```
CC   sensitive early-stage diagnosis and post-operative eradication of
CC   disease. The present DNA sequence encodes a peptide which was used in the
CC   invention
XX
SQ   Sequence 138 BP; 35 A; 37 C; 39 G; 27 T; 0 U; 0 Other;

  Query Match             4.7%;  Score 53.6;  DB 8;  Length 138;
  Best Local Similarity   93.3%;  Pred. No. 5.8e-05;
  Matches   56;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        235 TTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCG 294
              ||||||||||||||| || || ||||||||||||||| |||||||||||||||||||||||
Db         61 TTGTCGTGCATGGCCCAACATTCGCAGGAGTGGCATGACGTGGTCCTGACCGACTTACCG 120


RESULT 8
ABL25527
ID   ABL25527 standard; DNA; 1464 BP.
XX
AC   ABL25527;
XX
DT   26-MAR-2002  (first entry)
XX
DE   Drosophila melanogaster genomic polynucleotide SEQ ID NO 28054.
XX
KW   Drosophila; developmental biology; cell signalling; insecticide;
KW   pharmaceutical; gene; ds.
XX
OS   Drosophila melanogaster.
XX
PN   WO200171042-A2.
XX
PD   27-SEP-2001.
XX
PF   23-MAR-2001; 2001WO-US009231.
XX
PR   23-MAR-2000; 2000US-0191637P.
PR   11-JUL-2000; 2000US-00614150.
XX
PA   (PEKE ) PE CORP NY.
XX
PI   Venter JC,  Adams M,  Li PWD,  Myers EW;
XX
DR   WPI; 2001-656860/75.
XX
PT   New isolated nucleic acid detection reagent for detecting 1000 or more
PT   genes from Drosophila and for elucidating cell signaling and cell-cell
PT   interactions.
XX
PS   Claim 1; SEQ ID NO 28054; 21pp + Sequence Listing; English.
XX
CC   The invention relates to an isolated nucleic acid detection reagent
CC   capable of detecting 1000 or more genes from Drosophila. The invention is
CC   useful in developmental biology and in elucidating cell signalling and
CC   cell-cell interactions in higher eukaryotes for the development of
CC   insecticides, therapeutics and pharmaceutical drugs. The invention
CC   discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC   sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
CC   ABB72072). The sequence data for this patent did not form part of the
CC   printed specification, but was obtained in electronic format directly
CC   from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 1464 BP; 332 A; 427 C; 345 G; 360 T; 0 U; 0 Other;

  Query Match             4.2%;  Score 47.4;  DB 4;  Length 1464;
  Best Local Similarity   51.2%;  Pred. No. 0.0092;
  Matches  111;  Conservative    0;  Mismatches  106;  Indels    0;  Gaps    0;

Qy        129 GCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCC 188
              | | | ||| ||||       ||   ||   |||||| ||  | ||  | ||   || |
Db        433 GTATCTCCAGCTGCTGCTCCGGCCAATGTTGCTCCAGCTCCTGCTGCTCCTGTTGCTCCG 492

Qy        189 GCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATGGC 248
              || | ||| |    | ||  ||  |       ||  ||   | |  ||| || | || |
Db        493 GCTGCCCCAGCTGCCCCTGTGGTGCCTGTCGCTCCAGCTGCCCCTTCTGTTGTTCCTGTC 552

Qy        249 ACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATGTTCAC 308
              | || |||||    || |  | | | ||| ||    |   ||| | || || ||
Db        553 GCTCCTGTCGCCCCTGTAGTGGTTCATCCTGCTGCCCCCATACTCGTCCATCCTGCTCCA 612

Qy        309 GTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTC 345
              ||||||| ||  | | | |   | |   | | ||||
Db        613 GTTCCAGTGGCAGCTCCAGCTCCGGCCCCGATTGCTC 649


RESULT 9
ADA71938
ID   ADA71938 standard; DNA; 2000 BP.
XX
AC   ADA71938;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Rice gene, SEQ ID 5263.
XX
KW   Plant; bacterial infection; fungal infection; viral infection; rice;
KW   gene; ds.
XX
OS   Oryza sativa.
XX
PN   WO2003000898-A1.
XX
PD   03-JAN-2003.
XX
PF   22-JUN-2001; 2001WO-IB001105.
XX
PR   22-JUN-2001; 2001WO-IB001105.
XX
PA   (SYGN ) SYNGENTA PARTICIPATIONS AG.
XX
PI   Chang H,  Chen W,  Cooper B,  Glazebrook J,  Goff SA,  Hou Y;
PI   Katagiri F,  Quan S,  Tao Y,  Whitham S,  Xie Z,  Zhu T,  Zou G;
XX
DR   WPI; 2003-175290/17.
XX
PT   Identifying at least one gene involved in plant resistance or response to
PT   pathogenic infection for conferring resistance or tolerance to a plant to
PT   bacterial, fungal or viral infection by determining or detecting plant
PT   gene expression.
XX
PS   Claim 27; SEQ ID NO 5263; 899pp; English.
XX
CC   The present invention relates to a method (M1) for identifying genes
CC   involved in plant resistance or response to pathogenic infection. M1
CC   comprises identifying a gene whose expression is significantly altered in
CC   the incompatible interaction of plant gene expression relative to
CC   expression of the gene in an uninfected plant, in a mutant plant that
CC   does not express a gene associated with response to pathogenic infection,
CC   or in a corresponding incompatible or compatible interaction. (M1) is
CC   useful for conferring resistance to resistance or tolerance to a plant to
CC   bacterial, fungal or viral infection. The present sequence was used to
CC   illustrate the invention.
XX
SQ   Sequence 2000 BP; 336 A; 265 C; 284 G; 363 T; 0 U; 752 Other;

  Query Match             4.2%;  Score 47.4;  DB 8;  Length 2000;
  Best Local Similarity   10.0%;  Pred. No. 0.01;
  Matches   78;  Conservative  344;  Mismatches  355;  Indels    4;  Gaps    2;

Qy        217 GGCGCCCTCCTCGTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTG 276
              ::::  ::  ||:  | |  |:::    ::|:::  ::  :  ::| | ::  :: :||:
Db        159 KKSKGGSWGKTCRRGARGGSGWSSGAKYKSGSMSKRMWMSSCGRSGCGRRSAYSRYYGTS 218

Qy        277 GTCCTGACCGACTTACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGG 336
              ::: |   :  :     |   ::|  ::: | : |:|  ::::   :   : ::::::
Db        219 RKYGTYKKMTYYSASRCMRAYMTTSYSWACSSYTWCRSKRRSMMWKMMRKMRWSRSYGWY 278
```

```
Qy        337 GGGTAGCTCTTTTGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGG 396
              : ::    || ::::: ::  : : || :    :: |:| :      :::::::: :|
Db        279 SWSYKMWMCTAYKKSYYSRWCYMYRGGGWRGATRYWGRGYMSRMAMMYKKMYWYRGYKGM 338

Qy        397 GACGGGGGTAGGGCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTT 456
              ::    |: : :::| :   |  :  : :  |::   |::::: : ::  :  :  ::::
Db        339 KRGWWAGRMMMRSMCRWSKACYYMRWRMWRMTRRRRWAKKSSRTSRRKKRKWCMRKRKYK 398

Qy        457 CCGAAGATAGGGTCGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTG 516
              ::  :: :: :  :  :  ::|: : : |: |:|| :: : ::  :: : : ::::: :
Db        399 RMRGYSRMRSCKRARWMKRCRSGRAWKMGCRGCMTCRMKSYGMMRWKSWKRMASKYKWMS 458

Qy        517 ---ATGTTCTGGTGCGGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTC 573
                 :::::  ::| : |  :| ::| :   : :  : :::: :::::|:: : :: ::::
Db        459 RMYRWRKKKCSRTTMWGKTRGGMMGTMGRCRYKKRSGMKRKCRRRRWGRMYRMRWKRYYM 518

Qy        574 GAGTGGCACCTGTTCTCGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGCACTACGTA 633
              :|::    |  :::::::    | | : |: ::     ::: :: :::::      :::
Db        519 SARYTMRYCARKKYSYSAARKARCWYRGKGYYWAGMWMKRYKRMYMYKMMWWYKRKYSKC 578

Qy        634 CTCCGAGACGTGTTGGTGATGTGCGTCTTCTCGGAGAGGGACAG-AGGCCCATTTCATGG 692
              :::|::: :    ::  :|  : |: :: :  ::  :::: |:: |:: ::|: : : ||
Db        579 SWYCKMSYYASCMKSARKAGAKMCKRSKMSAWSKSMRSSRKCRKCASKRSSAKRYAMMGG 638

Qy        693 CTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATGCGCATAGTT 752
              :| |: :  :      :  :  : ::| |:   : :  : ::|::::::     :  ::::
Db        639 MTSGGSRMSRWKSYTCYWRKWGSMKSTCTWMYYMSKYTYAKYGSYWRYRYRAWCMYMWRWY 698

Qy        753 GCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTTGTCTTTCAATGTCCGGACCTGAAGTA 812
              :          : ::| : :  :::: : :|  : : :| ::  ::     :: :|:|:
Db        699 YYRYRSYMTYMAWYTSSTRMAMTGMKYSGRYWTSWYKYCKCSWKYRSMWYYWSWWWAKTW 758

Qy        813 GGGCCCAGACGTGGGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCGACATATGGT 872
              :    :| :: :    :  :::|   :    ::::: : :  :   :      :    :
Db        759 KMWRRYATRMMWMWYRYSMKWYTWCTMWGYWWYWWRTYMKMRYMWYKCTKTYWYWSATYW 818

Qy        873 CGTCTAGAATTGGAGGTACGGCAGGGCATTGCAATAGGTCTAGAGATTGCTGGAGCTCTT 932
              ||  | :: : :::  : |   :|: :: ::::::  :|  :: :|:|   ::  |
Db        819 TGTWAAWWMAKTKMRMGMTGAKTRGRARKARYWWKWATWCATKRWMTKGKGAKWAWTWMA 878

Qy        933 GGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGGTACCCGAAG 992
              : ::::    :   : :: :  ::   :::|:  :|  ::  :|:|  ::   |::|
Db        879 KAWRKYYWSWMRAWYYYYKTRRTRYKTCWWKARWGSWAYWRMWWKGSAKMWWMWKGGRWG 938

Qy        993 T 993
              :
Db        939 W 939
```

RESULT 10
ABL25526/c
ID ABL25526 standard; DNA; 4526 BP.
XX
AC ABL25526;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 28051.
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical; gene; ds.
XX
OS Drosophila melanogaster.
XX
PN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-US009231.
XX
PR 23-MAR-2000; 2000US-0191637P.
PR 11-JUL-2000; 2000US-00614150.
XX
PA (PEKE) PE CORP NY.
XX
PI Venter JC, Adams M, Li PWD, Myers EW;
XX
DR WPI; 2001-656860/75.
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signaling and cell-cell
PT interactions.
XX
PS Claim 1; SEQ ID NO 28051; 21pp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
CC ABB72072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 4526 BP; 1338 A; 912 C; 1011 G; 1265 T; 0 U; 0 Other;

Query Match 4.2%; Score 47.4; DB 4; Length 4526;
Best Local Similarity 51.2%; Pred. No. 0.015;
Matches 111; Conservative 0; Mismatches 106; Indels 0; Gaps 0;

```
Qy        129 GCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCC 188
              | | | ||| ||||        ||   ||   |||||| ||  | ||  | ||   || |
Db       2838 GTATCTCCAGCTGCTGCTCCGGCCAATGTTGCTCCAGCTCCTGCTGCTCCTGTTGCTCCG 2779

Qy        189 GCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATGGC 248
              ||  | |||  |    | ||  ||  |       ||  ||   | |  ||| || | || |
Db       2778 GCTGCCCCAGCTGCCCCTGTGGTGCCTGTCGCTCCAGCTGCCCCTTCTGTTGTTCCTGTC 2719

Qy        249 ACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATGTTCAC 308
              | || |||||    || |  |  | |  | ||| ||   |   ||| | || || ||
Db       2718 GCTCCTGTCGCCCCTGTAGTGGTTCATCCTGCTGCCCCCATACTCGTCCATCCTGCTCCA 2659

Qy        309 GTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTC 345
              ||||||| ||  | | | |    | |   | ||||
Db       2658 GTTCCAGTGGCAGCTCCAGCTCCGGCCCCGATTGCTC 2622
```

RESULT 11
ADA71938/c
ID ADA71938 standard; DNA; 2000 BP.
XX
AC ADA71938;
XX
DT 20-NOV-2003 (first entry)
XX
DE Rice gene, SEQ ID 5263.
XX
KW Plant; bacterial infection; fungal infection; viral infection; rice;
KW gene; ds.
XX
OS Oryza sativa.
XX
PN WO2003000898-A1.
XX
PD 03-JAN-2003.
XX
PF 22-JUN-2001; 2001WO-IB001105.
XX
PR 22-JUN-2001; 2001WO-IB001105.
XX
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
XX
PI Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;

PI Katagiri F, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;
XX
DR WPI; 2003-175290/17.
XX
PT Identifying at least one gene involved in plant resistance or response to
PT pathogenic infection for conferring resistance or tolerance to a plant to
PT bacterial, fungal or viral infection by determining or detecting plant
PT gene expression.
XX
PS Claim 27; SEQ ID NO 5263; 899pp; English.
XX
CC The present invention relates to a method (M1) for identifying genes
CC involved in plant resistance or response to pathogenic infection. M1
CC comprises identifying a gene whose expression is significantly altered in
CC the incompatible interaction of plant gene expression relative to
CC expression of the gene in an uninfected plant, in a mutant plant that
CC does not express a gene associated with response to pathogenic infection,
CC or in a corresponding incompatible or compatible interaction. (M1) is
CC useful for conferring resistance to resistance or tolerance to a plant to
CC bacterial, fungal or viral infection. The present sequence was used to
CC illustrate the invention.
XX
SQ Sequence 2000 BP; 336 A; 265 C; 284 G; 363 T; 0 U; 752 Other;

Query Match 4.1%; Score 47; DB 8; Length 2000;
Best Local Similarity 8.9%; Pred. No. 0.014;
Matches 78; Conservative 392; Mismatches 397; Indels 8; Gaps 2;

```
Qy        178 ATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTG 237
Db        879 MTKWAWTWMTCMCMAKWYMATGWATWMWWRYTMYTYCYAMTCAKCKYKMAMTKWWTTWAC 820

Qy        238 TCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTC 297
Db        819 AWRATSWRWRAMAGMRWKRYKMKRAYWWRWWRCWKAGWARWMKSRYRWKWKKYATRYYWK 760

Qy        298 CTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTT--TGGTAGA 355
Db        759 MWAMTWWWSWRRWKSYRMWSGMGRMRWSAWRYCSRMKCAKTKYASSARWTKRAKRSYRYR 700

Qy        356 GGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTAC 415
Db        699 RRWYWKRKGWTYRYRYWRSCRMTRARMSKRRKWAGASMKSCWMYWRGARSMWYSKYSCSA 640

Qy        416 TCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGT 475
Db        639 KCCKKTRYMTSSYMSTGMYGMYSSYKSMSWTSKMSYMGKMTCTMYTSMKGSTRRSKMGRW 580

Qy        476 AGCGGC------ACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCG 529
Db        579 SGMSRMYMRWWKKMRKRKYMRYMKWKCTWRRCMCYRWGYTMYTTSRSRMMYTGRYKARYT 520

Qy        530 GAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCT 589
Db        519 SKRRYMWYKYRKYCWYYYYGMYMKCSYMMRYGYCKACKKCCYAMCWKAAYSGMMMYWYRK 460

Qy        590 CGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGG 649
Db        459 YSKWMRMSTKYMWSMWYKKCRSMKYGAKGCYGCKMWTYCSYGYMKWYTYMGSYKYSRCYK 400

Qy        650 TGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCATTTCATGGCTAGGTCTTTCAAGTCC 709
Db        399 YMRMYMYKGWMYMMYYSAYSSMMTWYYYYAKYWKYWYKRRGTMSWYGKSYKKKYCTWWCY 340

Qy        710 TGCTGTGGTTTTGGAATTAATTTTGCTAGCAATGCGCATAGTTGCTGTAGTCAGTGTGGG 769
Db        339 MKCMRCYRWRKMMRKKTKYSKRCYCWRYATCYWCCCYRKRGWYSRRSMMRTAGKWKMRSW 280

Qy        770 TCAGCCACTCGAGATTTGTCTTTCAATGTCCGGACCTGAAGTAGGGCCCAGACGTGGGCT 829
Db        279 SRWCRSYSWYKMYKKMWKKSYYMSYGWARSSGTWSRSAAKRTYKGYSTSRRAKMMRACRM 220

Qy        830 AGGACTGGAACAGGTTTTACCTGGTCTGGGACCGACATATGGTCGTCTAGAATTGGAGGT 889
```

```
Db        219 YSACRRYSRTSYYCGCSYCGSSKWKYMSKSCSMRMTCSSWCSCCYTCYYGAMCWSCCMSM 160

Qy        890 ACGGCAGGGCATTGCAATAGGTCTAGAGATTGCTGGAGCTCTTGGAAGCGCTGGACGACG 949
Db        159 MYMGSCGCYTRGWKWRSKYSMCCKKYCSCCTKYCSYTGYYRYCKWYKYSYYKCYYCYCYW 100

Qy        950 TGCACGACCGTAAGAGGTTTAGGACGGTGGACGGTACCCGAAGTCCAGAACTCTGAGACC 1009
Db         99 YMSYMRYMMKCMCSRSCSSWMSCAYCSTSSTSRWMSMYYAAKMGMCGSSGMYRMSKSCKM 40

Qy       1010 TGAGAGACCCGCCCCAGGACCTTCGTAGGCCAATG 1044
Db         39 YSKYSSCKYTGSKKCTKRKYYYCYWSSGYSMWCTS 5
```

RESULT 12
ABD09099
ID ABD09099 standard; DNA; 1161 BP.
XX
AC ABD09099;
XX
DT 29-JUL-2004 (first entry)
XX
DE Pseudomonas aeruginosa polynucleotide #7703.
XX
KW Bacterial infection; gene; ds; Pseudomonas aeruginosa infection;
KW antibacterial.
XX
OS Pseudomonas aeruginosa.
XX
PN US6551795-B1.
XX
PD 22-APR-2003.
XX
PF 18-FEB-1999; 99US-00252991.
XX
PR 18-FEB-1998; 98US-0074788P.
PR 27-JUL-1998; 98US-0094190P.
XX
PA (GENO-) GENOME THERAPEUTICS CORP.
XX
PI Rubenfield MJ, Nolling J, Deloughery C, Bush D;
XX
DR WPI; 2003-615309/58.
DR P-PSDB; ABO75528.
XX
PT Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,
PT useful as molecular targets for diagnostics, prophylaxis and treatment of
PT pathological conditions resulting from bacterial infection.
XX
PS Disclosure; SEQ ID NO 7703; 455pp; English.
XX
CC The invention relates to Pseudomonas aeruginosa polypeptides and the
CC polynucleotides encoding them. The sequences are useful in diagnosis and
CC therapy of pathological conditions, as molecular targets for diagnostics,
CC prophylaxis and treatment of pathological conditions resulting from a
CC bacterial infection, for evaluating a compound, such as a polypeptide,
CC for the ability to bind a P. aeruginosa nucleic acid, as components of
CC effective antibacterial targets, as targets for antibacterial drugs,
CC including anti-P. aeruginosa drugs, as templates for recombinant
CC production of P. aeruginosa-derived peptides or polypeptides, as target
CC components for diagnosis and/or treatment of P. aeruginosa-caused
CC infection, and in detection of P. aeruginosa sequences or other sequences
CC of Pseudomonas species using biochip technology. Sequences ABD01397-
CC ABD17967 represent P. aeruginosa polynucleotides of the invention. Note:
CC The sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format from USPTO at
CC seqdata.uspto.gov/sequence.html
XX
SQ Sequence 1161 BP; 156 A; 367 C; 390 G; 248 T; 0 U; 0 Other;

Query Match 3.8%; Score 43.6; DB 11; Length 1161;

```
  Best Local Similarity   47.4%;  Pred. No. 0.1;
  Matches  130;  Conservative    0;  Mismatches  144;  Indels    0;  Gaps    0;

Qy        119 TCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCA 178
              ||||| | || |   | | |  ||  ||| | |     |      | |  ||| |
Db        332 TCCAGCCTTCGGAGATCGCCAAGGTCTGCGTGGTGATCTTCATGGCCGGCTACCTGATCC 391

Qy        179 TGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGT 238
                | || || | |  ||| | |    || |  | |||  |   | | ||||  |||||
Db        392 GCCGCCAGCAGGAGGTCCGGGAAAGCTGGATGGGCTTCTTCAAGCCCTTCGTGGTGTTGC 451

Qy        239 CGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCC 298
                |  |||||   || |  || |     || |||| | | |   ||||   ||  | |
Db        452 TGCCGATGGCCGGCCTGCTGCTGCGCGAGCCGGACTTCGGCGCCACCGTGGTAATGATGG 511

Qy        299 TCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGT 358
                |    | ||  |  |  |||  |  | ||  ||  ||  | |||  |   || |
Db        512 GCGCTGCCGCGGCCATGCTGTTCCTCGGCGGGGTGGGGCTGTTCCGCTTCGGCCTGATGG 571

Qy        359 TTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACAT 392
              | | | |  | ||||| ||  | |   | |  ||
Db        572 TGCTGCTGGCGGTCGGCGCGGTGGTCCTGCTGAT 605


RESULT 13
AAS51550
ID   AAS51550 standard; DNA; 1200 BP.
XX
AC   AAS51550;
XX
DT   13-FEB-2002  (first entry)
XX
DE   Pseudomonas aeruginosa DNA for cellular proliferation protein #135.
XX
KW   Antisense; ds; prokaryotic cellular proliferation gene; antibiotic;
KW   antibacterial; drug design.
XX
OS   Pseudomonas aeruginosa.
XX
PN   WO200170955-A2.
XX
PD   27-SEP-2001.
XX
PF   21-MAR-2001; 2001WO-US009180.
XX
PR   21-MAR-2000; 2000US-0191078P.
PR   23-MAY-2000; 2000US-0206848P.
PR   26-MAY-2000; 2000US-0207727P.
PR   23-OCT-2000; 2000US-0242578P.
PR   27-NOV-2000; 2000US-0253625P.
PR   22-DEC-2000; 2000US-0257931P.
PR   16-FEB-2001; 2001US-0269308P.
XX
PA   (ELIT-) ELITRA PHARM INC.
XX
PI   Haselbeck R,  Ohlsen KL,  Zyskind JW,  Wall D,  Trawick JD,  Carr GJ;
PI   Yamamoto RT,  Xu HH;
XX
DR   WPI; 2001-611495/70.
DR   P-PSDB; AAU33691.
XX
PT   New polynucleotides for the identification and development of
PT   antibiotics, comprise sequences of antisense nucleic acids.
XX
PS   Claim 27; SEQ ID NO 4132; 511pp; English.
XX
CC   The invention relates to antisense inhibitors of genes essential to
CC   prokaryotic cellular proliferation, their use in identifying the genes,
CC   their use in the discovery of novel antibiotics, the essential genes
CC   themselves and the encoded proteins. The prokaryotes used are Escherichia
CC   coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,
CC   Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also
CC   useful for the identification of potential new targets for antibiotic
CC   development. The antisense nucleic acids can also be used to identify
CC   proteins used in proliferation, to express these proteins, and to obtain
CC   antibodies capable of binding to the expressed proteins. The proteins can
CC   be used to screen compounds in rational drug discovery programmes. The
CC   antisense nucleic acid sequence is also useful to screen for homologous
CC   nucleic acids which are required for cell proliferation in a wide variety
CC   of organisms. The present sequence encodes an essential prokaryotic
CC   cellular proliferation protein. Note: The sequence data for this patent
CC   did not form part of the printed specification, but was obtained in
CC   electronic format directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 1200 BP; 157 A; 384 C; 402 G; 257 T; 0 U; 0 Other;

  Query Match             3.8%;  Score 43.6;  DB 4;  Length 1200;
  Best Local Similarity   47.4%;  Pred. No. 0.1;
  Matches  130;  Conservative    0;  Mismatches  144;  Indels    0;  Gaps    0;

Qy        119 TCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCA 178
              ||||| | || |   | | |  ||  ||| | |     |      | |  ||| |
Db        371 TCCAGCCTTCGGAGATCGCCAAGGTCTGCGTGGTGATCTTCATGGCCGGCTACCTGATCC 430

Qy        179 TGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGT 238
                | || || | |  ||| | |    || |  | |||  |   | | ||||  |||||
Db        431 GCCGCCAGCAGGAGGTCCGGGAAAGCTGGATGGGCTTCTTCAAGCCCTTCGTGGTGTTGC 490

Qy        239 CGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCC 298
                |  |||||   || |  || |     || |||| | | |   ||||   ||  | |
Db        491 TGCCGATGGCCGGCCTGCTGCTGCGCGAGCCGGACTTCGGCGCCACCGTGGTAATGATGG 550

Qy        299 TCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGT 358
                |    | ||  |  |  |||  |  | ||  ||  ||  | |||  |   || |
Db        551 GCGCTGCCGCGGCCATGCTGTTCCTCGGCGGGGTGGGGCTGTTCCGCTTCGGCCTGATGG 610

Qy        359 TTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACAT 392
              | | | |  | ||||| ||  | |   | |  ||
Db        611 TGCTGCTGGCGGTCGGCGCGGTGGTCCTGCTGAT 644


RESULT 14
ACA19541
ID   ACA19541 standard; DNA; 1200 BP.
XX
AC   ACA19541;
XX
DT   19-JUN-2003  (first entry)
XX
DE   Prokaryotic essential gene #1198.
XX
KW   Antisense; ds; prokaryotic essential gene; cell proliferation;
KW   drug design; gene.
XX
OS   Pseudomonas aeruginosa.
XX
PN   WO200277183-A2.
XX
PD   03-OCT-2002.
XX
PF   21-MAR-2002; 2002WO-US009107.
XX
PR   21-MAR-2001; 2001US-00815242.
PR   06-SEP-2001; 2001US-00948993.
PR   25-OCT-2001; 2001US-0342923P.
PR   08-FEB-2002; 2002US-00072851.
PR   06-MAR-2002; 2002US-0362699P.
XX
PA   (ELIT-) ELITRA PHARM INC.
XX
PI   Wang L,  Zamudio C,  Malone C,  Haselbeck R,  Ohlsen KL,  Zyskind JW;
PI   Wall D,  Trawick JD,  Carr GJ,  Yamamoto R,  Forsyth RA,  Xu HH;
XX
DR   WPI; 2003-029926/02.
DR   P-PSDB; ABU15671.
```

XX
PT New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX
PS Claim 14; SEQ ID NO 7411; 1766pp; English.
XX
CC The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide;(5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than S. aureus, S. typhimurium,
CC K. pneumoniae or P. aeruginosa. The present sequence is one of the target
CC prokaryotic essential genes. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1200 BP; 157 A; 384 C; 402 G; 257 T; 0 U; 0 Other;

Query Match 3.8%; Score 43.6; DB 8; Length 1200;
Best Local Similarity 47.4%; Pred. No. 0.1;
Matches 130; Conservative 0; Mismatches 144; Indels 0; Gaps 0;

Qy 119 TCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCA 178
Db 371 TCCAGCCTTCGGAGATCGCCAAGGTCTGCGTGGTGATCTTCATGGCCGGCTACCTGATCC 430

Qy 179 TGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGT 238
Db 431 GCCGCCAGCAGGAGGTCCGGGAAAGCTGGATGGGCTTCTTCAAGCCCTTCGTGGTGTTGC 490

Qy 239 CGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCC 298
Db 491 TGCCGATGGCCGGCCTGCTGCTGCGCGAGCCGGACTTCGGCGCCACCGTGGTAATGATGG 550

Qy 299 TCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGT 358
Db 551 GCGCTGCCGCGGCCATGCTGTTCCTCGGCGGGGTGGGGCTGTTCCGCTTCGGCCTGATGG 610

Qy 359 TTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACAT 392
Db 611 TGCTGCTGGCGGTCGGCGCGGTGGTCCTGCTGAT 644

RESULT 15
ABD09256/c
ID ABD09256 standard; DNA; 1287 BP.
XX
AC ABD09256;
XX
DT 29-JUL-2004 (first entry)

XX
DE Pseudomonas aeruginosa polynucleotide #7860.
XX
KW Bacterial infection; gene; ds; Pseudomonas aeruginosa infection;
KW antibacterial.
XX
OS Pseudomonas aeruginosa.
XX
PN US6551795-B1.
XX
PD 22-APR-2003.
XX
PF 18-FEB-1999; 99US-00252991.
XX
PR 18-FEB-1998; 98US-0074788P.
PR 27-JUL-1998; 98US-0094190P.
XX
PA (GENO-) GENOME THERAPEUTICS CORP.
XX
PI Rubenfield MJ, Nolling J, Deloughery C, Bush D;
XX
DR WPI; 2003-615309/58.
DR P-PSDB; ABO75685.
XX
PT Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,
PT useful as molecular targets for diagnostics, prophylaxis and treatment of
PT pathological conditions resulting from bacterial infection.
XX
PS Disclosure; SEQ ID NO 7860; 455pp; English.
XX
CC The invention relates to Pseudomonas aeruginosa polypeptides and the
CC polynucleotides encoding them. The sequences are useful in diagnosis and
CC therapy of pathological conditions, as molecular targets for diagnostics,
CC prophylaxis and treatment of pathological conditions resulting from a
CC bacterial infection, for evaluating a compound, such as a polypeptide,
CC for the ability to bind a P. aeruginosa nucleic acid, as components of
CC effective antibacterial targets, as targets for antibacterial drugs,
CC including anti-P. aeruginosa drugs, as templates for recombinant
CC production of P. aeruginosa-derived peptides or polypeptides, as target
CC components for diagnosis and/or treatment of P. aeruginosa-caused
CC infection, and in detection of P. aeruginosa sequences or other sequences
CC of Pseudomonas species using biochip technology. Sequences ABD01397-
CC ABD17967 represent P. aeruginosa polynucleotides of the invention. Note:
CC The sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format from USPTO at
CC seqdata.uspto.gov/sequence.html
XX
SQ Sequence 1287 BP; 276 A; 437 C; 408 G; 166 T; 0 U; 0 Other;

Query Match 3.8%; Score 43.6; DB 11; Length 1287;
Best Local Similarity 47.4%; Pred. No. 0.1;
Matches 130; Conservative 0; Mismatches 144; Indels 0; Gaps 0;

Qy 119 TCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCA 178
Db 908 TCCAGCCTTCGGAGATCGCCAAGGTCTGCGTGGTGATCTTCATGGCCGGCTACCTGATCC 849

Qy 179 TGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGT 238
Db 848 GCCGCCAGCAGGAGGTCCGGGAAAGCTGGATGGGCTTCTTCAAGCCCTTCGTGGTGTTGC 789

Qy 239 CGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCC 298
Db 788 TGCCGATGGCCGGCCTGCTGCTGCGCGAGCCGGACTTCGGCGCCACCGTGGTAATGATGG 729

Qy 299 TCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGT 358
Db 728 GCGCTGCCGCGGCCATGCTGTTCCTCGGCGGGGTGGGGCTGTTCCGCTTCGGCCTGATGG 669

Qy 359 TTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACAT 392
Db 668 TGCTGCTGGCGGTCGGCGCGGTGGTCCTGCTGAT 635

Search completed: October 17, 2004, 16:46:42
Job time : 590.736 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 17, 2004, 15:27:13 ; Search time 578.552 Seconds
(without alignments)
10035.691 Million cell updates/sec

Title: US-10-679-999-14
Perfect score: 1135
Sequence: 1 GTATACCTGTTTTGAGTGTG.....AGGCCCAACAATTACCTAGG 1135

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3403857 seqs, 2557783690 residues

Total number of hits satisfying chosen parameters: 6807714

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
18: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
19: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
20: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1135	100.0	1135	16	US-10-679-999-14	Sequence 14, Appl
2	1129	99.5	1150	16	US-10-679-999-11	Sequence 11, Appl
3	1117.8	98.5	1150	16	US-10-679-999-8	Sequence 8, Appli
4	1109.4	97.7	1135	16	US-10-679-999-17	Sequence 17, Appl
5	684.8	60.3	777	17	US-10-666-480-122	Sequence 122, App
6	676	59.6	780	17	US-10-666-480-62	Sequence 62, Appl
7	651.2	57.4	1142	15	US-10-157-408-9	Sequence 9, Appli
8	651.2	57.4	1142	15	US-10-097-044A-9	Sequence 9, Appli
9	651.2	57.4	1142	18	US-10-769-247-9	Sequence 9, Appli
10	616	54.3	7033	17	US-10-630-406-4	Sequence 4, Appli
11	494.4	43.6	2366	9	US-09-229-200A-12	Sequence 12, Appl
12	440.8	38.8	454	9	US-09-366-133-5	Sequence 5, Appli
13	440.8	38.8	454	14	US-10-214-037-5	Sequence 5, Appli
14	440.8	38.8	454	16	US-10-679-999-5	Sequence 5, Appli
15	378.4	33.3	491	9	US-09-366-133-2	Sequence 2, Appli
16	378.4	33.3	491	14	US-10-214-037-2	Sequence 2, Appli
17	378.4	33.3	491	16	US-10-679-999-2	Sequence 2, Appli
c 18	71	6.3	23770	14	US-10-035-637-8	Sequence 8, Appli
c 19	44.6	3.9	1188	17	US-10-437-963-65538	Sequence 65538, A
20	43.6	3.8	1200	9	US-09-815-242-4132	Sequence 4132, Ap
21	43.6	3.8	1200	16	US-10-282-122A-7411	Sequence 7411, Ap
c 22	43.2	3.8	2034	17	US-10-441-949-56	Sequence 56, Appl
23	43	3.8	468	15	US-10-157-408-12	Sequence 12, Appl
24	43	3.8	468	15	US-10-097-044A-12	Sequence 12, Appl
25	43	3.8	468	18	US-10-769-247-12	Sequence 12, Appl
26	43	3.8	8874	17	US-10-630-406-7	Sequence 7, Appli
c 27	42.4	3.7	1116	15	US-10-156-761-6640	Sequence 6640, Ap
c 28	42.4	3.7	9025608	15	US-10-156-761-1	Sequence 1, Appli
c 29	42.2	3.7	2034	17	US-10-441-949-57	Sequence 57, Appl
c 30	41.8	3.7	1182	16	US-10-354-437-15	Sequence 15, Appl
c 31	41.8	3.7	3489	11	US-09-894-273-1	Sequence 1, Appli
c 32	41.8	3.7	3489	15	US-10-294-804-1	Sequence 1, Appli
33	41.8	3.7	34460	13	US-10-087-192-115	Sequence 115, App
c 34	41.8	3.7	135638	15	US-10-314-657-1	Sequence 1, Appli
c 35	41.6	3.7	1986	17	US-10-441-949-47	Sequence 47, Appl
c 36	41.6	3.7	1986	17	US-10-441-949-51	Sequence 51, Appl
c 37	41.6	3.7	2034	17	US-10-441-949-49	Sequence 49, Appl
c 38	41.6	3.7	2034	17	US-10-441-949-50	Sequence 50, Appl
39	41.6	3.7	2171	9	US-09-925-300-721	Sequence 721, App
40	41.6	3.7	2172	16	US-10-264-049-843	Sequence 843, App
41	41.6	3.7	2300	9	US-09-823-245A-506	Sequence 506, App
42	41.6	3.7	2300	9	US-09-822-830A-33	Sequence 33, Appl
c 43	41.2	3.6	1236	14	US-10-077-584-3	Sequence 3, Appli
c 44	40.4	3.6	486	15	US-10-465-217-13	Sequence 13, Appl
45	40.4	3.6	754	9	US-09-229-200A-13	Sequence 13, Appl

ALIGNMENTS

```
RESULT 1
US-10-679-999-14
; Sequence 14, Application US/10679999
; Publication No. US20040067520A1
;  GENERAL INFORMATION:
;       APPLICANT: Mann, Michael B.
;                  Hecht, Randy I.
;       TITLE OF INVENTION: OB FUSION PROTEIN COMPOSITIONS AND
;                           METHODS
;       NUMBER OF SEQUENCES: 18
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Amgen Inc.
;            STREET: 1840 DeHavilland Drive
;            CITY: Thousand Oaks
;            STATE: CA
;            COUNTRY: USA
;            ZIP: 91320-1789
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/679,999
;            FILING DATE: 06-Oct-2003
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/09/568,528
;            FILING DATE: 09-May-2000
;            APPLICATION NUMBER: 09/267,517
;            FILING DATE: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Knight, Matthew W.
;            REGISTRATION NUMBER: 36,846
;            REFERENCE/DOCKET NUMBER: A-416
;  INFORMATION FOR SEQ ID NO: 14:
```

```
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 1135 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: double
;            TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-10-679-999-14

  Query Match            100.0%;  Score 1135;  DB 16;  Length 1135;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1135;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTATACCTGTTTTGAGTGTGTACAGGTGGAACAGGTCGAGGCCTTGAGGACCCCCCAGGA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GTATACCTGTTTTGAGTGTGTACAGGTGGAACAGGTCGAGGCCTTGAGGACCCCCCAGGA 60

Qy         61 AGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTC 120

Qy        121 CAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATG 180

Qy        181 CACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCG 240

Qy        241 TGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTC 300

Qy        301 ATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTT 360

Qy        361 CGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGAC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGAC 420

Qy        421 TGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGG 480

Qy        481 CACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGAC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGAC 540

Qy        541 CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTC 600

Qy        601 GTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTC 660

Qy        661 TTCTCGGAGAGGGACAGAGGCCCATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TTCTCGGAGAGGGACAGAGGCCCATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTT 720

Qy        721 TGGAATTAATTTTGCTAGCAATGCGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAATTAATTTTGCTAGCAATGCGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCG 780

Qy        781 AGATTTGTCTTTCAATGTCCGGACCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AGATTTGTCTTTCAATGTCCGGACCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAAC 840

Qy        841 AGGTTTTACCTGGTCTGGGACCGACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AGGTTTTACCTGGTCTGGGACCGACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCA 900

Qy        901 TTGCAATAGGTCTAGAGATTGCTGGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TTGCAATAGGTCTAGAGATTGCTGGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGT 960

Qy        961 AAGAGGTTTAGGACGGTGGACGGTACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AAGAGGTTTAGGACGGTGGACGGTACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCG 1020

Qy       1021 CCCCAGGACCTTCGTAGGCCAATGTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 CCCCAGGACCTTCGTAGGCCAATGTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCA 1080

Qy       1081 AGGGAAGTCCTGTACGAAACCGTCGACCTGGACAGAGGCCCAACAATTACCTAGG 1135
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 AGGGAAGTCCTGTACGAAACCGTCGACCTGGACAGAGGCCCAACAATTACCTAGG 1135


RESULT 2
US-10-679-999-11
; Sequence 11, Application US/10679999
; Publication No. US20040067520A1
;   GENERAL INFORMATION:
;        APPLICANT: Mann, Michael B.
;                   Hecht, Randy I.
;        TITLE OF INVENTION: OB FUSION PROTEIN COMPOSITIONS AND
;                            METHODS
;        NUMBER OF SEQUENCES: 18
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Amgen Inc.
;             STREET: 1840 DeHavilland Drive
;             CITY: Thousand Oaks
;             STATE: CA
;             COUNTRY: USA
;             ZIP: 91320-1789
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/679,999
;             FILING DATE: 06-Oct-2003
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/568,528
;             FILING DATE: 09-May-2000
;             APPLICATION NUMBER: 09/267,517
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Knight, Matthew W.
;             REGISTRATION NUMBER: 36,846
;             REFERENCE/DOCKET NUMBER: A-416
;   INFORMATION FOR SEQ ID NO: 11:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1150 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-679-999-11

  Query Match            99.5%;  Score 1129;  DB 16;  Length 1150;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1129;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 CTGTTTTGAGTGTGTACAGGTGGAACAGGTCGAGGCCTTGAGGACCCCCCAGGAAGTCAG 66
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         22 CTGTTTTGAGTGTGTACAGGTGGAACAGGTCGAGGCCTTGAGGACCCCCCAGGAAGTCAG 81

Qy         67 AAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGT 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         82 AAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGT 141
```

```
Qy        127 ACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTG 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        142 ACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTG 201

Qy        187 CCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATG 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        202 CCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATG 261

Qy        247 GCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATGTTC 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        262 GCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATGTTC 321

Qy        307 ACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTT 366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        322 ACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTT 381

Qy        367 CCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTC 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        382 CCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTC 441

Qy        427 TTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTC 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        442 TTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTC 501

Qy        487 ACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGG 546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        502 ACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGG 561

Qy        547 CTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCC 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        562 CTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCC 621

Qy        607 TTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCG 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        622 TTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCG 681

Qy        667 GAGAGGGACAGAGGCCCATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAAT 726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        682 GAGAGGGACAGAGGCCCATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAAT 741

Qy        727 TAATTTTGCTAGCAATGCGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTT 786
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        742 TAATTTTGCTAGCAATGCGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTT 801

Qy        787 GTCTTTCAATGTCCGGACCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTT 846
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        802 GTCTTTCAATGTCCGGACCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTT 861

Qy        847 TACCTGGTCTGGGACCGACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAA 906
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        862 TACCTGGTCTGGGACCGACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAA 921

Qy        907 TAGGTCTAGAGATTGCTGGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGG 966
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        922 TAGGTCTAGAGATTGCTGGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGG 981

Qy        967 TTTAGGACGGTGGACGGTACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAG 1026
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        982 TTTAGGACGGTGGACGGTACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAG 1041

Qy       1027 GACCTTCGTAGGCCAATGTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAA 1086
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1042 GACCTTCGTAGGCCAATGTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAA 1101

Qy       1087 GTCCTGTACGAAACCGTCGACCTGGACAGAGGCCCAACAATTACCTAGG 1135
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db       1102 GTCCTGTACGAAACCGTCGACCTGGACAGAGGCCCAACAATTACCTAGG 1150
```

RESULT 3
US-10-679-999-8
; Sequence 8, Application US/10679999

```
; Publication No. US20040067520A1
;   GENERAL INFORMATION:
;        APPLICANT: Mann, Michael B.
;                   Hecht, Randy I.
;        TITLE OF INVENTION: OB FUSION PROTEIN COMPOSITIONS AND
;                            METHODS
;        NUMBER OF SEQUENCES: 18
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Amgen Inc.
;             STREET: 1840 DeHavilland Drive
;             CITY: Thousand Oaks
;             STATE: CA
;             COUNTRY: USA
;             ZIP: 91320-1789
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/679,999
;             FILING DATE: 06-Oct-2003
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/568,528
;             FILING DATE: 09-May-2000
;             APPLICATION NUMBER: 09/267,517
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Knight, Matthew W.
;             REGISTRATION NUMBER: 36,846
;             REFERENCE/DOCKET NUMBER: A-416
;   INFORMATION FOR SEQ ID NO: 8:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1150 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-679-999-8

  Query Match            98.5%;  Score 1117.8;  DB 16;  Length 1150;
  Best Local Similarity  99.4%;  Pred. No. 0;
  Matches 1122;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          7 CTGTTTTGAGTGTGTACAGGTGGAACAGGTCGAGGCCTTGAGGACCCCCCAGGAAGTCAG 66
              |||||||||||||||| ||||| || ||||| || ||||||||||||||| || ||||||
Db         22 CTGTTTGAGTGTGTACGGGTGGCACGGGTCGTGGACTTGAGGACCCCCCTGGCAGTCAG 81

Qy         67 AAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGT 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         82 AAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGT 141

Qy        127 ACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTG 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        142 ACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTG 201

Qy        187 CCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATG 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        202 CCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATG 261

Qy        247 GCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATGTTC 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        262 GCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATGTTC 321

Qy        307 ACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTT 366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        322 ACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTT 381

Qy        367 CCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTC 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        382 CCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTC 441
```

```
Qy        427 TTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTC 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        442 TTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTC 501

Qy        487 ACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGG 546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        502 ACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGG 561

Qy        547 CTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCC 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        562 CTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCC 621

Qy        607 TTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCG 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        622 TTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCG 681

Qy        667 GAGAGGGACAGAGGCCCATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAAT 726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        682 GAGAGGGACAGAGGCCCATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAAT 741

Qy        727 TAATTTTGCTAGCAATGCGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTT 786
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        742 TAATTTTGCTAGCAATGCGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTT 801

Qy        787 GTCTTTCAATGTCCGGACCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTT 846
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        802 GTCTTTCAATGTCCGGACCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTT 861

Qy        847 TACCTGGTCTGGGACCGACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAA 906
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        862 TACCTGGTCTGGGACCGACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAA 921

Qy        907 TAGGTCTAGAGATTGCTGGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGG 966
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        922 TAGGTCTAGAGATTGCTGGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGG 981

Qy        967 TTTAGGACGGTGGACGGTACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAG 1026
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        982 TTTAGGACGGTGGACGGTACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAG 1041

Qy       1027 GACCTTCGTAGGCCAATGTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAA 1086
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1042 GACCTTCGTAGGCCAATGTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAA 1101

Qy       1087 GTCCTGTACGAAACCGTCGACCTGGACAGAGGCCCAACAATTACCTAGG 1135
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db       1102 GTCCTGTACGAAACCGTCGACCTGGACAGAGGCCCAACAATTACCTAGG 1150
```

```
RESULT 4
US-10-679-999-17
; Sequence 17, Application US/10679999
; Publication No. US20040067520A1
;   GENERAL INFORMATION:
;        APPLICANT: Mann, Michael B.
;                   Hecht, Randy I.
;        TITLE OF INVENTION: OB FUSION PROTEIN COMPOSITIONS AND
;                            METHODS
;        NUMBER OF SEQUENCES: 18
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Amgen Inc.
;             STREET: 1840 DeHavilland Drive
;             CITY: Thousand Oaks
;             STATE: CA
;             COUNTRY: USA
;             ZIP: 91320-1789
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/679,999
;             FILING DATE: 06-Oct-2003
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/568,528
;             FILING DATE: 09-May-2000
;             APPLICATION NUMBER: 09/267,517
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Knight, Matthew W.
;             REGISTRATION NUMBER: 36,846
;             REFERENCE/DOCKET NUMBER: A-416
;   INFORMATION FOR SEQ ID NO: 17:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1135 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-10-679-999-17

  Query Match            97.7%;  Score 1109.4;  DB 16;  Length 1135;
  Best Local Similarity  98.6%;  Pred. No. 0;
  Matches 1119;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;
```

```
Qy          1 GTATACCTGTTTTGAGTGTGTACAGGTGGAACAGGTCGAGGCCTTGAGGACCCCCCAGGA 60
              |||||||||||||||||||| ||||| || ||||||||||||||   || |||||
Db          1 GTATACCTGTTTTGAGTGTGTACGGGTGGCACGGGTCGAGGCCTTGAGCTTCCACCAGGC 60

Qy         61 AGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTC 120

Qy        121 CAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATG 180

Qy        181 CACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCG 240

Qy        241 TGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        241 TGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTTCGA 300

Qy        301 ATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTT 360
              |||   |||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATGCGTACGCGCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTT 360

Qy        361 CGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGAC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGAC 420

Qy        421 TGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGG 480

Qy        481 CACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGAC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGAC 540

Qy        541 CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTC 600

Qy        601 GTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTC 660

Qy        661 TTCTCGGAGAGGGACAGAGGCCCATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TTCTCGGAGAGGGACAGAGGCCCATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTT 720
```

```
Qy        721 TGGAATTAATTTTGCTAGCAATGCGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAATTAATTTTGCTAGCAATGCGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCG 780

Qy        781 AGATTTGTCTTTCAATGTCCGGACCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AGATTTGTCTTTCAATGTCCGGACCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAAC 840

Qy        841 AGGTTTTACCTGGTCTGGGACCGACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AGGTTTTACCTGGTCTGGGACCGACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCA 900

Qy        901 TTGCAATAGGTCTAGAGATTGCTGGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TTGCAATAGGTCTAGAGATTGCTGGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGT 960

Qy        961 AAGAGGTTTAGGACGGTGGACGGTACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AAGAGGTTTAGGACGGTGGACGGTACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCG 1020

Qy       1021 CCCCAGGACCTTCGTAGGCCAATGTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 CCCCAGGACCTTCGTAGGCCAATGTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCA 1080

Qy       1081 AGGGAAGTCCTGTACGAAACCGTCGACCTGGACAGAGGCCCAACAATTACCTAGG 1135
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 AGGGAAGTCCTGTACGAAACCGTCGACCTGGACAGAGGCCCAACAATTACCTAGG 1135
```

RESULT 5
US-10-666-480-122
; Sequence 122, Application US/10666480
; Publication No. US20040121959A1
; GENERAL INFORMATION:
; APPLICANT: Boone, Thomas C
; APPLICANT: Wild, Kenneth D
; APPLICANT: Sitney, Karen C
; APPLICANT: Min, Hosung
; APPLICANT: Kimmel, Bruce
; TITLE OF INVENTION: Peptides and Related Molecules That Modulate Nerve Growth Factor
; FILE REFERENCE: A-827US
; CURRENT APPLICATION NUMBER: US/10/666,480
; CURRENT FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: 60/412,524
; PRIOR FILING DATE: 2002-09-19
; NUMBER OF SEQ ID NOS: 286
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 122
; LENGTH: 777
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Expression vector
US-10-666-480-122

Query Match 60.3%; Score 684.8; DB 17; Length 777;
Best Local Similarity 99.7%; Pred. No. 4.1e-205;
Matches 686; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy          1 GTATACCTGTTTTGAGTGTGTACAGGTGGAACAGGTCGAGGCCTTGAGGACCCCCCAGGA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db         36 GTATACCTGTTTTGAGTGTGTACAGGTGGAACAGGTCGAGGCCTTGAGGACCCCCCTGGC 95

Qy         61 AGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         96 AGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTC 155

Qy        121 CAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        156 CAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATG 215

Qy        181 CACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        216 CACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCG 275

Qy        241 TGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        276 TGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTC 335

Qy        301 ATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        336 ATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTT 395

Qy        361 CGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGAC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        396 CGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGAC 455

Qy        421 TGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        456 TGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGG 515

Qy        481 CACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGAC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        516 CACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGAC 575

Qy        541 CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        576 CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTC 635

Qy        601 GTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        636 GTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTC 695

Qy        661 TTCTCGGAGAGGGACAGAGGCCCATTTC 688
              |||||||||||||||||||||||||||||
Db        696 TTCTCGGAGAGGGACAGAGGCCCATTTC 723
```

RESULT 6
US-10-666-480-62
; Sequence 62, Application US/10666480
; Publication No. US20040121959A1
; GENERAL INFORMATION:
; APPLICANT: Boone, Thomas C
; APPLICANT: Wild, Kenneth D
; APPLICANT: Sitney, Karen C
; APPLICANT: Min, Hosung
; APPLICANT: Kimmel, Bruce
; TITLE OF INVENTION: Peptides and Related Molecules That Modulate Nerve Growth Factor
; FILE REFERENCE: A-827US
; CURRENT APPLICATION NUMBER: US/10/666,480
; CURRENT FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: 60/412,524
; PRIOR FILING DATE: 2002-09-19
; NUMBER OF SEQ ID NOS: 286
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 62
; LENGTH: 780
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Expression vector component
US-10-666-480-62

Query Match 59.6%; Score 676; DB 17; Length 780;
Best Local Similarity 98.6%; Pred. No. 2.4e-202;
Matches 682; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

```
Qy          6 CCTGTTTTGAGTGTGTACAGGTGGAACAGGTCGAGGCCTTGAGGACCCCCCAGGAAGTCA 65
              |||||||||||||||||||||||||| ||||| || |||||||||||||| || ||||||
Db         89 CCTGTTTTGAGTGTGTACAGGTGGAACGGGTCGTGGACTTGAGGACCCCCCTGGCAGTCA 148

Qy         66 GAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTG 125
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        149 AAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTG 208
```

```
Qy        126 TACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCT 185
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        209 TACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCT 268

Qy        186 GCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCAT 245
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        269 GCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCAT 328

Qy        246 GGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATGTT 305
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        329 GGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATGTT 388

Qy        306 CACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTT 365
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        389 CACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTT 448

Qy        366 TCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTT 425
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        449 TCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTT 508

Qy        426 CTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCT 485
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        509 CTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCT 568

Qy        486 CACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAG 545
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        569 CACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAG 628

Qy        546 GCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCC 605
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        629 GCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCC 688

Qy        606 CTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTCTC 665
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        689 CTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTCTC 748

Qy        666 GGAGAGGGACAGAGGCCCATTTCATGGCTAGG 697
              |||||||||||||||||||||  |  |||||
Db        749 GGAGAGGGACAGAGGCCCATTTATTACCTAGG 780


RESULT 7
US-10-157-408-9
; Sequence 9, Application US/10157408
; Publication No. US20030104535A1
;   GENERAL INFORMATION:
;        APPLICANT: Capon, Daniel J.
;                   Gregory, Timothy J.
;        TITLE OF INVENTION: Adheson Variants
;        NUMBER OF SEQUENCES: 25
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Genentech, Inc.
;             STREET: 460 Point San Bruno Blvd
;             CITY: South San Francisco
;             STATE: California
;             COUNTRY: USA
;             ZIP: 94080
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: patin (Genentech)
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/157,408
;             FILING DATE: 28-May-2002
;             CLASSIFICATION: 435
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/457,918
;             FILING DATE: 1-JUN-1995
;             APPLICATION NUMBER: 08/236311
;             FILING DATE: 02-MAY-1994
;             APPLICATION NUMBER: 07/936190
;             FILING DATE: 26-AUG-1992
;             APPLICATION NUMBER: 07/842777
;             FILING DATE: 18-FEB-1992
;             APPLICATION NUMBER: 07/250785
;             FILING DATE: 28-SEP-1988
;             APPLICATION NUMBER: 07/104329
;             FILING DATE: 02-OCT-1987
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Kubinec, Jeffrey S.
;             REGISTRATION NUMBER: 36,575
;             REFERENCE/DOCKET NUMBER: P0444P1C3
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 415/225-8228
;             TELEFAX: 415/952-9881
;             TELEX: 910/371-7168
;   INFORMATION FOR SEQ ID NO: 9:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1142 bases
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-157-408-9

  Query Match           57.4%;  Score 651.2;  DB 15;  Length 1142;
  Best Local Similarity  97.8%;  Pred. No. 1.8e-194;
  Matches  673;  Conservative    0;  Mismatches    8;  Indels    7;  Gaps    1;

Qy          7 CTGTTTTGAGTGTGTACAGGTGGAACAGGTCGAGGCCTTGAGGACCCCCCAGGAAGTCAG 66
              |||||||||||||||| ||||| || ||||| || ||||||||||||||| || ||||||
Db        440 CTGTTTTGAGTGTGTACGGGTGGCACGGGTCGTGGACTTGAGGACCCCCCTGGCAGTCAG 499

Qy         67 AAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGT 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        500 AAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGT 559

Qy        127 ACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTG 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        560 ACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTG 619

Qy        187 CCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATG 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        620 CCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATG 679

Qy        247 GCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATGTTC 306
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        680 GCCCACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATGTTC 739

Qy        307 ACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTT 366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        740 ACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTT 799

Qy        367 CCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTC 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        800 CCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTC 859

Qy        427 TTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTC 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        860 TTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTC 919

Qy        487 ACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGG 546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        920 ACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGG 979

Qy        547 CTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCC 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        980 CTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCC 1039

Qy        607 TTGCAGAAGAGTACGAGGC-------ACTACGTACTCCGAGACGTGTTGGTGATGTGCGT 659
              |||||||||||||||||||       ||||||||||||||||||||||||||||||||||
Db       1040 TTGCAGAAGAGTACGAGGCACTACGTACTACGTACTCCGAGACGTGTTGGTGATGTGCGT 1099

Qy        660 CTTCTCGGAGAGGGACAGAGGCCCATTT 687
```

```
                    ||||||||||||||||||||||||||||
Db       1100 CTTCTCGGAGAGGGACAGAGGCCCATTT 1127


RESULT 8
US-10-097-044A-9
; Sequence 9, Application US/10097044A
; Publication No. US20030143220A1
;   GENERAL INFORMATION:
;        APPLICANT: Capon, Daniel J.
;                   Gregory, Timothy J.
;        TITLE OF INVENTION: Adheson Variants
;        NUMBER OF SEQUENCES: 25
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Genentech, Inc.
;             STREET: 460 Point San Bruno Blvd
;             CITY: South San Francisco
;             STATE: California
;             COUNTRY: USA
;             ZIP: 94080
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: patin (Genentech)
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/097,044A
;             FILING DATE: 28-May-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/457,918
;             FILING DATE: 1-JUN-1995
;             APPLICATION NUMBER: 08/236311
;             FILING DATE: 02-MAY-1994
;             APPLICATION NUMBER: 07/936190
;             FILING DATE: 26-AUG-1992
;             APPLICATION NUMBER: 07/842777
;             FILING DATE: 18-FEB-1992
;             APPLICATION NUMBER: 07/250785
;             FILING DATE: 28-SEP-1988
;             APPLICATION NUMBER: 07/104329
;             FILING DATE: 02-OCT-1987
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Kubinec, Jeffrey S.
;             REGISTRATION NUMBER: 36,575
;             REFERENCE/DOCKET NUMBER: P0444P1C3
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 415/225-8228
;             TELEFAX: 415/952-9881
;             TELEX: 910/371-7168
;   INFORMATION FOR SEQ ID NO: 9:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1142 bases
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-097-044A-9

  Query Match             57.4%;  Score 651.2;  DB 15;  Length 1142;
  Best Local Similarity   97.8%;  Pred. No. 1.8e-194;
  Matches  673;  Conservative    0;  Mismatches    8;  Indels    7;  Gaps    1;

Qy          7 CTGTTTTGAGTGTGTACAGGTGGAACAGGTCGAGGCCTTGAGGACCCCCCAGGAAGTCAG 66
              |||||||||||||||| ||||| || |||||  || ||||||||||||||  || ||||||
Db        440 CTGTTTTGAGTGTGTACGGGTGGCACGGGTCGTGGACTTGAGGACCCCCCTGGCAGTCAG 499

Qy         67 AAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGT 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        500 AAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGT 559

Qy        127 ACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTG 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        560 ACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTG 619

Qy        187 CCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATG 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        620 CCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATG 679

Qy        247 GCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATGTTC 306
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        680 GCCCACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATGTTC 739

Qy        307 ACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTT 366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        740 ACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTT 799

Qy        367 CCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTC 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        800 CCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTC 859

Qy        427 TTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTC 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        860 TTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTC 919

Qy        487 ACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGG 546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        920 ACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGG 979

Qy        547 CTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCC 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        980 CTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCC 1039

Qy        607 TTGCAGAAGAGTACGAGGC-------ACTACGTACTCCGAGACGTGTTGGTGATGTGCGT 659
              |||||||||||||||||||       ||||||||||||||||||||||||||||||||||
Db       1040 TTGCAGAAGAGTACGAGGCACTACGTACTACGTACTCCGAGACGTGTTGGTGATGTGCGT 1099

Qy        660 CTTCTCGGAGAGGGACAGAGGCCCATTT 687
              ||||||||||||||||||||||||||||
Db       1100 CTTCTCGGAGAGGGACAGAGGCCCATTT 1127


RESULT 9
US-10-769-247-9
; Sequence 9, Application US/10769247
; Publication No. US20040197809A1
;   GENERAL INFORMATION:
;        APPLICANT: Capon, Daniel J.
;                   Gregory, Timothy J.
;        TITLE OF INVENTION: Adheson Variants
;        NUMBER OF SEQUENCES: 25
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Genentech, Inc.
;             STREET: 460 Point San Bruno Blvd
;             CITY: South San Francisco
;             STATE: California
;             COUNTRY: USA
;             ZIP: 94080
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: patin (Genentech)
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/769,247
;             FILING DATE: 30-Jan-2004
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/457,918
;             FILING DATE: 1-JUN-1995
;             APPLICATION NUMBER: 08/236311
;             FILING DATE: 02-MAY-1994
;             APPLICATION NUMBER: 07/936190
;             FILING DATE: 26-AUG-1992
;             APPLICATION NUMBER: 07/842777
;             FILING DATE: 18-FEB-1992
```

```
;             APPLICATION NUMBER: 07/250785
;             FILING DATE: 28-SEP-1988
;             APPLICATION NUMBER: 07/104329
;             FILING DATE: 02-OCT-1987
;       ATTORNEY/AGENT INFORMATION:
;             NAME: Kubinec, Jeffrey S.
;             REGISTRATION NUMBER: 36,575
;             REFERENCE/DOCKET NUMBER: P0444P1C3
;       TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 415/225-8228
;             TELEFAX: 415/952-9881
;             TELEX: 910/371-7168
;   INFORMATION FOR SEQ ID NO: 9:
;       SEQUENCE CHARACTERISTICS:
;             LENGTH: 1142 bases
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-769-247-9

  Query Match             57.4%;  Score 651.2;  DB 18;  Length 1142;
  Best Local Similarity   97.8%;  Pred. No. 1.8e-194;
  Matches  673;  Conservative    0;  Mismatches    8;  Indels    7;  Gaps    1;

Qy          7 CTGTTTTGAGTGTGTACAGGTGGAACAGGTCGAGGCCTTGAGGACCCCCCCAGGAAGTCAG 66
              |||||||||||||||| ||||| || ||||| || |||||||||||||| || ||||||
Db        440 CTGTTTTGAGTGTGTACGGGTGGCACGGGTCGTGGACTTGAGGACCCCCCTGGCAGTCAG 499

Qy         67 AAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGT 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        500 AAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGT 559

Qy        127 ACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTG 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        560 ACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTG 619

Qy        187 CCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATG 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        620 CCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATG 679

Qy        247 GCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATGTTC 306
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        680 GCCCACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATGTTC 739

Qy        307 ACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTT 366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        740 ACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTT 799

Qy        367 CCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTC 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        800 CCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTC 859

Qy        427 TTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTC 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        860 TTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTC 919

Qy        487 ACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGG 546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        920 ACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGG 979

Qy        547 CTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCC 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        980 CTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCC 1039

Qy        607 TTGCAGAAGAGTACGAGGC-------ACTACGTACTCCGAGACGTGTTGGTGATGTGCGT 659
              ||||||||||||||||||       ||||||||||||||||||||||||||||||||||
Db       1040 TTGCAGAAGAGTACGAGGCACTACGTACTACGTACTCCGAGACGTGTTGGTGATGTGCGT 1099

Qy        660 CTTCTCGGAGAGGGACAGAGGCCCATTT 687
              |||||||||||||||||||||||||||
Db       1100 CTTCTCGGAGAGGGACAGAGGCCCATTT 1127
```

```
RESULT 10
US-10-630-406-4
; Sequence 4, Application US/10630406
; Publication No. US20040105855A1
; GENERAL INFORMATION:
;  APPLICANT: Jure-Kunkel, Maria
;  APPLICANT:  Ganguly, Subinay
;  APPLICANT:  Abraham, Ralph
;  APPLICANT:  Hollenbaugh, Diane L.
;  APPLICANT:  Rillema, Jill
;  APPLICANT:  Thorne, Barbara
;  APPLICANT:  Shuford, Walter W.
;  APPLICANT:  Mittler, Robert S.
;  TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST HUMAN 4-1BB
;  FILE REFERENCE: D0288 NP
;  CURRENT APPLICATION NUMBER: US/10/630,406
;  CURRENT FILING DATE:  2003-07-30
;  PRIOR APPLICATION NUMBER: US 60/399,646
;  PRIOR FILING DATE: 2002-07-30
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
;   LENGTH: 7033
;   TYPE: DNA
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Synthetic
US-10-630-406-4

  Query Match             54.3%;  Score 616;  DB 17;  Length 7033;
  Best Local Similarity   94.1%;  Pred. No. 4.5e-183;
  Matches  640;  Conservative    0;  Mismatches   40;  Indels    0;  Gaps    0;

Qy         15 AGTGTGTACAGGTGGAACAGGTCGAGGCCTTGAGGACCCCCCCAGGAAGTCAGAAGGAGAA 74
              ||   | || |||||||| ||||| || ||   |||||||||| || |||||||||| ||
Db       1400 AGGTGGAACGGGTGGAACGGGTCGTGGACTCAAGGACCCCCCTGGTAGTCAGAAGGACAA 1459

Qy         75 GGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGCACCA 134
              |||||||||||||||||||| ||||||||||||||||||||||||||||| ||||||||
Db       1460 GGGGGGTTTTGGGTTCCTGTGAGAGTACTAGAGGGCCTGGGGACTCCAGTGCACGCACCA 1519

Qy        135 CCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGCACCT 194
              |||||||||||||| |||||||| |||||| |||||||||||||||||||| ||||||||
Db       1520 CCACCTGCACTCGGTCCTTCTGGGGCTCCAGGTCAAGTTGACCATGCACCTACCGCACCT 1579

Qy        195 CCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATGGCACACCA 254
              |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db       1580 CCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCAAGTTGTCGTGCATGGCACACCA 1639

Qy        255 GTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATGTTCACGTTCCA 314
              |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db       1640 GTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTGCCGTTCCTCATGTTCACGTTCCA 1699

Qy        315 GAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTTCCCGTCGG 374
              |||||||||||| ||||||   || ||||||||||||||||||||||||||||||||||||
Db       1700 GAGGTTGTTTCCGGAGGGCAGGAGGTAGCTCTTTTGGTAGAGGTTTCGGTTTCCCGTCGG 1759

Qy        375 GGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTCTTGGTCCA 434
              |||||| |||||||||||||||||||||||||||||| ||| ||| ||||||||||||||||
Db       1760 GGCTCTCGGTGTCCACATGTGGGACGGGGGTAGGGTCCTCCTCTACTGGTTCTTGGTCCA 1819

Qy        435 GTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCACCCTCTC 494
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db       1820 GTCGGACTGGACGGACCAGTTTCCGAAGATGGGGTCGCTGTAGCGGCACCTCACCCTCTC 1879

Qy        495 GTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGGCTGCCGAG 554
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1880 GTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGGCTGCCGAG 1939

Qy        555 GAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCCTTGCAGAA 614
              |||||||||||||||| ||| |||||||||||||||||||||| ||||||| |||||
Db       1940 GAAGAAGGAGATGTCGTCCGATTGGCACCTGTTCTCGTCCACCGTCCTCCCCTTACAGAA 1999
```

```
Qy        615 GAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCGGAGAGGGA 674
              ||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db       2000 GAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGTGTCTTCTCGGAGAGGGA 2059

Qy        675 CAGAGGCCCATTTCATGGCT 694
              ||||| |||||||  | | |
Db       2060 CAGAGACCCATTTACTAGAT 2079


RESULT 11
US-09-229-200A-12
; Sequence 12, Application US/09229200A
; Patent No. US20020099179A1
;   GENERAL INFORMATION:
;        APPLICANT: Jolliffe et al.
;        TITLE OF INVENTION: CD4 Specific Recombinant Antibody
;        NUMBER OF SEQUENCES: 28
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Johnson & Johnson
;             STREET: One Johnson & Johnson Plaza
;             CITY: New Brunswick
;             STATE: NJ
;             COUNTRY: USA
;             ZIP: 08933-7003
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
;             COMPUTER: IBM
;             OPERATING SYSTEM: PC-DOS
;             SOFTWARE: <Unknown>
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/229,200A
;             FILING DATE: 13-Jan-1999
;             CLASSIFICATION: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: John W. Wallen, III
;             REGISTRATION NUMBER: 35,403
;             REFERENCE/DOCKET NUMBER: ORT-948
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (858) 784-3239
;             TELEFAX: (908) 524-2808
;   INFORMATION FOR SEQ ID NO: 12:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 2366
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: linear
;        ANTI-SENSE: no
;        SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-229-200A-12

  Query Match             43.6%;  Score 494.4;  DB 9;  Length 2366;
  Best Local Similarity   82.4%;  Pred. No. 6.7e-145;
  Matches  623;  Conservative    0;  Mismatches   36;  Indels   97;  Gaps    1;

Qy          29 GAACAGGTCGAGGCCTTGAGGACCCCCCAGGAAGTCAGAAGGAGAAGGGGGGTTTTGGGT 88
               |||   |||| || ||  |||||||||| || |||||||||| ||||||||||||||||
Db        1264 GAAGGAGTCGTGGACTCAAGGACCCCCCTGGTAGTCAGAAGGACAAGGGGGGTTTTGGGT 1323

Qy          89 TCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGCACCACCACCTGCACTCGG 148
               ||||||| |||||||||||||||||||||||||| ||||||||||||||||||||||||
Db        1324 TCCTGTGAGAGTACTAGAGGGCCTGGGGACTCCAGTGCACGCACCACCACCTGCACTCGG 1383

Qy         149 TGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGT 208
               | ||||||||| |||||| |||||||||||||||||| |||||||||||||||||||||
Db        1384 TCCTTCTGGGGCTCCAGGTCAAGTTGACCATGCACCTACCGCACCTCCACGTATTACGGT 1443

Qy         209 TCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGC 268
               ||||||||||||||   ||||||| ||||||||||||||||||||||||||||||||||
Db        1444 TCTGTTTCGGCGCCCGTCTCGTCAAGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGC 1503

Qy         269 AGGACGTGGTCCTGACCGACTTACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGG 328
               |||||||||||||||||||| |||||||||||||||||||||||||||||||||| ||
Db        1504 AGGACGTGGTCCTGACCGACTTGCCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCCGG 1563

Qy         329 AGGGTCGGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTT---------------------- 365
               ||||  || |||||||||||||||||||||||||||||
Db        1564 AGGGCAGGAGGTAGCTCTTTTGGTAGAGGTTTCGGTTTCCACCCTGGGTGCCCCACGCTC 1623

Qy         366 ------------------------------------------------------------ 365

Db        1624 CCGGTGTGCCTGTCTCCGGTCGAGCCGGGTGGGAGACGGGACCCTCACTGGCGACACGGT 1683

Qy         366 --------------TCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCC 411
                             ||||||||||||||| |||||||||||||||||||||||||||| |
Db        1684 TGGAGACAGGGATGTCCCGTCGGGGCTCTCGGTGTCCACATGTGGGACGGGGGTAGGGTC 1743

Qy         412 CTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCG 471
               || ||| ||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db        1744 CTCCTCTACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATGGGGTCG 1803

Qy         472 CTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGA 531
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1804 CTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGA 1863

Qy         532 GGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCG 591
               |||||||||||||||||||||||||||||||||||||||||| ||| ||||||||||||||
Db        1864 GGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTCCGATTGGCACCTGTTCTCG 1923

Qy         592 TCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTG 651
               ||||||||| ||||| | ||||||||||||||||||||||||||||||||||||||||||
Db        1924 TCCACCGTCCTCCCCCTACAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTG 1983

Qy         652 ATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCATTT 687
               ||||| |||||||||||||||||||| |||||||
Db        1984 ATGTGTGTCTTCTCGGAGAGGGACAGAGACCCATTT 2019


RESULT 12
US-09-366-133-5
; Sequence 5, Application US/09366133
; Patent No. US20020009798A1
;  GENERAL INFORMATION:
;    APPLICANT:  Pelleymounter, Mary Ann
;    APPLICANT:  Hecht, Randy I
;    APPLICANT:  Mann, Michael B
;    TITLE OF INVENTION:  OB PROTEIN COMPOSITIONS AND METHODS
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Amgen Inc.
;      STREET:  1840 Dehavilland Drive
;      CITY:  Thousand Oaks
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  91230-1789
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/366,133
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/920,608
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Pessin, Karol M.
;      REFERENCE/DOCKET NUMBER:  A-345
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  454 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
```

```
;    MOLECULE TYPE:  cDNA
US-09-366-133-5

  Query Match             38.8%;  Score 440.8;  DB 9;  Length 454;
  Best Local Similarity   98.5%;  Pred. No. 2.9e-128;
  Matches  445;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy        684 ATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATG 743
              ||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 ATACCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATG 62

Qy        744 CGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTTGTCTTTCAATGTCCGGA 803
              ||||||||||||||||||||||||||||||||||||||||||||||    ||||||||||
Db         63 CGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTTGTCGCACAATGTCCGGA 122

Qy        804 CCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCG 863
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 CCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCG 182

Qy        864 ACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAATAGGTCTAGAGATTGCT 923
              |||||||||||||||||||||||||||||||||||||| | ||||||||||||||||||
Db        183 ACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAAGAAGTCTAGAGATTGCT 242

Qy        924 GGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGG 983
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        243 GGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGG 302

Qy        984 TACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCAAT 1043
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        303 TACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCAAT 362

Qy       1044 GTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAAGTCCTGTACGAAACCGT 1103
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        363 GTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAAGTCCTGTACGAAACCGT 422

Qy       1104 CGACCTGGACAGAGGCCCAACAATTACCTAGG 1135
              |||||||||||||||||||||||||||||||
Db        423 CGACCTGGACAGAGGCCCAACAATTACCTAGG 454


RESULT 13
US-10-214-037-5
; Sequence 5, Application US/10214037
; Publication No. US20030054997A1
;   GENERAL INFORMATION:
;        APPLICANT: Pelleymounter, Mary Ann
;                   Hecht, Randy I
;                   Mann, Michael B
;        TITLE OF INVENTION: OB PROTEIN COMPOSITIONS AND METHODS
;        NUMBER OF SEQUENCES: 6
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Amgen Inc.
;             STREET: 1840 Dehavilland Drive
;             CITY: Thousand Oaks
;             STATE: California
;             COUNTRY: U.S.A.
;             ZIP: 91230-1789
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/214,037
;             FILING DATE: 05-Aug-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/920,608
;             FILING DATE: 07-JUN-1995
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Pessin, Karol M.
;             REFERENCE/DOCKET NUMBER: A-345
;   INFORMATION FOR SEQ ID NO: 5:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 454 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-214-037-5

  Query Match             38.8%;  Score 440.8;  DB 14;  Length 454;
  Best Local Similarity   98.5%;  Pred. No. 2.9e-128;
  Matches  445;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy        684 ATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATG 743
              ||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 ATACCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATG 62

Qy        744 CGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTTGTCTTTCAATGTCCGGA 803
              ||||||||||||||||||||||||||||||||||||||||||||||    ||||||||||
Db         63 CGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTTGTCGCACAATGTCCGGA 122

Qy        804 CCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCG 863
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 CCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCG 182

Qy        864 ACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAATAGGTCTAGAGATTGCT 923
              |||||||||||||||||||||||||||||||||||||| | ||||||||||||||||||
Db        183 ACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAAGAAGTCTAGAGATTGCT 242

Qy        924 GGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGG 983
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        243 GGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGG 302

Qy        984 TACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCAAT 1043
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        303 TACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCAAT 362

Qy       1044 GTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAAGTCCTGTACGAAACCGT 1103
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        363 GTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAAGTCCTGTACGAAACCGT 422

Qy       1104 CGACCTGGACAGAGGCCCAACAATTACCTAGG 1135
              |||||||||||||||||||||||||||||||
Db        423 CGACCTGGACAGAGGCCCAACAATTACCTAGG 454


RESULT 14
US-10-679-999-5
; Sequence 5, Application US/10679999
; Publication No. US20040067520A1
;   GENERAL INFORMATION:
;        APPLICANT: Mann, Michael B.
;                   Hecht, Randy I.
;        TITLE OF INVENTION: OB FUSION PROTEIN COMPOSITIONS AND
;                            METHODS
;        NUMBER OF SEQUENCES: 18
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Amgen Inc.
;             STREET: 1840 DeHavilland Drive
;             CITY: Thousand Oaks
;             STATE: CA
;             COUNTRY: USA
;             ZIP: 91320-1789
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/679,999
;             FILING DATE: 06-Oct-2003
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
```

```
;             APPLICATION NUMBER: US/09/568,528
;             FILING DATE: 09-May-2000
;             APPLICATION NUMBER: 09/267,517
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Knight, Matthew W.
;             REGISTRATION NUMBER: 36,846
;             REFERENCE/DOCKET NUMBER: A-416
;   INFORMATION FOR SEQ ID NO: 5:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 454 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-679-999-5

  Query Match             38.8%;  Score 440.8;  DB 16;  Length 454;
  Best Local Similarity   98.5%;  Pred. No. 2.9e-128;
  Matches  445;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy        684 ATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATG 743
              ||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 ATACCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATG 62

Qy        744 CGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTTGTCTTTCAATGTCCGGA 803
              ||||||||||||||||||||||||||||||||||||||||||||||||   ||||||||||
Db         63 CGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTTGTCGCACAATGTCCGGA 122

Qy        804 CCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCG 863
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 CCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCG 182

Qy        864 ACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAATAGGTCTAGAGATTGCT 923
              |||||||||||||||||||||||||||||||||||||||||| | ||||||||||||||
Db        183 ACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAAGAAGTCTAGAGATTGCT 242

Qy        924 GGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGG 983
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        243 GGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGG 302

Qy        984 TACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCAAT 1043
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        303 TACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCAAT 362

Qy       1044 GTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAAGTCCTGTACGAAACCGT 1103
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        363 GTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAAGTCCTGTACGAAACCGT 422

Qy       1104 CGACCTGGACAGAGGCCCAACAATTACCTAGG 1135
              |||||||||||||||||||||||||||||||
Db        423 CGACCTGGACAGAGGCCCAACAATTACCTAGG 454


RESULT 15
US-09-366-133-2
; Sequence 2, Application US/09366133
; Patent No. US20020009798A1
;  GENERAL INFORMATION:
;    APPLICANT:  Pelleymounter, Mary Ann
;    APPLICANT:  Hecht, Randy I
;    APPLICANT:  Mann, Michael B
;    TITLE OF INVENTION:  OB PROTEIN COMPOSITIONS AND METHODS
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Amgen Inc.
;      STREET:  1840 Dehavilland Drive
;      CITY:  Thousand Oaks
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  91230-1789
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/366,133
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/920,608
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Pessin, Karol M.
;      REFERENCE/DOCKET NUMBER:  A-345
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  491 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-366-133-2

  Query Match             33.3%;  Score 378.4;  DB 9;  Length 491;
  Best Local Similarity   89.8%;  Pred. No. 1.4e-108;
  Matches  406;  Conservative    0;  Mismatches   46;  Indels    0;  Gaps    0;

Qy        684 ATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATG 743
              ||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         40 ATACCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATG 99

Qy        744 CGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTTGTCTTTCAATGTCCGGA 803
              ||||||||||||||||||||||||||||||||||  | ||||||||  ||||| || ||
Db        100 CGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCAGAGGCGATTTGTCGCACAATGGCCAGA 159

Qy        804 CCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCG 863
              |||||||||||||||||||||||||||||| | ||||||||||||||||||||||||||
Db        160 CCTGAAGTAGGGCCCAGACGTGGGCTAGGATTCGAACAGGTTTTACCTGGTCTGGGACCG 219

Qy        864 ACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAATAGGTCTAGAGATTGCT 923
              |||||||||||| | |||||||| |||||||  ||||||| | |||||| |||||||
Db        220 ACATATGGTCGTCCACAATTGGAGGGACGGCAGGGTCTTGCAAGAAGTCTAGCGATTGCT 279

Qy        924 GGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGG 983
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        280 GGAGCTCTTGGAAGCGCTGGACGACGTGGACGACCGTAAGAGGTTTAGGACGAGGGACGG 339

Qy        984 TACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCAAT 1043
                | | |||||||| |||  | |||  || |||| ||||||||||||||||||    ||
Db        340 CGTCTGGAGTCCAGAAGTCTTTGGCCTTAGGGACCTGCCCCAGGACCTTCGTAGGGACAT 399

Qy       1044 GTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAAGTCCTGTACGAAACCGT 1103
              ||||||||||||||||||||||||||||||||||||||||||||||||||  |||  |||
Db        400 GTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAAGTCCTGTAGGAAGTCGT 459

Qy       1104 CGACCTGGACAGAGGCCCAACAATTACCTAGG 1135
              ||||||| | |||||||  ||||||||||||
Db        460 CGACCTGCAAAGAGGCCTTACAATTACCTAGG 491


Search completed: October 17, 2004, 18:18:51
Job time : 585.552 secs
```

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 17, 2004, 15:34:57 ; Search time 4354.1 Seconds
(without alignments)
11298.387 Million cell updates/sec

Title: US-10-679-999-16
Perfect score: 1135
Sequence: 1 CATATGGACAAAACTCACAC.....TCCGGGTTGTTAATGGATCC 1135

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1135	100.0	1135	6	BD056523	BD056523 OB fusion
2	1109.4	97.7	1135	6	BD056521	BD056521 OB fusion
3	1105	97.4	1150	6	BD056517	BD056517 OB fusion
4	1103.4	97.2	1150	6	BD056519	BD056519 OB fusion
5	662.4	58.4	748	6	AR437973	AR437973 Sequence
6	662.4	58.4	748	6	AX304259	AX304259 Sequence
7	662.4	58.4	757	6	AR437967	AR437967 Sequence
8	662.4	58.4	757	6	AX304247	AX304247 Sequence
9	662.4	58.4	763	6	AR437969	AR437969 Sequence
10	662.4	58.4	763	6	AX304251	AX304251 Sequence
11	662.4	58.4	794	6	AR437913	AR437913 Sequence
12	662.4	58.4	794	6	AX303197	AX303197 Sequence
13	662.4	58.4	812	6	AR437917	AR437917 Sequence
14	662.4	58.4	812	6	AX303207	AX303207 Sequence
15	662.4	58.4	859	6	AX327583	AX327583 Sequence
16	662.4	58.4	861	6	BD263009	BD263009 Dimeric t
17	662.4	58.4	861	6	AR437914	AR437914 Sequence
18	662.4	58.4	861	6	AX303199	AX303199 Sequence
19	660.8	58.2	773	6	AR437971	AR437971 Sequence
20	660.8	58.2	773	6	AX304255	AX304255 Sequence
21	659.2	58.1	2190	6	AX268713	AX268713 Sequence
22	659.2	58.1	2220	6	AX268719	AX268719 Sequence
23	659	58.1	1288	6	AX039180	AX039180 Sequence
24	658.8	58.0	1304	6	AX319686	AX319686 Sequence
25	658.8	58.0	1377	6	AX056749	AX056749 Sequence
26	658.6	58.0	1467	6	AR435734	AR435734 Sequence
27	658.6	58.0	1494	6	AR435733	AR435733 Sequence
28	658.6	58.0	1578	6	AR435732	AR435732 Sequence
29	658.4	58.0	684	6	BD262999	BD262999 Dimeric t
30	658.4	58.0	684	6	AR437912	AR437912 Sequence
31	658.4	58.0	684	6	AX140509	AX140509 Sequence
32	658.4	58.0	684	6	AX303193	AX303193 Sequence
33	658.4	58.0	684	6	AX318309	AX318309 Sequence
34	658.4	58.0	684	6	AX320751	AX320751 Sequence
35	658.4	58.0	684	6	AX327476	AX327476 Sequence
36	658.4	58.0	684	6	AX328218	AX328218 Sequence
37	658.4	58.0	684	6	AX354762	AX354762 Sequence
38	658.4	58.0	4661	6	AX359936	AX359936 Sequence
39	658.4	58.0	4661	6	AX382150	AX382150 Sequence
40	658	58.0	1304	6	AX039184	AX039184 Sequence
41	658	58.0	2196	6	AX268709	AX268709 Sequence
42	658	58.0	2226	6	AX268715	AX268715 Sequence
43	657.8	58.0	1720	6	AR381777	AR381777 Sequence
44	657.8	58.0	1720	6	AX180193	AX180193 Sequence
45	657.8	58.0	1720	6	AX180693	AX180693 Sequence

ALIGNMENTS

RESULT 1
BD056523
LOCUS BD056523 1135 bp DNA linear PAT 27-AUG-2002
DEFINITION OB fusion protein compositions and methods.
ACCESSION BD056523
VERSION BD056523.1 GI:22602129
KEYWORDS JP 2001512417-A/11.
SOURCE Aequorea victoria
ORGANISM Aequorea victoria
Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae; Aequorea.
REFERENCE 1 (bases 1 to 1135)
AUTHORS Mann,M.B. and Hecht,R.I.
TITLE OB fusion protein compositions and methods
JOURNAL Patent: JP 2001512417-A 11 21-AUG-2001;

```
            AMGEN INC
COMMENT     PN   JP 2001512417-A/11
            PD   21-AUG-2001
            PF   11-DEC-1997 JP 1998528896
            PR   20-DEC-1996 US    08/770973
            PI   MICHAEL BENJAMIN MANN,RANDY IRA HECHT
            PC   C07K14/575,A61K38/00,A61P3/04,A61P3/06,A61P3/10,A61P9/10, PC
            A61P43/00,
            PC   C12N15/09,C12N15/00,A61K37/02
            CC   Strandedness: Double;
            CC   Topology: Linear;
            CC   /note= 'Met = ATG'
            FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
     source          1. .1135
                     /organism="Aequorea victoria"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:6100"
ORIGIN

  Query Match             100.0%;  Score 1135;  DB 6;  Length 1135;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-233;
  Matches 1135;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CATATGGACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CATATGGACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCG 60

Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120

Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180

Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240

Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCT 300

Qy        301 TACGCATGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TACGCATGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360

Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420

Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480

Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540

Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600

Qy        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660

Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTTCAGGACGACACCAAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTTCAGGACGACACCAAA 720

Qy        721 ACCTTAATTAAAACGATCGTTACGCGTATCAACGACATCAGTCACACCCAGTCGGTGAGC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ACCTTAATTAAAACGATCGTTACGCGTATCAACGACATCAGTCACACCCAGTCGGTGAGC 780

Qy        781 TCTAAACAGAAAGTTACAGGCCTGGACTTCATCCCGGGTCTGCACCCGATCCTGACCTTG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TCTAAACAGAAAGTTACAGGCCTGGACTTCATCCCGGGTCTGCACCCGATCCTGACCTTG 840

Qy        841 TCCAAAATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACCTCCATGCCGTCCCGT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TCCAAAATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACCTCCATGCCGTCCCGT 900

Qy        901 AACGTTATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTGCTGCACGTGCTGGCA 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 AACGTTATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTGCTGCACGTGCTGGCA 960

Qy        961 TTCTCCAAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACTCTGGACTCTCTGGGC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TTCTCCAAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACTCTGGACTCTCTGGGC 1020

Qy       1021 GGGGTCCTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTGTCCCGTCTGCAGGGT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GGGGTCCTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTGTCCCGTCTGCAGGGT 1080

Qy       1081 TCCCTTCAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGTTAATGGATCC 1135
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TCCCTTCAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGTTAATGGATCC 1135


RESULT 2
BD056521
LOCUS       BD056521                1135 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  OB fusion protein compositions and methods.
ACCESSION   BD056521
VERSION     BD056521.1  GI:22602127
KEYWORDS    JP 2001512417-A/9.
SOURCE      Aequorea victoria
  ORGANISM  Aequorea victoria
            Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
            Aequoreidae; Aequorea.
REFERENCE   1  (bases 1 to 1135)
  AUTHORS   Mann,M.B. and Hecht,R.I.
  TITLE     OB fusion protein compositions and methods
  JOURNAL   Patent: JP 2001512417-A 9 21-AUG-2001;
            AMGEN INC
COMMENT     PN   JP 2001512417-A/9
            PD   21-AUG-2001
            PF   11-DEC-1997 JP 1998528896
            PR   20-DEC-1996 US    08/770973
            PI   MICHAEL BENJAMIN MANN,RANDY IRA HECHT
            PC   C07K14/575,A61K38/00,A61P3/04,A61P3/06,A61P3/10,A61P9/10, PC
            A61P43/00,
            PC   C12N15/09,C12N15/00,A61K37/02
            CC   Strandedness: Double;
            CC   Topology: Linear;
            CC   /note= 'Met = ATG'
            FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
     source          1. .1135
                     /organism="Aequorea victoria"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:6100"
ORIGIN

  Query Match             97.7%;  Score 1109.4;  DB 6;  Length 1135;
  Best Local Similarity   98.6%;  Pred. No. 3.5e-228;
  Matches 1119;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          1 CATATGGACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCG 60
              |||||||||||||||||||| |||| || ||||||||||||||    || |||||
Db          1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGTCCT 60

Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
Qy       121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
Db       121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
Qy       181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
Db       181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
Qy       241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCT 300
Db       241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300
Qy       301 TACGCATGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
Db       301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
Qy       361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
Db       361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
Qy       421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
Db       421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
Qy       481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
Db       481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
Qy       541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
Db       541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
Qy       601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
Db       601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
Qy       661 AAGAGCCTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTTCAGGACGACACCAAA 720
Db       661 AAGAGCCTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTTCAGGACGACACCAAA 720
Qy       721 ACCTTAATTAAAACGATCGTTACGCGTATCAACGACATCAGTCACACCCAGTCGGTGAGC 780
Db       721 ACCTTAATTAAAACGATCGTTACGCGTATCAACGACATCAGTCACACCCAGTCGGTGAGC 780
Qy       781 TCTAAACAGAAAGTTACAGGCCTGGACTTCATCCCGGGTCTGCACCCGATCCTGACCTTG 840
Db       781 TCTAAACAGAAAGTTACAGGCCTGGACTTCATCCCGGGTCTGCACCCGATCCTGACCTTG 840
Qy       841 TCCAAAATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACCTCCATGCCGTCCCGT 900
Db       841 TCCAAAATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACCTCCATGCCGTCCCGT 900
Qy       901 AACGTTATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTGCTGCACGTGCTGGCA 960
Db       901 AACGTTATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTGCTGCACGTGCTGGCA 960
Qy       961 TTCTCCAAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACTCTGGACTCTCTGGGC 1020
Db       961 TTCTCCAAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACTCTGGACTCTCTGGGC 1020
Qy      1021 GGGGTCCTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTGTCCCGTCTGCAGGGT 1080
Db      1021 GGGGTCCTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTGTCCCGTCTGCAGGGT 1080
Qy      1081 TCCCTTCAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGTTAATGGATCC 1135
Db      1081 TCCCTTCAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGTTAATGGATCC 1135
```

RESULT 3
BD056517

```
LOCUS       BD056517                1150 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  OB fusion protein compositions and methods.
ACCESSION   BD056517
VERSION     BD056517.1  GI:22602123
KEYWORDS    JP 2001512417-A/5.
SOURCE      Aequorea victoria
  ORGANISM  Aequorea victoria
            Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
            Aequoreidae; Aequorea.
REFERENCE   1  (bases 1 to 1150)
  AUTHORS   Mann,M.B. and Hecht,R.I.
  TITLE     OB fusion protein compositions and methods
  JOURNAL   Patent: JP 2001512417-A 5 21-AUG-2001;
            AMGEN INC
COMMENT     PN   JP 2001512417-A/5
            PD   21-AUG-2001
            PF   11-DEC-1997 JP 1998528896
            PR   20-DEC-1996 US    08/770973
            PI   MICHAEL BENJAMIN MANN,RANDY IRA HECHT
            PC   C07K14/575,A61K38/00,A61P3/04,A61P3/06,A61P3/10,A61P9/10, PC
            A61P43/00,
            PC   C12N15/09,C12N15/00,A61K37/02
            CC   Strandedness: Double;
            CC   Topology: Linear;
            CC   /note= 'Met = ATG'
            FH   Key             Location/Qualifiers.
FEATURES                Location/Qualifiers
     source             1. .1150
                        /organism="Aequorea victoria"
                        /mol_type="genomic DNA"
                        /db_xref="taxon:6100"
ORIGIN
```

Query Match 97.4%; Score 1105; DB 6; Length 1150;
Best Local Similarity 98.7%; Pred. No. 3.1e-227;
Matches 1114; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

```
Qy          7 GACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCGTCAGTC 66
Db         22 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC 81
Qy         67 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 126
Db         82 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 141
Qy        127 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 186
Db        142 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 201
Qy        187 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 246
Db        202 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 261
Qy        247 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCTTACGCA 306
Db        262 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 321
Qy        307 TGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 366
Db        322 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 381
Qy        367 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 426
Db        382 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 441
Qy        427 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 486
Db        442 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 501
Qy        487 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 546
Db        502 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 561
```

```
Qy        547 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        562 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 621

Qy        607 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        622 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 681

Qy        667 CTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTTCAGGACGACACCAAAACCTTA 726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        682 CTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTTCAGGACGACACCAAAACCTTA 741

Qy        727 ATTAAAACGATCGTTACGCGTATCAACGACATCAGTCACACCCAGTCGGTGAGCTCTAAA 786
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        742 ATTAAAACGATCGTTACGCGTATCAACGACATCAGTCACACCCAGTCGGTGAGCTCTAAA 801

Qy        787 CAGAAAGTTACAGGCCTGGACTTCATCCCGGGTCTGCACCCGATCCTGACCTTGTCCAAA 846
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        802 CAGAAAGTTACAGGCCTGGACTTCATCCCGGGTCTGCACCCGATCCTGACCTTGTCCAAA 861

Qy        847 ATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACCTCCATGCCGTCCCGTAACGTT 906
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        862 ATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACCTCCATGCCGTCCCGTAACGTT 921

Qy        907 ATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTGCTGCACGTGCTGGCATTCTCC 966
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        922 ATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTGCTGCACGTGCTGGCATTCTCC 981

Qy        967 AAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACTCTGGACTCTCTGGGCGGGGTC 1026
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        982 AAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACTCTGGACTCTCTGGGCGGGGTC 1041

Qy       1027 CTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTGTCCCGTCTGCAGGGTTCCCTT 1086
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1042 CTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTGTCCCGTCTGCAGGGTTCCCTT 1101

Qy       1087 CAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGTTAATGGATCC 1135
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db       1102 CAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGTTAATGGATCC 1150
```

```
RESULT 4
BD056519
LOCUS       BD056519                1150 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  OB fusion protein compositions and methods.
ACCESSION   BD056519
VERSION     BD056519.1  GI:22602125
KEYWORDS    JP 2001512417-A/7.
SOURCE      Aequorea victoria
  ORGANISM  Aequorea victoria
            Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
            Aequoreidae; Aequorea.
REFERENCE   1  (bases 1 to 1150)
  AUTHORS   Mann,M.B. and Hecht,R.I.
  TITLE     OB fusion protein compositions and methods
  JOURNAL   Patent: JP 2001512417-A 7 21-AUG-2001;
            AMGEN INC
COMMENT     PN   JP 2001512417-A/7
            PD   21-AUG-2001
            PF   11-DEC-1997 JP 1998528896
            PR   20-DEC-1996 US    08/770973
            PI   MICHAEL BENJAMIN MANN,RANDY IRA HECHT
            PC   C07K14/575,A61K38/00,A61P3/04,A61P3/06,A61P3/10,A61P9/10, PC
            A61P43/00,
            PC   C12N15/09,C12N15/00,A61K37/02
            CC   Strandedness: Double;
            CC   Topology: Linear;
            CC   /note= 'Met = ATG'
            FH   Key             Location/Qualifiers.
FEATURES                Location/Qualifiers
     source             1. .1150
                        /organism="Aequorea victoria"
                        /mol_type="genomic DNA"
                        /db_xref="taxon:6100"
ORIGIN
```

```
  Query Match             97.2%;  Score 1103.4;  DB 6;  Length 1150;
  Best Local Similarity   98.6%;  Pred. No. 6.9e-227;
  Matches 1113;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          7 GACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCGTCAGTC 66
              |||||||||||||||| ||||| || ||||||||||||||    || ||||| |||||||
Db         22 GACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGTCCTTCAGTC 81

Qy         67 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         82 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 141

Qy        127 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        142 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 201

Qy        187 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        202 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 261

Qy        247 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCTTACGCA 306
              |||||||||||||||||||||||||||||||||||||||||||||||| | |||
Db        262 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 321

Qy        307 TGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 366
              ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        322 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 381

Qy        367 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        382 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 441

Qy        427 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        442 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 501

Qy        487 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        502 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 561

Qy        547 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        562 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 621

Qy        607 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        622 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 681

Qy        667 CTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTTCAGGACGACACCAAAACCTTA 726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        682 CTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTTCAGGACGACACCAAAACCTTA 741

Qy        727 ATTAAAACGATCGTTACGCGTATCAACGACATCAGTCACACCCAGTCGGTGAGCTCTAAA 786
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        742 ATTAAAACGATCGTTACGCGTATCAACGACATCAGTCACACCCAGTCGGTGAGCTCTAAA 801

Qy        787 CAGAAAGTTACAGGCCTGGACTTCATCCCGGGTCTGCACCCGATCCTGACCTTGTCCAAA 846
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        802 CAGAAAGTTACAGGCCTGGACTTCATCCCGGGTCTGCACCCGATCCTGACCTTGTCCAAA 861

Qy        847 ATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACCTCCATGCCGTCCCGTAACGTT 906
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        862 ATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACCTCCATGCCGTCCCGTAACGTT 921

Qy        907 ATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTGCTGCACGTGCTGGCATTCTCC 966
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        922 ATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTGCTGCACGTGCTGGCATTCTCC 981

Qy        967 AAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACTCTGGACTCTCTGGGCGGGGTC 1026
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        982 AAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACTCTGGACTCTCTGGGCGGGGTC 1041

Qy       1027 CTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTGTCCCGTCTGCAGGGTTCCCTT 1086
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1042 CTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTGTCCCGTCTGCAGGGTTCCCTT 1101

Qy       1087 CAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGTTAATGGATCC 1135
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1102 CAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGTTAATGGATCC 1150


RESULT 5
AR437973
LOCUS       AR437973                748 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 1067 from patent US 6660843.
ACCESSION   AR437973
VERSION     AR437973.1  GI:40203312
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 748)
  AUTHORS   Feige,U. and Liu,C.-F.
  TITLE     Modified peptides as therapeutic agents
  JOURNAL   Patent: US 6660843-A 1067 09-DEC-2003;
FEATURES             Location/Qualifiers
     source          1. .748
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match           58.4%;  Score 662.4;  DB 6;  Length 748;
  Best Local Similarity  97.7%;  Pred. No. 4.9e-132;
  Matches  672;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          1 CATATGGACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCG 60
              |||||||||||||||||||| ||||| || ||||||||||||||   || || |||
Db          1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCG 60

Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120

Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180

Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240

Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCT 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300

Qy        301 TACGCATGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
              |||   |||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360

Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420

Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480

Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540

Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600

Qy        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660

Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
              ||||||||||||||||||||||||||||
Db        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688


RESULT 6
AX304259
LOCUS       AX304259                748 bp    DNA     linear   PAT 30-NOV-2001
DEFINITION  Sequence 1067 from Patent WO0183525.
ACCESSION   AX304259
VERSION     AX304259.1  GI:17383760
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Feige,U., Liu,C.F., Cheetham,J.C., Boone,T.C. and Gudas,J.M.
  TITLE     Modified peptides as therapeutic agents
  JOURNAL   Patent: WO 0183525-A 1067 08-NOV-2001;
            Amgen Inc., (US)
FEATURES             Location/Qualifiers
     source          1. .748
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Fc-MMP INHIBITOR"
     CDS             4. .735
                     /note="unnamed protein product"
                     /codon_start=1
                     /transl_table=11
                     /protein_id="CAD13122.1"
                     /db_xref="GI:17383761"
                     /db_xref="REMTREMBL:CAD13122"
                     /translation="MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV
                     VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKC
                     KVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAV
                     EWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYT
                     QKSLSLSPGKGGGGGCTTHWGFTLC"
ORIGIN

  Query Match           58.4%;  Score 662.4;  DB 6;  Length 748;
  Best Local Similarity  97.7%;  Pred. No. 4.9e-132;
  Matches  672;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          1 CATATGGACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCG 60
              |||||||||||||||||||| ||||| || ||||||||||||||   || || |||
Db          1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCG 60

Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120

Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180

Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240

Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCT 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300

Qy        301 TACGCATGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
              |||   |||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
```

```
Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420

Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480

Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540

Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600

Qy        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660

Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
              |||||||||||||||||||||||||||||
Db        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
```

RESULT 7
AR437967
LOCUS AR437967 757 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 1055 from patent US 6660843.
ACCESSION AR437967
VERSION AR437967.1 GI:40203306
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 757)
AUTHORS Feige,U. and Liu,C.-F.
TITLE Modified peptides as therapeutic agents
JOURNAL Patent: US 6660843-A 1055 09-DEC-2003;
FEATURES Location/Qualifiers
source 1. .757
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN

Query Match 58.4%; Score 662.4; DB 6; Length 757;
Best Local Similarity 97.7%; Pred. No. 4.9e-132;
Matches 672; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

```
Qy          1 CATATGGACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCG 60
              |||||||||||||||||||||||| ||||| || ||||||||||||||   || || |||
Db          1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCG 60

Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120

Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180

Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240

Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCT 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300

Qy        301 TACGCATGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
              |||  |||  ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
```

```
Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420

Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480

Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540

Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600

Qy        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660

Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
              |||||||||||||||||||||||||||||
Db        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
```

RESULT 8
AX304247
LOCUS AX304247 757 bp DNA linear PAT 30-NOV-2001
DEFINITION Sequence 1055 from Patent WO0183525.
ACCESSION AX304247
VERSION AX304247.1 GI:17383748
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Feige,U., Liu,C.F., Cheetham,J.C., Boone,T.C. and Gudas,J.M.
TITLE Modified peptides as therapeutic agents
JOURNAL Patent: WO 0183525-A 1055 08-NOV-2001;
Amgen Inc., (US)
FEATURES Location/Qualifiers
source 1. .757
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Fc-TNF-ALPHA INHIBITORS"
CDS 4. .750
/note="unnamed protein product"
/codon_start=1
/transl_table=11
/protein_id="CAD13116.1"
/db_xref="GI:17383749"
/db_xref="REMTREMBL:CAD13116"
/translation="MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV
VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKC
KVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAV
EWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYT
QKSLSLSPGKGGGGGDFLPHYKNTSLGHRP"
ORIGIN

Query Match 58.4%; Score 662.4; DB 6; Length 757;
Best Local Similarity 97.7%; Pred. No. 4.9e-132;
Matches 672; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

```
Qy          1 CATATGGACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCG 60
              |||||||||||||||||||||||| ||||| || ||||||||||||||   || || |||
Db          1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCG 60

Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
```

```
Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180

Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240

Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300

Qy        301 TACGCATGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
              |||   |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360

Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420

Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480

Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540

Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600

Qy        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660

Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
              |||||||||||||||||||||||||||
Db        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
```

```
RESULT 9
AR437969
LOCUS       AR437969                763 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 1059 from patent US 6660843.
ACCESSION   AR437969
VERSION     AR437969.1  GI:40203308
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 763)
  AUTHORS   Feige,U. and Liu,C.-F.
  TITLE     Modified peptides as therapeutic agents
  JOURNAL   Patent: US 6660843-A 1059 09-DEC-2003;
FEATURES             Location/Qualifiers
     source          1. .763
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match           58.4%;  Score 662.4;  DB 6;  Length 763;
  Best Local Similarity   97.7%;  Pred. No. 4.9e-132;
  Matches  672;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          1 CATATGGACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCG 60
              |||||||||||||||||||||| ||||| || ||||||||||||||   || || |||
Db          1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCG 60

Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
```

```
Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180

Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240

Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300

Qy        301 TACGCATGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
              |||   |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360

Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420

Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480

Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540

Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600

Qy        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660

Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
              |||||||||||||||||||||||||||
Db        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
```

```
RESULT 10
AX304251
LOCUS       AX304251                763 bp    DNA     linear   PAT 30-NOV-2001
DEFINITION  Sequence 1059 from Patent WO0183525.
ACCESSION   AX304251
VERSION     AX304251.1  GI:17383752
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Feige,U., Liu,C.F., Cheetham,J.C., Boone,T.C. and Gudas,J.M.
  TITLE     Modified peptides as therapeutic agents
  JOURNAL   Patent: WO 0183525-A 1059 08-NOV-2001;
            Amgen Inc., (US)
FEATURES             Location/Qualifiers
     source          1. .763
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Fc-IL-1 ANTAGONIST"
     CDS             4. .750
                     /note="unnamed protein product"
                     /codon_start=1
                     /transl_table=11
                     /protein_id="CAD13118.1"
                     /db_xref="GI:17383753"
                     /db_xref="REMTREMBL:CAD13118"
                     /translation="MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV
                     VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKC
                     KVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAV
                     EWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYT
```

QKSLSLSPGKGGGGGFEWTPGYWQPYALPL"
ORIGIN

Query Match 58.4%; Score 662.4; DB 6; Length 763;
Best Local Similarity 97.7%; Pred. No. 4.9e-132;
Matches 672; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

```
Qy          1 CATATGGACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCG 60
              |||||||||||||||||||||||| ||||| || ||||||||||||||||    || || |||
Db          1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCG 60

Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120

Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180

Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240

Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCT 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300

Qy        301 TACGCATGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
              |||   |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360

Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420

Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480

Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540

Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600

Qy        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660

Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
              |||||||||||||||||||||||||||
Db        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
```

RESULT 11
AR437913
LOCUS AR437913 794 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 5 from patent US 6660843.
ACCESSION AR437913
VERSION AR437913.1 GI:40203252
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 794)
AUTHORS Feige,U. and Liu,C.-F.
TITLE Modified peptides as therapeutic agents
JOURNAL Patent: US 6660843-A 5 09-DEC-2003;
FEATURES Location/Qualifiers
source 1. .794
/organism="unknown"

/mol_type="genomic DNA"
ORIGIN

Query Match 58.4%; Score 662.4; DB 6; Length 794;
Best Local Similarity 97.7%; Pred. No. 4.9e-132;
Matches 672; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

```
Qy          1 CATATGGACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCG 60
              |||||||||||||||||||||||| ||||| || ||||||||||||||||    || || |||
Db         36 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCG 95

Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         96 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 155

Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        156 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 215

Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        216 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 275

Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCT 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        276 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 335

Qy        301 TACGCATGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
              |||   |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        336 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 395

Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        396 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 455

Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        456 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 515

Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        516 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 575

Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        576 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 635

Qy        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        636 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 695

Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
              |||||||||||||||||||||||||||
Db        696 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 723
```

RESULT 12
AX303197
LOCUS AX303197 794 bp DNA linear PAT 30-NOV-2001
DEFINITION Sequence 5 from Patent WO0183525.
ACCESSION AX303197
VERSION AX303197.1 GI:17383677
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Feige,U., Liu,C.F., Cheetham,J.C., Boone,T.C. and Gudas,J.M.
TITLE Modified peptides as therapeutic agents
JOURNAL Patent: WO 0183525-A 5 08-NOV-2001;
Amgen Inc., (US)
FEATURES Location/Qualifiers
source 1. .794

```
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Fc-TMP"
     CDS             39. .782
                     /note="unnamed protein product"
                     /codon_start=1
                     /transl_table=11
                     /protein_id="CAD13102.1"
                     /db_xref="GI:17383678"
                     /db_xref="REMTREMBL:CAD13102"
                     /translation="MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV
                     VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKC
                     KVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAV
                     EWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYT
                     QKSLSLSPGKGGGGGIEGPTLRQWLAARA"
ORIGIN

  Query Match             58.4%;  Score 662.4;  DB 6;  Length 794;
  Best Local Similarity   97.7%;  Pred. No. 4.9e-132;
  Matches  672;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          1 CATATGGACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCG 60
              ||||||||||||||||||||||| ||||| || |||||||||||||||    || || |||
Db         36 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCG 95

Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         96 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 155

Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        156 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 215

Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        216 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 275

Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCT 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        276 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 335

Qy        301 TACGCATGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
              |||   |||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db        336 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 395

Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        396 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 455

Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        456 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 515

Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        516 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 575

Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        576 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 635

Qy        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        636 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 695

Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
              ||||||||||||||||||||||||||||
Db        696 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 723
```

RESULT 13
AR437917

```
LOCUS       AR437917                812 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 15 from patent US 6660843.
ACCESSION   AR437917
VERSION     AR437917.1  GI:40203256
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 812)
  AUTHORS   Feige,U. and Liu,C.-F.
  TITLE     Modified peptides as therapeutic agents
  JOURNAL   Patent: US 6660843-A 15 09-DEC-2003;
FEATURES             Location/Qualifiers
     source          1. .812
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             58.4%;  Score 662.4;  DB 6;  Length 812;
  Best Local Similarity   97.7%;  Pred. No. 4.9e-132;
  Matches  672;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          1 CATATGGACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCG 60
              ||||||||||||||||||||||| ||||| || |||||||||||||||    || || |||
Db         36 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCG 95

Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         96 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 155

Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        156 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 215

Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        216 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 275

Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCT 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        276 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 335

Qy        301 TACGCATGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
              |||   |||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db        336 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 395

Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        396 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 455

Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        456 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 515

Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        516 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 575

Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        576 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 635

Qy        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        636 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 695

Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
              ||||||||||||||||||||||||||||
Db        696 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 723
```

RESULT 14
AX303207

```
LOCUS       AX303207                812 bp    DNA     linear   PAT 30-NOV-2001
DEFINITION  Sequence 15 from Patent WO0183525.
ACCESSION   AX303207
VERSION     AX303207.1  GI:17383685
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Feige,U., Liu,C.F., Cheetham,J.C., Boone,T.C. and Gudas,J.M.
  TITLE     Modified peptides as therapeutic agents
  JOURNAL   Patent: WO 0183525-A 15 08-NOV-2001;
            Amgen Inc., (US)
FEATURES             Location/Qualifiers
     source          1. .812
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="EMP-Fc"
     CDS             39. .800
                     /note="unnamed protein product"
                     /codon_start=1
                     /transl_table=11
                     /protein_id="CAD13106.1"
                     /db_xref="GI:17383686"
                     /db_xref="REMTREMBL:CAD13106"
                     /translation="MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV
                     VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKC
                     KVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAV
                     EWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYT
                     QKSLSLSPGKGGGGGGGTYSCHFGPLTWVCKPQGG"
ORIGIN

  Query Match           58.4%;  Score 662.4;  DB 6;  Length 812;
  Best Local Similarity  97.7%;  Pred. No. 4.9e-132;
  Matches  672;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          1 CATATGGACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCG 60
              ||||||||||||||||||||||| ||||| || ||||||||||||||   || || |||
Db         36 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCG 95

Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         96 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 155

Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        156 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 215

Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        216 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 275

Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCT 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        276 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 335

Qy        301 TACGCATGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
              |||   |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        336 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 395

Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        396 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 455

Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        456 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 515

Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        516 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 575

Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        576 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 635

Qy        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        636 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 695

Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
              |||||||||||||||||||||||||||
Db        696 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 723


RESULT 15
AX327583
LOCUS       AX327583                859 bp    DNA     linear   PAT 07-JAN-2002
DEFINITION  Sequence 108 from Patent WO0181377.
ACCESSION   AX327583
VERSION     AX327583.1  GI:18097963
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Feige,U., Kohno,T., Lacey,D.L. and Boone,T.C.
  TITLE     Integrin/adhesion antagonists
  JOURNAL   Patent: WO 0181377-A 108 01-NOV-2001;
            Amgen, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .859
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Echistatin Fc-peptide"
     misc_feature    1
                     /note="NdeI site"
     CDS             4. .852
                     /note="unnamed protein product"
                     /codon_start=1
                     /transl_table=11
                     /protein_id="CAD20426.1"
                     /db_xref="GI:18097964"
                     /db_xref="REMTREMBL:CAD20426"
                     /translation="MDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV
                     VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKC
                     KVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAV
                     EWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYT
                     QKSLSLSPGKGGGGGECESGPCCRNCKFLKEGTICKRARGDDMDDYCNGKTCDCPRNP
                     HKGPAT"
     misc_feature    854
                     /note="BamHI site"
ORIGIN

  Query Match           58.4%;  Score 662.4;  DB 6;  Length 859;
  Best Local Similarity  97.7%;  Pred. No. 4.8e-132;
  Matches  672;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          1 CATATGGACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCG 60
              ||||||||||||||||||||||| ||||| || ||||||||||||||   || || |||
Db          1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCG 60

Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120

Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180

Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
```

```
Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300

Qy        301 TACGCATGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
              |||   |||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360

Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420

Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480

Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540

Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600

Qy        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660

Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
              ||||||||||||||||||||||||||||
Db        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
```

Search completed: October 18, 2004, 01:19:56
Job time : 4356.1 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 17, 2004, 15:27:13 ; Search time 3993.73 Seconds
(without alignments)
10355.995 Million cell updates/sec

Title: US-10-679-999-16
Perfect score: 1135
Sequence: 1 CATATGGACAAAACTCACAC.....TCCGGGTTGTTAATGGATCC 1135

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	657	57.9	871	4	BG753979	BG753979 602709506
2	657	57.9	983	5	BQ708975	BQ708975 AGENCOURT
3	656.2	57.8	843	4	BM007897	BM007897 603617582
4	656	57.8	941	5	BQ712021	BQ712021 AGENCOURT
5	655.4	57.7	925	5	BQ709152	BQ709152 AGENCOURT
6	655.4	57.7	1022	3	CR611254	CR611254 full-leng
7	655.4	57.7	1048	3	CR595172	CR595172 full-leng
8	655.4	57.7	1090	3	CR612308	CR612308 full-leng
9	655.4	57.7	1091	3	CR604961	CR604961 full-leng
10	655.4	57.7	1093	3	CR616804	CR616804 full-leng
11	655.4	57.7	1098	3	CR626477	CR626477 full-leng
12	655.4	57.7	1100	3	CR612813	CR612813 full-leng
13	655.4	57.7	1102	3	CR601777	CR601777 full-leng
14	655.4	57.7	1102	3	CR625051	CR625051 full-leng
15	655.4	57.7	1103	3	CR595194	CR595194 full-leng
16	655.4	57.7	1104	3	CR591904	CR591904 full-leng
17	655.4	57.7	1106	3	CR613460	CR613460 full-leng
18	655.4	57.7	1106	3	CR620071	CR620071 full-leng
19	655.4	57.7	1107	3	CR598548	CR598548 full-leng
20	655.4	57.7	1109	3	CR614200	CR614200 full-leng
21	655.4	57.7	1109	3	CR619687	CR619687 full-leng
22	655.4	57.7	1111	3	CR606782	CR606782 full-leng
23	655.4	57.7	1114	3	CR593349	CR593349 full-leng
24	655.4	57.7	1114	3	CR618075	CR618075 full-leng
25	655.4	57.7	1118	3	CR613511	CR613511 full-leng
26	655.4	57.7	1120	3	CR619868	CR619868 full-leng
27	655.4	57.7	1124	3	CR611468	CR611468 full-leng
28	655.4	57.7	1136	3	CR598462	CR598462 full-leng
29	655.4	57.7	1142	3	CR598316	CR598316 full-leng
30	655.4	57.7	1179	3	CR607277	CR607277 full-leng
31	655.4	57.7	1287	3	CR611016	CR611016 full-leng
32	655.4	57.7	1289	3	CR594000	CR594000 full-leng
33	654.6	57.7	973	5	BQ706204	BQ706204 AGENCOURT
34	654.4	57.7	851	5	BX346946	BX346946 BX346946
35	653.8	57.6	919	5	BQ709339	BQ709339 AGENCOURT
36	653.2	57.6	897	5	BQ709144	BQ709144 AGENCOURT
37	652.2	57.5	947	5	BQ709771	BQ709771 AGENCOURT
38	652	57.4	881	5	BQ711291	BQ711291 AGENCOURT
c 39	650	57.3	1013	5	BX360518	BX360518 BX360518
40	649.6	57.2	757	4	BG674795	BG674795 602620925
41	649.6	57.2	914	5	BQ712363	BQ712363 AGENCOURT
42	647.8	57.1	856	5	BQ709859	BQ709859 AGENCOURT
43	645	56.8	892	4	BG397723	BG397723 602438784
44	645	56.8	897	4	BM008412	BM008412 603617406
45	645	56.8	902	5	BU146962	BU146962 AGENCOURT

ALIGNMENTS

RESULT 1
BG753979
LOCUS BG753979 871 bp mRNA linear EST 15-MAY-2001
DEFINITION 602709506F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4846201 5', mRNA sequence.
ACCESSION BG753979
VERSION BG753979.1 GI:14064632
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 871)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1686 row: k column: 02
High quality sequence stop: 848.
FEATURES Location/Qualifiers
source 1. .871
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4846201"
/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_48"
/note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
ORIGIN

```
 Query Match             57.9%;  Score 657;  DB 4;  Length 871;
 Best Local Similarity   97.8%;  Pred. No. 1.4e-160;
 Matches  666;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          7 GACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCGTCAGTC 66
              |||||||||||||||||||||||||||||||||| || ||||||   || || |||||||||
Db         37 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC 96

Qy         67 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         97 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 156

Qy        127 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        157 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 216

Qy        187 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        217 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 276

Qy        247 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCTTACGCA 306
              |||||||||||||||||||||||||||||||||||||||||||||||||| |  |||
Db        277 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 336

Qy        307 TGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 366
              |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        337 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 396

Qy        367 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        397 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 456

Qy        427 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        457 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 516

Qy        487 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        517 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 576

Qy        547 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        577 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 636

Qy        607 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        637 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 696

Qy        667 CTCTCCCTGTCTCCGGGTAAA 687
              |||||||||||||||||||||
Db        697 CTCTCCCTGTCTCCGGGTAAA 717
```

```
RESULT 2
BQ708975
LOCUS       BQ708975                983 bp    mRNA    linear   EST 16-JUL-2002
DEFINITION  AGENCOURT_8353514 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6279683
            5', mRNA sequence.
ACCESSION   BQ708975
VERSION     BQ708975.1  GI:21847874
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 983)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2469  row: k  column: 12
            High quality sequence stop: 604.
FEATURES             Location/Qualifiers
     source          1. .983
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6279683"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_113"
                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
ORIGIN
```

```
 Query Match             57.9%;  Score 657;  DB 5;  Length 983;
 Best Local Similarity   97.8%;  Pred. No. 1.5e-160;
 Matches  666;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          7 GACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCGTCAGTC 66
              |||||||||||||||||||||||||||||||||| || ||||||   || || |||||||||
Db         24 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC 83

Qy         67 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         84 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 143

Qy        127 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        144 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 203

Qy        187 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        204 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 263

Qy        247 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCTTACGCA 306
              |||||||||||||||||||||||||||||||||||||||||||||||||| |  |||
Db        264 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 323

Qy        307 TGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 366
              |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        324 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 383

Qy        367 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        384 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 443

Qy        427 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        444 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 503

Qy        487 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        504 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 563

Qy        547 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        564 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 623

Qy        607 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        624 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 683
```

```
Qy        667 CTCTCCCTGTCTCCGGGTAAA 687
              |||||||||||||||||||||
Db        684 CTCTCCCTGTCTCCGGGTAAA 704
```

RESULT 3
BM007897
LOCUS BM007897 843 bp mRNA linear EST 30-OCT-2001
DEFINITION 603617582F1 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:5450469 5', mRNA sequence.
ACCESSION BM007897
VERSION BM007897.1 GI:16522238
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 843)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1939 row: d column: 22
High quality sequence stop: 833.

FEATURES Location/Qualifiers
source 1. .843
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5450469"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_113"
/note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 57.8%; Score 656.2; DB 4; Length 843;
Best Local Similarity 97.4%; Pred. No. 2.3e-160;
Matches 667; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

```
Qy          7 GACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCGTCAGTC 66
              |||||||||||||||||||||||||||||| || ||||||   || || |||||||||
Db        108 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC 167

Qy         67 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        168 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 227

Qy        127 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        228 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 287

Qy        187 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        288 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 347

Qy        247 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCTTACGCA 306
              |||||||||||||||||||||||||||||||||||||||||||||||||||  |  |||
Db        348 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 407

Qy        307 TGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 366
              |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        408 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 467

Qy        367 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        468 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 527

Qy        427 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        528 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 587

Qy        487 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        588 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 647

Qy        547 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        648 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 707

Qy        607 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 666
              |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db        708 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCATTACACGCAGAAGAGC 767

Qy        667 CTCTCCCTGTCTCCGGGTAAAGTAC 691
              |||||||||||||||||||  ||
Db        768 CTCTCCCTGTCTCCGGGTAAATGAC 792
```

RESULT 4
BQ712021
LOCUS BQ712021 941 bp mRNA linear EST 16-JUL-2002
DEFINITION AGENCOURT_8418162 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6281403 5', mRNA sequence.
ACCESSION BQ712021
VERSION BQ712021.1 GI:21850920
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 941)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2474 row: c column: 04
High quality sequence stop: 638.

FEATURES Location/Qualifiers
source 1. .941
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6281403"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_113"
/note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 57.8%; Score 656; DB 5; Length 941;
Best Local Similarity 97.7%; Pred. No. 2.6e-160;
Matches 665; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

```
Qy          7 GACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCGTCAGTC 66
              |||||||||||||||||||||||||||||||| || ||||||   || || |||||||||
Db         50 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC 109

Qy         67 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        110 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 169

Qy        127 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        170 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 229

Qy        187 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        230 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 289

Qy        247 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCTTACGCA 306
              |||||||||||||||||||||||||||||||||||||||||||||||| | |||
Db        290 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 349

Qy        307 TGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 366
              |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        350 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 409

Qy        367 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        410 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 469

Qy        427 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        470 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 529

Qy        487 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        530 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 589

Qy        547 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        590 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 649

Qy        607 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 666
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        650 AACGTCTTCTCATGCTCCGTGATGCATGANGCTCTGCACAACCACTACACGCAGAAGAGC 709

Qy        667 CTCTCCCTGTCTCCGGGTAAA 687
              |||||||||||||||||||||
Db        710 CTCTCCCTGTCTCCGGGTAAA 730
```

RESULT 5
BQ709152
LOCUS BQ709152 925 bp mRNA linear EST 16-JUL-2002
DEFINITION AGENCOURT_8485151 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6301245 5', mRNA sequence.
ACCESSION BQ709152
VERSION BQ709152.1 GI:21848051
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 925)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2516 row: m column: 22
High quality sequence stop: 739.

FEATURES Location/Qualifiers
source 1. .925
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6301245"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_113"
/note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 57.7%; Score 655.4; DB 5; Length 925;
Best Local Similarity 97.7%; Pred. No. 3.8e-160;
Matches 665; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

```
Qy          7 GACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCGTCAGTC 66
              |||||||||||||||||||||||||||||||| || ||||||   || || |||||||||
Db         48 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC 107

Qy         67 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        108 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 167

Qy        127 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        168 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 227

Qy        187 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        228 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 287

Qy        247 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCTTACGCA 306
              |||||||||||||||||||||||||||||||||||||||||||||||| | |||
Db        288 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 347

Qy        307 TGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 366
              |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        348 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 407

Qy        367 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        408 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 467

Qy        427 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        468 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 527

Qy        487 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        528 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 587

Qy        547 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        588 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 647

Qy        607 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 666
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        648 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACACAGAAGAGC 707

Qy        667 CTCTCCCTGTCTCCGGGTAAA 687
              |||||||||||||||||||||
Db        708 CTCTCCCTGTCTCCGGGTAAA 728


RESULT 6
CR611254
LOCUS       CR611254                1022 bp    mRNA    linear   HTC 21-JUL-2004
DEFINITION  full-length cDNA clone CS0DE007YJ17 of Placenta of Homo sapiens
            (human).
ACCESSION   CR611254
VERSION     CR611254.1  GI:50492061
KEYWORDS    HTC; CNSLT_cDNA.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1022)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished
  REMARK    Contact : Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue
REFERENCE   2  (bases 1 to 1022)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen.
FEATURES             Location/Qualifiers
     source          1. .1022
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DE007YJ17"
                     /tissue_type="Placenta"
                     /plasmid="pCMVSPORT_6"
ORIGIN

  Query Match           57.7%;  Score 655.4;  DB 3;  Length 1022;
  Best Local Similarity   97.7%;  Pred. No. 3.9e-160;
  Matches  665;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          7 GACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCGTCAGTC 66
              |||||||||||||||||||||||||||||||| || ||||||   || || |||||||||
Db        323 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC 382

Qy         67 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        383 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 442

Qy        127 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        443 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 502

Qy        187 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        503 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 562

Qy        247 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCTTACGCA 306
              |||||||||||||||||||||||||||||||||||||||||||||||||||  |  |||
Db        563 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 622

Qy        307 TGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 366
              |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        623 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 682

Qy        367 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        683 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 742

Qy        427 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        743 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 802

Qy        487 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        803 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 862

Qy        547 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        863 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 922

Qy        607 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 666
              |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db        923 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACACAGAAGAGC 982

Qy        667 CTCTCCCTGTCTCCGGGTAAA 687
              |||||||||||||||||||||
Db        983 CTCTCCCTGTCTCCGGGTAAA 1003


RESULT 7
CR595172
LOCUS       CR595172                1048 bp    mRNA    linear   HTC 21-JUL-2004
DEFINITION  full-length cDNA clone CS0DI040YA16 of Placenta Cot 25-normalized
            of Homo sapiens (human).
ACCESSION   CR595172
VERSION     CR595172.1  GI:50475979
KEYWORDS    HTC; CNSLT_cDNA.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1048)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished
  REMARK    Contact : Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue
REFERENCE   2  (bases 1 to 1048)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen.
FEATURES             Location/Qualifiers
     source          1. .1048
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DI040YA16"
                     /tissue_type="Placenta Cot 25-normalized"
                     /plasmid="pCMVSPORT_6"
ORIGIN

  Query Match           57.7%;  Score 655.4;  DB 3;  Length 1048;
  Best Local Similarity   97.7%;  Pred. No. 3.9e-160;
  Matches  665;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          7 GACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCGTCAGTC 66
              |||||||||||||||||||||||||||||||| || ||||||   || || |||||||||
```

```
Db        336 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC 395

Qy         67 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        396 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 455

Qy        127 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        456 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 515

Qy        187 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        516 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 575

Qy        247 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCTTACGCA 306
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        576 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 635

Qy        307 TGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 366
              ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        636 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 695

Qy        367 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        696 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 755

Qy        427 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        756 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 815

Qy        487 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        816 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 875

Qy        547 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        876 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 935

Qy        607 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 666
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        936 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACACAGAAGAGC 995

Qy        667 CTCTCCCTGTCTCCGGGTAAA 687
              |||||||||||||||||||||
Db        996 CTCTCCCTGTCTCCGGGTAAA 1016
```

```
RESULT 8
CR612308
LOCUS       CR612308               1090 bp    mRNA    linear   HTC 21-JUL-2004
DEFINITION  full-length cDNA clone CS0DI071YG21 of Placenta Cot 25-normalized
            of Homo sapiens (human).
ACCESSION   CR612308
VERSION     CR612308.1  GI:50493115
KEYWORDS    HTC; CNSLT_cDNA.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1090)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished
  REMARK    Contact : Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue
REFERENCE   2  (bases 1 to 1090)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen.
FEATURES             Location/Qualifiers
     source          1. .1090
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DI071YG21"
                     /tissue_type="Placenta Cot 25-normalized"
                     /plasmid="pCMVSPORT_6"
ORIGIN
```

```
  Query Match             57.7%;  Score 655.4;  DB 3;  Length 1090;
  Best Local Similarity   97.7%;  Pred. No. 3.9e-160;
  Matches  665;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          7 GACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCGTCAGTC 66
              |||||||||||||||||||||||||||||||| || ||||||   || || |||||||||
Db        323 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC 382

Qy         67 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        383 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 442

Qy        127 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        443 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 502

Qy        187 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        503 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 562

Qy        247 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCTTACGCA 306
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        563 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 622

Qy        307 TGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 366
              ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        623 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 682

Qy        367 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        683 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 742

Qy        427 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        743 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 802

Qy        487 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        803 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 862

Qy        547 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        863 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 922

Qy        607 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 666
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        923 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACACAGAAGAGC 982

Qy        667 CTCTCCCTGTCTCCGGGTAAA 687
              |||||||||||||||||||||
Db        983 CTCTCCCTGTCTCCGGGTAAA 1003
```

```
RESULT 9
CR604961
LOCUS       CR604961               1091 bp    mRNA    linear   HTC 21-JUL-2004
DEFINITION  full-length cDNA clone CS0DI009YJ10 of Placenta Cot 25-normalized
            of Homo sapiens (human).
ACCESSION   CR604961
```

```
VERSION     CR604961.1  GI:50485768
KEYWORDS    HTC; CNSLT_cDNA.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1091)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished
  REMARK    Contact : Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue
REFERENCE   2  (bases 1 to 1091)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen.
FEATURES             Location/Qualifiers
     source          1. .1091
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DI009YJ10"
                     /tissue_type="Placenta Cot 25-normalized"
                     /plasmid="pCMVSPORT_6"
ORIGIN

  Query Match           57.7%;  Score 655.4;  DB 3;  Length 1091;
  Best Local Similarity  97.7%;  Pred. No. 3.9e-160;
  Matches  665;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          7 GACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCGTCAGTC 66
              |||||||||||||||||||||||||||||||| || ||||||   || || |||||||||
Db        323 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC 382

Qy         67 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        383 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 442

Qy        127 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        443 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 502

Qy        187 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        503 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 562

Qy        247 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCTTACGCA 306
              |||||||||||||||||||||||||||||||||||||||||||||||| |  |||
Db        563 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 622

Qy        307 TGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 366
              |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        623 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 682

Qy        367 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        683 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 742

Qy        427 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        743 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 802

Qy        487 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        803 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 862

Qy        547 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        863 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 922

Qy        607 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 666
              |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db        923 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACACAGAAGAGC 982

Qy        667 CTCTCCCTGTCTCCGGGTAAA 687
              |||||||||||||||||||||
Db        983 CTCTCCCTGTCTCCGGGTAAA 1003


RESULT 10
CR616804
LOCUS       CR616804               1093 bp    mRNA    linear   HTC 21-JUL-2004
DEFINITION  full-length cDNA clone CS0DI048YC07 of Placenta Cot 25-normalized
            of Homo sapiens (human).
ACCESSION   CR616804
VERSION     CR616804.1  GI:50497611
KEYWORDS    HTC; CNSLT_cDNA.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1093)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished
  REMARK    Contact : Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue
REFERENCE   2  (bases 1 to 1093)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen.
FEATURES             Location/Qualifiers
     source          1. .1093
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DI048YC07"
                     /tissue_type="Placenta Cot 25-normalized"
                     /plasmid="pCMVSPORT_6"
ORIGIN

  Query Match           57.7%;  Score 655.4;  DB 3;  Length 1093;
  Best Local Similarity  97.7%;  Pred. No. 3.9e-160;
  Matches  665;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          7 GACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCGTCAGTC 66
              |||||||||||||||||||||||||||||||| || ||||||   || || |||||||||
Db        323 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC 382

Qy         67 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        383 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 442

Qy        127 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        443 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 502

Qy        187 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        503 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 562
```

```
Qy        247 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCTTACGCA 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||| | |||
Db        563 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 622

Qy        307 TGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 366
              |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        623 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 682

Qy        367 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        683 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 742

Qy        427 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        743 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 802

Qy        487 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        803 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 862

Qy        547 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        863 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 922

Qy        607 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 666
              |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db        923 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACACAGAAGAGC 982

Qy        667 CTCTCCCTGTCTCCGGGTAAA 687
              |||||||||||||||||||||
Db        983 CTCTCCCTGTCTCCGGGTAAA 1003
```

```
RESULT 11
CR626477
LOCUS       CR626477               1098 bp    mRNA    linear   HTC 21-JUL-2004
DEFINITION  full-length cDNA clone CS0CAP001YI13 of Thymus of Homo sapiens
            (human).
ACCESSION   CR626477
VERSION     CR626477.1  GI:50507284
KEYWORDS    HTC; CNSLT_cDNA.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1098)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished
  REMARK    Contact : Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue
REFERENCE   2  (bases 1 to 1098)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen.
FEATURES             Location/Qualifiers
     source          1. .1098
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0CAP001YI13"
                     /tissue_type="Thymus"
                     /plasmid="pCMVSPORT_6"
ORIGIN
```

```
Query Match           57.7%;  Score 655.4;  DB 3;  Length 1098;
Best Local Similarity 97.7%;  Pred. No. 3.9e-160;
Matches  665;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          7 GACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCGTCAGTC 66
              |||||||||||||||||||||||||||||||| || ||||||   || || ||||||||||
Db        323 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC 382

Qy         67 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        383 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 442

Qy        127 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        443 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 502

Qy        187 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        503 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 562

Qy        247 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCTTACGCA 306
              |||||||||||||||||||||||||||||||||||||||||||||||||| | |||
Db        563 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 622

Qy        307 TGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 366
              |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        623 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 682

Qy        367 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        683 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 742

Qy        427 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        743 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 802

Qy        487 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        803 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 862

Qy        547 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        863 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 922

Qy        607 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 666
              |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db        923 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACACAGAAGAGC 982

Qy        667 CTCTCCCTGTCTCCGGGTAAA 687
              |||||||||||||||||||||
Db        983 CTCTCCCTGTCTCCGGGTAAA 1003
```

```
RESULT 12
CR612813
LOCUS       CR612813               1100 bp    mRNA    linear   HTC 21-JUL-2004
DEFINITION  full-length cDNA clone CS0DI081YF02 of Placenta Cot 25-normalized
            of Homo sapiens (human).
ACCESSION   CR612813
VERSION     CR612813.1  GI:50493620
KEYWORDS    HTC; CNSLT_cDNA.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1100)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished
  REMARK    Contact : Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue
```

```
REFERENCE   2  (bases 1 to 1100)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen.
FEATURES             Location/Qualifiers
     source          1. .1100
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DI081YF02"
                     /tissue_type="Placenta Cot 25-normalized"
                     /plasmid="pCMVSPORT_6"
ORIGIN

  Query Match           57.7%;  Score 655.4;  DB 3;  Length 1100;
  Best Local Similarity  97.7%;  Pred. No. 3.9e-160;
  Matches  665;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          7 GACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCGTCAGTC 66
              |||||||||||||||||||||||||||||||| || ||||||   || || |||||||||
Db        319 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC 378

Qy         67 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        379 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 438

Qy        127 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        439 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 498

Qy        187 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        499 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 558

Qy        247 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCTTACGCA 306
              |||||||||||||||||||||||||||||||||||||||||||||||| |  |||
Db        559 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 618

Qy        307 TGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 366
              |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        619 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 678

Qy        367 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        679 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 738

Qy        427 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        739 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 798

Qy        487 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        799 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 858

Qy        547 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        859 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 918

Qy        607 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 666
              |||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db        919 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACACAGAAGAGC 978

Qy        667 CTCTCCCTGTCTCCGGGTAAA 687
              |||||||||||||||||||||
Db        979 CTCTCCCTGTCTCCGGGTAAA 999
```

```
RESULT 13
CR601777
LOCUS       CR601777               1102 bp    mRNA    linear   HTC 21-JUL-2004
DEFINITION  full-length cDNA clone CS0CAP008YF07 of Thymus of Homo sapiens
            (human).
ACCESSION   CR601777
VERSION     CR601777.1  GI:50482584
KEYWORDS    HTC; CNSLT_cDNA.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1102)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished
  REMARK    Contact : Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue
REFERENCE   2  (bases 1 to 1102)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen.
FEATURES             Location/Qualifiers
     source          1. .1102
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0CAP008YF07"
                     /tissue_type="Thymus"
                     /plasmid="pCMVSPORT_6"
ORIGIN

  Query Match           57.7%;  Score 655.4;  DB 3;  Length 1102;
  Best Local Similarity  97.7%;  Pred. No. 3.9e-160;
  Matches  665;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          7 GACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCGTCAGTC 66
              |||||||||||||||||||||||||||||||| || ||||||   || || |||||||||
Db        319 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC 378

Qy         67 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        379 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 438

Qy        127 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        439 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 498

Qy        187 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        499 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 558

Qy        247 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCTTACGCA 306
              |||||||||||||||||||||||||||||||||||||||||||||||| |  |||
Db        559 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 618

Qy        307 TGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 366
              |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        619 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 678

Qy        367 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        679 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 738
```

```
Qy        427 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        739 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 798

Qy        487 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        799 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 858

Qy        547 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        859 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 918

Qy        607 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 666
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        919 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACACAGAAGAGC 978

Qy        667 CTCTCCCTGTCTCCGGGTAAA 687
              |||||||||||||||||||||
Db        979 CTCTCCCTGTCTCCGGGTAAA 999
```

```
RESULT 14
CR625051
LOCUS       CR625051               1102 bp    mRNA    linear   HTC 21-JUL-2004
DEFINITION  full-length cDNA clone CS0DI059YL06 of Placenta Cot 25-normalized
            of Homo sapiens (human).
ACCESSION   CR625051
VERSION     CR625051.1  GI:50505858
KEYWORDS    HTC; CNSLT_cDNA.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1102)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished
  REMARK    Contact : Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue
REFERENCE   2  (bases 1 to 1102)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen.
FEATURES             Location/Qualifiers
     source          1. .1102
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DI059YL06"
                     /tissue_type="Placenta Cot 25-normalized"
                     /plasmid="pCMVSPORT_6"
ORIGIN

  Query Match             57.7%;  Score 655.4;  DB 3;  Length 1102;
  Best Local Similarity   97.7%;  Pred. No. 3.9e-160;
  Matches  665;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          7 GACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCGTCAGTC 66
              |||||||||||||||||||||||||||||||| || ||||||   || || |||||||||
Db        323 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC 382

Qy         67 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        383 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 442
```

```
Qy        127 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        443 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 502

Qy        187 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        503 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 562

Qy        247 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCTTACGCA 306
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        563 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 622

Qy        307 TGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 366
              |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        623 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 682

Qy        367 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        683 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 742

Qy        427 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        743 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 802

Qy        487 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        803 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 862

Qy        547 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        863 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 922

Qy        607 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 666
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        923 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACACAGAAGAGC 982

Qy        667 CTCTCCCTGTCTCCGGGTAAA 687
              |||||||||||||||||||||
Db        983 CTCTCCCTGTCTCCGGGTAAA 1003
```

```
RESULT 15
CR595194
LOCUS       CR595194               1103 bp    mRNA    linear   HTC 21-JUL-2004
DEFINITION  full-length cDNA clone CS0DE010YH13 of Placenta of Homo sapiens
            (human).
ACCESSION   CR595194
VERSION     CR595194.1  GI:50476001
KEYWORDS    HTC; CNSLT_cDNA.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1103)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished
  REMARK    Contact : Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue
REFERENCE   2  (bases 1 to 1103)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen.
FEATURES             Location/Qualifiers
     source          1. .1103
```

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DE010YH13"
/tissue_type="Placenta"
/plasmid="pCMVSPORT_6"

ORIGIN

Query Match 57.7%; Score 655.4; DB 3; Length 1103;
Best Local Similarity 97.7%; Pred. No. 3.9e-160;
Matches 665; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

```
Qy          7 GACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCGTCAGTC 66
              ||||||||||||||||||||||||||||||| || ||||||   || || |||||||||
Db        319 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC 378

Qy         67 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        379 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 438

Qy        127 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        439 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 498

Qy        187 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        499 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 558

Qy        247 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCTTACGCA 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||  |  |||
Db        559 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 618

Qy        307 TGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 366
              |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        619 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 678

Qy        367 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        679 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 738

Qy        427 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        739 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 798

Qy        487 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        799 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 858

Qy        547 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        859 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 918

Qy        607 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 666
              |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db        919 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACACAGAAGAGC 978

Qy        667 CTCTCCCTGTCTCCGGGTAAA 687
              |||||||||||||||||||||
Db        979 CTCTCCCTGTCTCCGGGTAAA 999
```

Search completed: October 18, 2004, 03:14:40
Job time : 3995.86 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 17, 2004, 15:27:12 ; Search time 588.611 Seconds
(without alignments)
10122.301 Million cell updates/sec

Title: US-10-679-999-16
Perfect score: 1135
Sequence: 1 CATATGGACAAAACTCACAC.....TCCGGGTTGTTAATGGATCC 1135

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_23Sep04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1135	100.0	1135	2	AAV32903	Aav32903 Recombina
2	1109.4	97.7	1135	2	AAV32902	Aav32902 Recombina
3	1109.4	97.7	1135	2	AAV69686	Aav69686 Recombina
4	1105	97.4	1150	2	AAV32900	Aav32900 Recombina
5	1105	97.4	1150	2	AAV69685	Aav69685 Recombina
6	1103.4	97.2	1150	2	AAV32901	Aav32901 Recombina
7	662.4	58.4	748	6	ABL35776	Abl35776 Fc-MMP in
8	662.4	58.4	757	3	AAA69501	Aaa69501 Fc-TNF-al
9	662.4	58.4	757	6	ABL35770	Abl35770 Fc-TNF-al
10	662.4	58.4	763	3	AAA69503	Aaa69503 Fc-IL-1 a
11	662.4	58.4	777	12	ADM17769	Adm17769 Fc C-term
12	662.4	58.4	794	3	AAA69444	Aaa69444 Fc-TMP nu
13	662.4	58.4	794	6	ABL35761	Abl35761 Fc-TPO mi
14	662.4	58.4	812	3	AAA69448	Aaa69448 Fc-EMP nu
15	662.4	58.4	812	6	ABL35765	Abl35765 Fc-EPO mi
16	662.4	58.4	837	11	ADN59745	Adn59745 Vector 20
17	662.4	58.4	859	6	ABK24109	Abk24109 DNA encod
18	662.4	58.4	861	3	AAA29229	Aaa29229 Human IgG
19	662.4	58.4	861	3	AAA69445	Aaa69445 Fc-TMP-TM
20	662.4	58.4	861	6	ABL35762	Abl35762 Fc-TMP-TM
21	660.8	58.2	748	3	AAA69507	Aaa69507 Fc-MMP in
22	660.8	58.2	763	6	ABL35772	Abl35772 Fc-interl
23	660.8	58.2	773	3	AAA69505	Aaa69505 Fc-VEGF a
24	660.8	58.2	773	6	ABL35774	Abl35774 Fc-VEGF a
25	659.4	58.1	7285	10	ABT33869	Abt33869 TALL-1 re
26	659.2	58.1	1002	12	ADN97484	Adn97484 Artificia
27	659.2	58.1	2154	12	ADN97490	Adn97490 Artificia
28	659.2	58.1	2160	12	ADN97488	Adn97488 Artificia
29	659.2	58.1	2190	4	ABA02694	Aba02694 Humanised
30	659.2	58.1	2220	4	ABA02700	Aba02700 Humanised
31	659	58.1	1288	3	AAC67833	Aac67833 Fc-huAGP-
32	658.8	58.0	1304	6	AAK98732	Aak98732 DNA of a
33	658.8	58.0	1377	5	AAA91076	Aaa91076 Flt1 rece
34	658.8	58.0	1377	6	ABQ74610	Abq74610 Modified
35	658.6	58.0	1467	3	AAA52132	Aaa52132 Human FGF
36	658.6	58.0	1494	3	AAA52131	Aaa52131 Human FGF
37	658.6	58.0	1578	3	AAA52130	Aaa52130 Human FGF
38	658.4	58.0	684	3	AAA29220	Aaa29220 Human IgG
39	658.4	58.0	684	3	AAA69443	Aaa69443 Human IgG
40	658.4	58.0	684	5	AAH25762	Aah25762 Human IgG
41	658.4	58.0	684	6	ABA03672	Aba03672 Human IgG
42	658.4	58.0	684	6	ABK24097	Abk24097 Human cDN
43	658.4	58.0	684	6	AAD23840	Aad23840 Human imm
44	658.4	58.0	684	6	ABL35760	Abl35760 Human imm
45	658.4	58.0	684	6	AAI67658	Aai67658 Human imm

ALIGNMENTS

RESULT 1
AAV32903
ID AAV32903 standard; cDNA; 1135 BP.
XX
AC AAV32903;
XX
DT 18-NOV-1998 (first entry)
XX
DE Recombinant human MetFc-OB variant 3 cDNA.
XX
KW Recombinant human MetFc-OB variant 3 cDNA; chimeric; immunoglobulin;
KW high blood lipid level; arterial sclerosis; stroke; Fc-OB fusion protein;
KW diabetes; ds.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT CDS 4. .1128
FT /*tag= a
FT /product= "Recombinant human Fc-OB variant 3"
FT mat_peptide 7. .1125
FT /*tag= b
FT misc_feature 685. .1125
FT /*tag= c
FT /note= "Encodes for the OB part of the fusion protein"
XX
PN WO9828427-A1.
XX
PD 02-JUL-1998.
XX
PF 11-DEC-1997; 97WO-US023183.
XX
PR 20-DEC-1996; 96US-00770973.
XX
PA (AMGE-) AMGEN INC.
XX
PI Mann MB, Hecht RI;
XX
DR WPI; 1998-377658/32.
DR P-PSDB; AAW49076.
XX
PT New fusion proteins of OB and Fc - used for treating e.g. excess weight,
PT diabetes, arterial sclerosis, arterial plaque, high blood lipid level,

```
PT   gall stones or stroke.
XX
PS   Disclosure; Fig 6A-6C; 107pp; English.
XX
CC   The present sequence represents a recombinant human MetFc-OB variant 3
CC   cDNA which encodes a recombinant human Fc-OB fusion variant 3 protein
CC   having the L16E, E99A, K101A and K103A substitutions when compared with
CC   the template protein shown in AAW49075. The invention provides Fc-OB
CC   fusion proteins whereby the Fc region of an immunoglobulin or its
CC   analogue is linked, either directly or indirectly using a linker, to the
CC   N-terminus of an OB protein or its analogue. The Fc-OB fusion proteins
CC   are claimed to demonstrate increased stability and clearance rate and
CC   decreased degradation as compared to OB protein or a fusion of Fc to the
CC   C-terminus of the OB protein. These Fc-OB fusion proteins are also
CC   claimed to be useful for treating excess weight in an individual or
CC   animal or for treating co-morbidities associated with excess fat such as
CC   diabetes, high blood lipid level, arterial sclerosis and stroke
XX
SQ   Sequence 1135 BP; 270 A; 365 C; 283 G; 217 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 1135;  DB 2;  Length 1135;
  Best Local Similarity   100.0%;  Pred. No. 3e-253;
  Matches 1135;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CATATGGACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CATATGGACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCG 60

Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120

Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180

Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240

Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCT 300

Qy        301 TACGCATGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TACGCATGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360

Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420

Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480

Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540

Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600

Qy        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660

Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTTCAGGACGACACCAAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTTCAGGACGACACCAAA 720

Qy        721 ACCTTAATTAAAACGATCGTTACGCGTATCAACGACATCAGTCACACCCAGTCGGTGAGC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ACCTTAATTAAAACGATCGTTACGCGTATCAACGACATCAGTCACACCCAGTCGGTGAGC 780

Qy        781 TCTAAACAGAAAGTTACAGGCCTGGACTTCATCCCGGGTCTGCACCCGATCCTGACCTTG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TCTAAACAGAAAGTTACAGGCCTGGACTTCATCCCGGGTCTGCACCCGATCCTGACCTTG 840

Qy        841 TCCAAAATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACCTCCATGCCGTCCCGT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TCCAAAATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACCTCCATGCCGTCCCGT 900

Qy        901 AACGTTATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTGCTGCACGTGCTGGCA 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 AACGTTATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTGCTGCACGTGCTGGCA 960

Qy        961 TTCTCCAAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACTCTGGACTCTCTGGGC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TTCTCCAAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACTCTGGACTCTCTGGGC 1020

Qy       1021 GGGGTCCTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTGTCCCGTCTGCAGGGT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GGGGTCCTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTGTCCCGTCTGCAGGGT 1080

Qy       1081 TCCCTTCAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGTTAATGGATCC 1135
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TCCCTTCAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGTTAATGGATCC 1135


RESULT 2
AAV32902
ID   AAV32902 standard; cDNA; 1135 BP.
XX
AC   AAV32902;
XX
DT   18-NOV-1998  (first entry)
XX
DE   Recombinant human MetFc-OB variant 2 cDNA.
XX
KW   Recombinant human MetFc-OB variant 2 cDNA; chimeric; immunoglobulin;
KW   high blood lipid level; arterial sclerosis; stroke; Fc-OB fusion protein;
KW   diabetes; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             4. .1128
FT                   /*tag= a
FT                   /product= "Recombinant human Fc-OB variant 2"
FT   mat_peptide     7. .1125
FT                   /*tag= b
FT   misc_feature    685. .1125
FT                   /*tag= c
FT                   /note= "Encodes for the OB part of the fusion protein"
XX
PN   WO9828427-A1.
XX
PD   02-JUL-1998.
XX
PF   11-DEC-1997;   97WO-US023183.
XX
PR   20-DEC-1996;   96US-00770973.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Mann MB,  Hecht RI;
XX
DR   WPI; 1998-377658/32.
DR   P-PSDB; AAW49075.
XX
PT   New fusion proteins of OB and Fc - used for treating e.g. excess weight,
PT   diabetes, arterial sclerosis, arterial plaque, high blood lipid level,
PT   gall stones or stroke.
```

XX
PS Disclosure; Fig 5A-5C; 107pp; English.
XX
CC The present sequence represents a recombinant human MetFc-OB variant 2
CC cDNA which encodes a recombinant human Fc-OB fusion variant 2 protein
CC having a 5 residue deletion of residues 2-6 of the wild-type Fc-OB
CC protein sequence shown in AAW49073. The invention provides Fc-OB fusion
CC proteins whereby the Fc region of an immunoglobulin or its analogue is
CC linked, either directly or indirectly using a linker, to the N-terminus
CC of an OB protein or its analogue. The Fc-OB fusion proteins are claimed
CC to demonstrate increased stability and clearance rate and decreased
CC degradation as compared to OB protein or a fusion of Fc to the C-terminus
CC of the OB protein. These Fc-OB fusion proteins are also claimed to be
CC useful for treating excess weight in an individual or animal or for
CC treating co-morbidities associated with excess fat such as diabetes, high
CC blood lipid level, arterial sclerosis and stroke
XX
SQ Sequence 1135 BP; 271 A; 361 C; 283 G; 220 T; 0 U; 0 Other;

Query Match 97.7%; Score 1109.4; DB 2; Length 1135;
Best Local Similarity 98.6%; Pred. No. 2.5e-247;
Matches 1119; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

```
Qy          1 CATATGGACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCG 60
              ||||||||||||||||||||||| ||||| || |||||||||||||||   || |||||
Db          1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGTCCT 60

Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120

Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180

Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240

Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCT 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300

Qy        301 TACGCATGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
              |||   |||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360

Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420

Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480

Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540

Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600

Qy        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660

Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTTCAGGACGACACCAAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTTCAGGACGACACCAAA 720

Qy        721 ACCTTAATTAAAACGATCGTTACGCGTATCAACGACATCAGTCACACCCAGTCGGTGAGC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ACCTTAATTAAAACGATCGTTACGCGTATCAACGACATCAGTCACACCCAGTCGGTGAGC 780

Qy        781 TCTAAACAGAAAGTTACAGGCCTGGACTTCATCCCGGGTCTGCACCCGATCCTGACCTTG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TCTAAACAGAAAGTTACAGGCCTGGACTTCATCCCGGGTCTGCACCCGATCCTGACCTTG 840

Qy        841 TCCAAAATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACCTCCATGCCGTCCCGT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TCCAAAATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACCTCCATGCCGTCCCGT 900

Qy        901 AACGTTATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTGCTGCACGTGCTGGCA 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 AACGTTATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTGCTGCACGTGCTGGCA 960

Qy        961 TTCTCCAAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACTCTGGACTCTCTGGGC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TTCTCCAAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACTCTGGACTCTCTGGGC 1020

Qy       1021 GGGGTCCTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTGTCCCGTCTGCAGGGT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GGGGTCCTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTGTCCCGTCTGCAGGGT 1080

Qy       1081 TCCCTTCAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGTTAATGGATCC 1135
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TCCCTTCAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGTTAATGGATCC 1135
```

RESULT 3
AAV69686
ID AAV69686 standard; DNA; 1135 BP.
XX
AC AAV69686;
XX
DT 05-FEB-1999 (first entry)
XX
DE Recombinant human metFc-OB protein variant encoding DNA.
XX
KW Recombinant; metFc-OB protein; Fc region; immunoglobulin; Ig; OB;
KW obesity; human; adiposity; blood lipid; diabetes type II; insulin;
KW hypoglycaemic; antihypertensive; diuretic; appetite suppressant;
KW suspension; variant; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 4. .1128
FT /*tag= a
FT /product= "metFc-OB protein variant"
XX
PN WO9846257-A1.
XX
PD 22-OCT-1998.
XX
PF 16-APR-1998; 98WO-US007828.
XX
PR 17-APR-1997; 97US-00843971.
PR 14-APR-1998; 98US-00059467.
XX
PA (AMGE-) AMGEN INC.
XX
PI Brems DN, French DL, Speed MA;
XX
DR WPI; 1998-594525/50.
DR P-PSDB; AAW83963.
XX
PT Concentrated suspension of fusion of obesity protein with Fc
PT immunoglobulin fragment - stable at physiological pH, used for e.g.
PT reduction of weight and blood lipid levels, and for treatment of type II
PT diabetes.
XX
PS Disclosure; Fig 6A-C; 47pp; English.
XX
CC This DNA encodes a recombinant metFc-OB protein variant which consists of

```
CC   an Fc region of human immunoglobulin (Ig) fused to a human OB (obesity)
CC   protein. The invention provides a human OB protein suspension that
CC   contains at least 0.5 mg/ml of the human OB protein derivatised by
CC   attachment of the Fc region of an Ig to the N-terminus of OB, and has a
CC   pH 6-8. The suspensions are used to reduce weight, adiposity and blood
CC   lipid levels, to treat or prevent diabetes type II, and to increase lean
CC   mass and insulin sensitivity. They may be used in conjunction with
CC   insulin, hypoglycaemics, antihypertensives, diuretics, appetite
CC   suppressants etc. These suspensions are stable and active at
CC   physiological pH and are ready-for-use formulations that do not require
CC   freezing or freeze drying. As they are very concentrated, only small
CC   volumes are required and they provide a sustained-release effect, with
CC   increased potency and reduced frequency of injection
XX
SQ   Sequence 1135 BP; 271 A; 361 C; 283 G; 220 T; 0 U; 0 Other;

  Query Match             97.7%;  Score 1109.4;  DB 2;  Length 1135;
  Best Local Similarity   98.6%;  Pred. No. 2.5e-247;
  Matches 1119;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          1 CATATGGACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCG 60
              |||||||||||||||||||||| ||||| || ||||||||||||||    || |||||
Db          1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGTCCT 60

Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120

Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180

Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240

Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCT 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300

Qy        301 TACGCATGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
              |||   |||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360

Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420

Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480

Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540

Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600

Qy        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660

Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTTCAGGACGACACCAAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTTCAGGACGACACCAAA 720

Qy        721 ACCTTAATTAAAACGATCGTTACGCGTATCAACGACATCAGTCACACCCAGTCGGTGAGC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ACCTTAATTAAAACGATCGTTACGCGTATCAACGACATCAGTCACACCCAGTCGGTGAGC 780

Qy        781 TCTAAACAGAAAGTTACAGGCCTGGACTTCATCCCGGGTCTGCACCCGATCCTGACCTTG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TCTAAACAGAAAGTTACAGGCCTGGACTTCATCCCGGGTCTGCACCCGATCCTGACCTTG 840

Qy        841 TCCAAAATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACCTCCATGCCGTCCCGT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TCCAAAATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACCTCCATGCCGTCCCGT 900

Qy        901 AACGTTATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTGCTGCACGTGCTGGCA 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 AACGTTATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTGCTGCACGTGCTGGCA 960

Qy        961 TTCTCCAAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACTCTGGACTCTCTGGGC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TTCTCCAAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACTCTGGACTCTCTGGGC 1020

Qy       1021 GGGGTCCTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTGTCCCGTCTGCAGGGT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GGGGTCCTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTGTCCCGTCTGCAGGGT 1080

Qy       1081 TCCCTTCAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGTTAATGGATCC 1135
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TCCCTTCAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGTTAATGGATCC 1135


RESULT 4
AAV32900
ID   AAV32900 standard; cDNA; 1150 BP.
XX
AC   AAV32900;
XX
DT   18-NOV-1998  (first entry)
XX
DE   Recombinant human MetFc-OB cDNA.
XX
KW   Recombinant human MetFc-OB cDNA; chimeric; immunoglobulin; diabetes;
KW   high blood lipid level; arterial sclerosis; stroke; Fc-OB fusion protein;
KW   ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             4. .1143
FT                   /*tag=  a
FT                   /product= "Recombinant human Fc-OB"
FT   mat_peptide     7. .1140
FT                   /*tag=  b
FT   misc_feature    700. .1140
FT                   /*tag=  c
FT                   /note= "Encodes for the OB part of the fusion protein"
FT
XX
PN   WO9828427-A1.
XX
PD   02-JUL-1998.
XX
PF   11-DEC-1997;   97WO-US023183.
XX
PR   20-DEC-1996;   96US-00770973.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Mann MB,  Hecht RI;
XX
DR   WPI; 1998-377658/32.
DR   P-PSDB; AAW49073.
XX
PT   New fusion proteins of OB and Fc - used for treating e.g. excess weight,
PT   diabetes, arterial sclerosis, arterial plaque, high blood lipid level,
PT   gall stones or stroke.
XX
PS   Disclosure; Fig 3A-3C; 107pp; English.
XX
CC   The present sequence represents a recombinant human MetFc-OB cDNA which
```

CC encodes a recombinant human Fc-OB fusion protein. The invention provides
CC Fc-OB fusion proteins whereby the Fc region of an immunoglobulin or its
CC analogue is linked, either directly or indirectly using a linker, to the
CC N-terminus of an OB protein or its analogue. The Fc-OB fusion proteins
CC are claimed to demonstrate increased stability and clearance rate and
CC decreased degradation as compared to OB protein or a fusion of Fc to the
CC C-terminus of the OB protein. These Fc-OB fusion proteins are also
CC claimed to be useful for treating excess weight in an individual or
CC animal or for treating co-morbidities associated with excess fat such as
CC diabetes, high blood lipid level, arterial sclerosis and stroke
XX
SQ Sequence 1150 BP; 278 A; 367 C; 286 G; 219 T; 0 U; 0 Other;

Query Match 97.4%; Score 1105; DB 2; Length 1150;
Best Local Similarity 98.7%; Pred. No. 2.7e-246;
Matches 1114; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

```
Qy          7 GACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCGTCAGTC 66
              ||||||||||||||||||||||||||||||| || ||||||  || || |||||||||
Db         22 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC 81

Qy         67 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         82 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 141

Qy        127 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        142 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 201

Qy        187 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        202 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 261

Qy        247 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCTTACGCA 306
              |||||||||||||||||||||||||||||||||||||||||||||||||| |  |||
Db        262 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 321

Qy        307 TGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 366
              |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        322 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 381

Qy        367 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        382 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 441

Qy        427 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        442 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 501

Qy        487 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        502 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 561

Qy        547 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        562 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 621

Qy        607 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        622 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 681

Qy        667 CTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTTCAGGACGACACCAAAACCTTA 726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        682 CTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTTCAGGACGACACCAAAACCTTA 741

Qy        727 ATTAAAACGATCGTTACGCGTATCAACGACATCAGTCACACCCAGTCGGTGAGCTCTAAA 786
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        742 ATTAAAACGATCGTTACGCGTATCAACGACATCAGTCACACCCAGTCGGTGAGCTCTAAA 801

Qy        787 CAGAAAGTTACAGGCCTGGACTTCATCCCGGGTCTGCACCCGATCCTGACCTTGTCCAAA 846
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        802 CAGAAAGTTACAGGCCTGGACTTCATCCCGGGTCTGCACCCGATCCTGACCTTGTCCAAA 861

Qy        847 ATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACCTCCATGCCGTCCCGTAACGTT 906
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        862 ATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACCTCCATGCCGTCCCGTAACGTT 921

Qy        907 ATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTGCTGCACGTGCTGGCATTCTCC 966
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        922 ATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTGCTGCACGTGCTGGCATTCTCC 981

Qy        967 AAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACTCTGGACTCTCTGGGCGGGGTC 1026
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        982 AAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACTCTGGACTCTCTGGGCGGGGTC 1041

Qy       1027 CTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTGTCCCGTCTGCAGGGTTCCCTT 1086
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1042 CTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTGTCCCGTCTGCAGGGTTCCCTT 1101

Qy       1087 CAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGTTAATGGATCC 1135
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db       1102 CAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGTTAATGGATCC 1150
```

RESULT 5
AAV69685
ID AAV69685 standard; DNA; 1150 BP.
XX
AC AAV69685;
XX
DT 05-FEB-1999 (first entry)
XX
DE Recombinant human metFc-OB protein encoding DNA.
XX
KW Recombinant; metFc-OB protein; Fc region; immunoglobulin; Ig; OB;
KW obesity; human; adiposity; blood lipid; diabetes type II; insulin;
KW hypoglycaemic; antihypertensive; diuretic; appetite suppressant;
KW suspension; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 4. .1143
FT /*tag= a
FT /product= "metFc-OB protein"
XX
PN WO9846257-A1.
XX
PD 22-OCT-1998.
XX
PF 16-APR-1998; 98WO-US007828.
XX
PR 17-APR-1997; 97US-00843971.
PR 14-APR-1998; 98US-00059467.
XX
PA (AMGE-) AMGEN INC.
XX
PI Brems DN, French DL, Speed MA;
XX
DR WPI; 1998-594525/50.
DR P-PSDB; AAW83962.
XX
PT Concentrated suspension of fusion of obesity protein with Fc
PT immunoglobulin fragment - stable at physiological pH, used for e.g.
PT reduction of weight and blood lipid levels, and for treatment of type II
PT diabetes.
XX
PS Disclosure; Fig 5A-C; 47pp; English.
XX
CC This DNA encodes a recombinant metFc-OB protein which consists of an Fc
CC region of human immunoglobulin (Ig) fused to a human OB (obesity)
CC protein. The invention provides a human OB protein suspension that
CC contains at least 0.5 mg/ml of the human OB protein derivatised by
CC attachment of the Fc region of an Ig to the N-terminus of OB, and has a
CC pH 6-8. The suspensions are used to reduce weight, adiposity and blood
CC lipid levels, to treat or prevent diabetes type II, and to increase lean

```
CC   mass and insulin sensitivity. They may be used in conjunction with
CC   insulin, hypoglycaemics, antihypertensives, diuretics, appetite
CC   suppressants etc. These suspensions are stable and active at
CC   physiological pH and are ready-for-use formulations that do not require
CC   freezing or freeze drying. As they are very concentrated, only small
CC   volumes are required and they provide a sustained-release effect, with
CC   increased potency and reduced frequency of injection
XX
SQ   Sequence 1150 BP; 278 A; 367 C; 286 G; 219 T; 0 U; 0 Other;

  Query Match             97.4%;  Score 1105;  DB 2;  Length 1150;
  Best Local Similarity   98.7%;  Pred. No. 2.7e-246;
  Matches 1114;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          7 GACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCGTCAGTC 66
              |||||||||||||||||||||||||||||||| || ||||||   || || |||||||||
Db         22 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC 81

Qy         67 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         82 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 141

Qy        127 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        142 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 201

Qy        187 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        202 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 261

Qy        247 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCTTACGCA 306
              |||||||||||||||||||||||||||||||||||||||||||||||| |   |||
Db        262 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 321

Qy        307 TGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 366
              |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        322 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 381

Qy        367 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        382 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 441

Qy        427 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        442 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 501

Qy        487 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        502 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 561

Qy        547 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        562 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 621

Qy        607 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        622 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 681

Qy        667 CTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTTCAGGACGACACCAAAACCTTA 726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        682 CTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTTCAGGACGACACCAAAACCTTA 741

Qy        727 ATTAAAACGATCGTTACGCGTATCAACGACATCAGTCACACCCAGTCGGTGAGCTCTAAA 786
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        742 ATTAAAACGATCGTTACGCGTATCAACGACATCAGTCACACCCAGTCGGTGAGCTCTAAA 801

Qy        787 CAGAAAGTTACAGGCCTGGACTTCATCCCGGGTCTGCACCCGATCCTGACCTTGTCCAAA 846
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        802 CAGAAAGTTACAGGCCTGGACTTCATCCCGGGTCTGCACCCGATCCTGACCTTGTCCAAA 861

Qy        847 ATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACCTCCATGCCGTCCCGTAACGTT 906
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        862 ATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACCTCCATGCCGTCCCGTAACGTT 921

Qy        907 ATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTGCTGCACGTGCTGGCATTCTCC 966
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        922 ATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTGCTGCACGTGCTGGCATTCTCC 981

Qy        967 AAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACTCTGGACTCTCTGGGCGGGGTC 1026
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        982 AAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACTCTGGACTCTCTGGGCGGGGTC 1041

Qy       1027 CTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTGTCCCGTCTGCAGGGTTCCCTT 1086
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1042 CTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTGTCCCGTCTGCAGGGTTCCCTT 1101

Qy       1087 CAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGTTAATGGATCC 1135
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db       1102 CAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGTTAATGGATCC 1150


RESULT 6
AAV32901
ID   AAV32901 standard; cDNA; 1150 BP.
XX
AC   AAV32901;
XX
DT   18-NOV-1998  (first entry)
XX
DE   Recombinant human MetFc-OB variant 1 cDNA.
XX
KW   Recombinant human MetFc-OB variant 1 cDNA; chimeric; immunoglobulin;
KW   high blood lipid level; arterial sclerosis; stroke; Fc-OB fusion protein;
KW   diabetes; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             4. .1143
FT                   /*tag= a
FT                   /product= "Recombinant human Fc-OB variant 1"
FT   mat_peptide     7. .1140
FT                   /*tag= b
FT   mutation        19. .21
FT                   /*tag= c
FT                   /note= "Changed from TGT in wild-type (AAV32900) to GCT
FT                   in mutant"
FT   misc_feature    700. .1140
FT                   /*tag= d
FT                   /note= "Encodes for the OB part of the fusion protein"
XX
PN   WO9828427-A1.
XX
PD   02-JUL-1998.
XX
PF   11-DEC-1997;   97WO-US023183.
XX
PR   20-DEC-1996;   96US-00770973.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Mann MB,  Hecht RI;
XX
DR   WPI; 1998-377658/32.
DR   P-PSDB; AAW49074.
XX
PT   New fusion proteins of OB and Fc - used for treating e.g. excess weight,
PT   diabetes, arterial sclerosis, arterial plaque, high blood lipid level,
PT   gall stones or stroke.
XX
PS   Disclosure; Fig 4A-4C; 107pp; English.
XX
CC   The present sequence represents a recombinant human MetFc-OB variant 1
CC   cDNA which encodes a recombinant human Fc-OB fusion variant 1 protein
CC   having a C6A substitution when compared with the wild-type Fc-OB protein
```

CC sequence shown in AAW49073. The invention provides Fc-OB fusion proteins
CC whereby the Fc region of an immunoglobulin or its analogue is linked,
CC either directly or indirectly using a linker, to the N-terminus of an OB
CC protein or its analogue. The Fc-OB fusion proteins are claimed to
CC demonstrate increased stability and clearance rate and decreased
CC degradation as compared to OB protein or a fusion of Fc to the C-terminus
CC of the OB protein. These Fc-OB fusion proteins are also claimed to be
CC useful for treating excess weight in an individual or animal or for
CC treating co-morbidities associated with excess fat such as diabetes, high
CC blood lipid level, arterial sclerosis and stroke
XX
SQ Sequence 1150 BP; 277 A; 365 C; 285 G; 223 T; 0 U; 0 Other;

Query Match 97.2%; Score 1103.4; DB 2; Length 1150;
Best Local Similarity 98.6%; Pred. No. 6.3e-246;
Matches 1113; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

```
Qy          7 GACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCGTCAGTC 66
              |||||||||||||||| ||||| || ||||||||||||||   || ||||| ||||||
Db         22 GACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGTCCTTCAGTC 81

Qy         67 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         82 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 141

Qy        127 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        142 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 201

Qy        187 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        202 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 261

Qy        247 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCTTACGCA 306
              |||||||||||||||||||||||||||||||||||||||||||||||||||| |  |||
Db        262 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 321

Qy        307 TGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 366
              |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        322 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 381

Qy        367 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        382 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 441

Qy        427 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        442 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 501

Qy        487 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        502 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 561

Qy        547 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        562 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 621

Qy        607 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        622 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 681

Qy        667 CTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTTCAGGACGACACCAAAACCTTA 726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        682 CTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTTCAGGACGACACCAAAACCTTA 741

Qy        727 ATTAAAACGATCGTTACGCGTATCAACGACATCAGTCACACCCAGTCGGTGAGCTCTAAA 786
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        742 ATTAAAACGATCGTTACGCGTATCAACGACATCAGTCACACCCAGTCGGTGAGCTCTAAA 801

Qy        787 CAGAAAGTTACAGGCCTGGACTTCATCCCGGGTCTGCACCCGATCCTGACCTTGTCCAAA 846
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        802 CAGAAAGTTACAGGCCTGGACTTCATCCCGGGTCTGCACCCGATCCTGACCTTGTCCAAA 861

Qy        847 ATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACCTCCATGCCGTCCCGTAACGTT 906
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        862 ATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACCTCCATGCCGTCCCGTAACGTT 921

Qy        907 ATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTGCTGCACGTGCTGGCATTCTCC 966
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        922 ATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTGCTGCACGTGCTGGCATTCTCC 981

Qy        967 AAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACTCTGGACTCTCTGGGCGGGGTC 1026
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        982 AAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACTCTGGACTCTCTGGGCGGGGTC 1041

Qy       1027 CTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTGTCCCGTCTGCAGGGTTCCCTT 1086
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1042 CTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTGTCCCGTCTGCAGGGTTCCCTT 1101

Qy       1087 CAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGTTAATGGATCC 1135
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db       1102 CAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGTTAATGGATCC 1150
```

RESULT 7
ABL35776
ID ABL35776 standard; DNA; 748 BP.
XX
AC ABL35776;
XX
DT 05-APR-2002 (first entry)
XX
DE Fc-MMP inhibitor fusion amino acid SEQ ID NO:1068.
XX
KW Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; IgG; EPO;
KW erythropoietin; TPO; tumour necrosis factor alpha inhibitor;
KW TNF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TMP;
KW TPO mimetic peptide; EPO mimetic peptide; EMP; VEGF antagonist;
KW MMP inhibitor; antiinflammatory; antitumour; immunosuppressive;
KW cytostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological;
KW antianaemic; anorectic; antiinfertility; haemostatic; dermatological;
KW neuroprotective; inflammatory disease; autoimmune disease; tumour growth;
KW cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity;
KW sleep disorder; neurological degenerative disease; anaemia;
KW thrombocytopaenia; metastatic tumour; systemic lupus erythematosus;
KW Fanconi's syndrome; gene; ds.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200183525-A2.
XX
PD 08-NOV-2001.
XX
PF 02-MAY-2001; 2001WO-US014310.
XX
PR 03-MAY-2000; 2000US-00563286.
XX
PA (AMGE-) AMGEN INC.
XX
PI Feige U, Liu C, Cheetham JC, Boone TC, Gudas JM;
XX
DR WPI; 2002-130313/17.
DR P-PSDB; ABB73426.
XX
PT Novel vehicle-peptide molecule or its multimers useful for treating
PT inflammatory and autoimmune diseases, cancer, rheumatoid arthritis,
PT diabetic retinopathy, obesity, sleep disorders and infertility.
XX
PS Example 7; Fig 25A-B; 176pp; English.
XX
CC The present invention describes a vehicle-peptide molecule (I) or its
CC multimers. (I) can have antiinflammatory, antitumour, immunosuppressive,
CC cytostatic, antirheumatic, antiarthritic, antidiabetic, ophthalmological,
CC antianaemic, anorectic, antiinfertility, haemostatic, dermatological and
CC neuroprotective activities. (I) can be used as a therapeutic or

CC prophylactic agent as well as for screening purposes. (I) is useful for
CC diagnosing diseases characterised by dysfunction of their associated
CC protein of interest, for identifying normal or abnormal proteins of
CC interest, as a part of diagnostic kit to detect the presence of their
CC proteins of interest in a biological sample. Additionally, (I) is useful
CC for treating inflammatory and autoimmune diseases, tumour growth, cancer,
CC rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders,
CC infertility, and neurological degenerative diseases. (I), comprising EPO-
CC mimetic compounds are useful for treating disorders characterised by low
CC red blood cell levels such as anaemia. The TPO-mimetic comprising
CC compounds are useful for treating conditions that involve an existing
CC megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet
CC deficiency, such as thrombocytopaenia, aplastic anaemia, metastatic
CC tumour which result in thrombocytopaenia, systemic lupus erythematosus,
CC and Fanconi's syndrome. ABB72403 to ABB73426 and ABL35695 to ABL35777
CC represent amino acid and nucleic acid sequences used in the
CC exemplification of the present invention
XX
SQ Sequence 748 BP; 180 A; 240 C; 201 G; 127 T; 0 U; 0 Other;

Query Match 58.4%; Score 662.4; DB 6; Length 748;
Best Local Similarity 97.7%; Pred. No. 9.8e-144;
Matches 672; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

```
Qy          1 CATATGGACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCG 60
              |||||||||||||||||||||||| ||||| || ||||||||||||||    || || |||
Db          1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCG 60

Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120

Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180

Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240

Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCT 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300

Qy        301 TACGCATGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
              |||   |||  ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360

Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420

Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480

Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540

Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600

Qy        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660

Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
              |||||||||||||||||||||||||||
Db        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
```

RESULT 8
AAA69501
ID AAA69501 standard; DNA; 757 BP.
XX
AC AAA69501;
XX
DT 31-OCT-2000 (first entry)
XX
DE Fc-TNF-alpha inhibitor fusion nucleotide sequence SEQ ID NO:1055.
XX
KW Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
KW autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;
KW immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP;
KW inhibitor; erythropoietin; thrombopoietin; interleukin 1;
KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
KW vascular endothelial growth factor; matrix metalloproteinase; asthma;
KW thrombosis; pharmaceutical; ds.
XX
OS Synthetic.
XX
PN WO200024782-A2.
XX
PD 04-MAY-2000.
XX
PF 25-OCT-1999; 99WO-US025044.
XX
PR 23-OCT-1998; 98US-0105371P.
PR 22-OCT-1999; 99US-00428082.
XX
PA (AMGE-) AMGEN INC.
XX
PI Feige U, Liu C, Cheetham J, Boone TC;
XX
DR WPI; 2000-350702/30.
DR P-PSDB; AAB17951.
XX
PT Novel composition of matter comprising an Fc domain and pharmacologically
PT active peptides, useful for treating cancer and autoimmune diseases.
XX
PS Example 4; Page 566-568; 608pp; English.
XX
CC The present invention describes composition of matter (I) comprising an
CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
CC (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
CC independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-
CC (L2)d-P2-(L3)e-P^3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2,
CC P3, and P4 = are each independently sequences of pharmacologically active
CC peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b,
CC c, d, e, and f = are each independently 0 or 1, provided that at least 1
CC of a and b is 1. The composition can have cytostatic, antiasthmatic,
CC thrombolytic and immunosuppressive activities. DNAs, vectors and host
CC cells from the present invention can be used for producing pharmaceutical
CC compositions. The compositions are useful for treating cancer, asthma,
CC thrombosis, or autoimmune diseases. The use of an Fc domain (rather than
CC a Fab domain) can provide a longer half-life or incorporate functions
CC such as Fc receptor binding, protein A binding, complement fixation, and
CC possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to
CC AAB18003 represent nucleotide and amino acid sequences used in the
CC exemplification of the present invention
XX
SQ Sequence 757 BP; 185 A; 244 C; 200 G; 128 T; 0 U; 0 Other;

Query Match 58.4%; Score 662.4; DB 3; Length 757;
Best Local Similarity 97.7%; Pred. No. 9.8e-144;
Matches 672; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

```
Qy          1 CATATGGACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCG 60
              |||||||||||||||||||||||| ||||| || ||||||||||||||    || || |||
Db          1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCG 60

Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
```

```
Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180

Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240

Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300

Qy        301 TACGCATGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
              |||   |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360

Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420

Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480

Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540

Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600

Qy        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660

Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
              ||||||||||||||||||||||||||||
Db        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
```

RESULT 9
ABL35770
ID ABL35770 standard; DNA; 757 BP.
XX
AC ABL35770;
XX
DT 05-APR-2002 (first entry)
XX
DE Fc-TNF-alpha inhibitor fusion amino acid SEQ ID NO:1056.
XX
KW Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; IgG; EPO;
KW erythropoietin; TPO; tumour necrosis factor alpha inhibitor;
KW TNF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TMP;
KW TPO mimetic peptide; EPO mimetic peptide; EMP; VEGF antagonist;
KW MMP inhibitor; antiinflammatory; antitumour; immunosuppressive;
KW cytostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological;
KW antianaemic; anorectic; antiinfertility; haemostatic; dermatological;
KW neuroprotective; inflammatory disease; autoimmune disease; tumour growth;
KW cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity;
KW sleep disorder; neurological degenerative disease; anaemia;
KW thrombocytopaenia; metastatic tumour; systemic lupus erythematosus;
KW Fanconi's syndrome; gene; ds.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200183525-A2.
XX
PD 08-NOV-2001.
XX
PF 02-MAY-2001; 2001WO-US014310.
XX
PR 03-MAY-2000; 2000US-00563286.
XX
PA (AMGE-) AMGEN INC.
XX
PI Feige U, Liu C, Cheetham JC, Boone TC, Gudas JM;
XX
DR WPI; 2002-130313/17.
DR P-PSDB; ABB73420.
XX
PT Novel vehicle-peptide molecule or its multimers useful for treating
PT inflammatory and autoimmune diseases, cancer, rheumatoid arthritis,
PT diabetic retinopathy, obesity, sleep disorders and infertility.
XX
PS Example 4; Fig 19A-B; 176pp; English.
XX
CC The present invention describes a vehicle-peptide molecule (I) or its
CC multimers. (I) can have antiinflammatory, antitumour, immunosuppressive,
CC cytostatic, antirheumatic, antiarthritic, antidiabetic, ophthalmological,
CC antianaemic, anorectic, antiinfertility, haemostatic, dermatological and
CC neuroprotective activities. (I) can be used as a therapeutic or
CC prophylactic agent as well as for screening purposes. (I) is useful for
CC diagnosing diseases characterised by dysfunction of their associated
CC protein of interest, for identifying normal or abnormal proteins of
CC interest, as a part of diagnostic kit to detect the presence of their
CC proteins of interest in a biological sample. Additionally, (I) is useful
CC for treating inflammatory and autoimmune diseases, tumour growth, cancer,
CC rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders,
CC infertility, and neurological degenerative diseases. (I), comprising EPO-
CC mimetic compounds are useful for treating disorders characterised by low
CC red blood cell levels such as anaemia. The TPO-mimetic comprising
CC compounds are useful for treating conditions that involve an existing
CC megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet
CC deficiency, such as thrombocytopaenia, aplastic anaemia, metastatic
CC tumour which result in thrombocytopaenia, systemic lupus erythematosus,
CC and Fanconi's syndrome. ABB72403 to ABB73426 and ABL35695 to ABL35777
CC represent amino acid and nucleic acid sequences used in the
CC exemplification of the present invention
XX
SQ Sequence 757 BP; 185 A; 244 C; 200 G; 128 T; 0 U; 0 Other;

Query Match 58.4%; Score 662.4; DB 6; Length 757;
Best Local Similarity 97.7%; Pred. No. 9.8e-144;
Matches 672; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

```
Qy          1 CATATGGACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCG 60
              |||||||||||||||||||||| ||||| || ||||||||||||||   || || |||
Db          1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCG 60

Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120

Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180

Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240

Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300

Qy        301 TACGCATGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
              |||   |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360

Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
```

```
Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480

Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540

Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600

Qy        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660

Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
              |||||||||||||||||||||||||||||
Db        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
```

RESULT 10
AAA69503
ID AAA69503 standard; DNA; 763 BP.
XX
AC AAA69503;
XX
DT 31-OCT-2000 (first entry)
XX
DE Fc-IL-1 antagonist fusion nucleotide sequence SEQ ID NO:1059.
XX
KW Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
KW autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;
KW immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP;
KW inhibitor; erythropoietin; thrombopoietin; interleukin 1;
KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
KW vascular endothelial growth factor; matrix metalloproteinase; asthma;
KW thrombosis; pharmaceutical; ds.
XX
OS Synthetic.
XX
PN WO200024782-A2.
XX
PD 04-MAY-2000.
XX
PF 25-OCT-1999; 99WO-US025044.
XX
PR 23-OCT-1998; 98US-0105371P.
PR 22-OCT-1999; 99US-00428082.
XX
PA (AMGE-) AMGEN INC.
XX
PI Feige U, Liu C, Cheetham J, Boone TC;
XX
DR WPI; 2000-350702/30.
DR P-PSDB; AAB17953.
XX
PT Novel composition of matter comprising an Fc domain and pharmacologically
PT active peptides, useful for treating cancer and autoimmune diseases.
XX
PS Example 5; Page 572-573; 608pp; English.
XX
CC The present invention describes composition of matter (I) comprising an
CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
CC (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
CC independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-
CC (L2)d-P2-(L3)e-P^3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2,
CC P3, and P4 = are each independently sequences of pharmacologically active
CC peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b,
CC c, d, e, and f = are each independently 0 or 1, provided that at least 1
CC of a and b is 1. The composition can have cytostatic, antiasthmatic,
CC thrombolytic and immunosuppressive activities. DNAs, vectors and host
CC cells from the present invention can be used for producing pharmaceutical
CC compositions. The compositions are useful for treating cancer, asthma,
CC thrombosis, or autoimmune diseases. The use of an Fc domain (rather than
CC a Fab domain) can provide a longer half-life or incorporate functions
CC such as Fc receptor binding, protein A binding, complement fixation, and
CC possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to
CC AAB18003 represent nucleotide and amino acid sequences used in the
CC exemplification of the present invention
XX
SQ Sequence 763 BP; 182 A; 243 C; 208 G; 130 T; 0 U; 0 Other;

```
  Query Match             58.4%;  Score 662.4;  DB 3;  Length 763;
  Best Local Similarity   97.7%;  Pred. No. 9.8e-144;
  Matches  672;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          1 CATATGGACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCG 60
              |||||||||||||||||||||||| ||||| || ||||||||||||||||   || || |||
Db          1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCG 60

Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120

Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180

Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240

Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCT 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300

Qy        301 TACGCATGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
              |||   |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360

Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420

Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480

Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540

Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600

Qy        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660

Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
              |||||||||||||||||||||||||||||
Db        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
```

RESULT 11
ADM17769
ID ADM17769 standard; DNA; 777 BP.
XX
AC ADM17769;
XX
DT 17-JUN-2004 (first entry)
XX
DE Fc C-terminal vector related oligonucleotide SEQ ID NO:121.
XX

KW nerve growth factor modulator; NGF modulator; analgesic; NGF inhibitor;
KW nerve growth factor inhibitor; neurologic pain; diabetic neuropathy;
KW post-herpetic neuralgia; inflammatory pain; migraine; asthma;
KW hyperactive bladder; psoriasis; cancer; acute pain; dental pain;
KW surgical pain; pain; causalgia; demyelinating disease;
KW trigeminal neuralgia; chronic alcoholism; stroke; thalamic pain syndrome;
KW diabetes; acquired immuno deficiency syndrome; AIDS; headache;
KW inflammation; arthritis; rheumatic disease; lupus; osteoarthritis;
KW inflammatory bowel disorder; inflammatory eye disorder; sunburn;
KW carditis; dermatitis; myositis; neuritis; collagen vascular disease;
KW chronic inflammatory condition; neuropathic pain; genitourinary; wound;
KW burn; allergic skin reaction; pruritus; vitiligo;
KW gastrointestinal disorder; colitis; gastric ulceration; duodenal ulcer;
KW ss.
XX
OS Synthetic.
XX
PN WO2004026329-A1.
XX
PD 01-APR-2004.
XX
PF 19-SEP-2003; 2003WO-US029866.
XX
PR 19-SEP-2002; 2002US-0412524P.
PR 18-SEP-2003; 2003US-00666480.
XX
PA (AMGE-) AMGEN INC.
XX
PI Boone TC, Wild KD, Sitney KC, Min H, Kimmel B;
XX
DR WPI; 2004-283150/26.
XX
PT Novel peptide capable of modulating nerve growth factor activity, useful
PT for treating disease or disorder e.g., acute pain, dental pain, cancer,
PT migraine and collagen vascular disease.
XX
PS Example 2; SEQ ID NO 121; 267pp; English.
XX
CC The present invention describes a peptide (I) that is capable of
CC modulating nerve growth factor (NGF) activity. Also described: (1)
CC modified peptide (II) comprising (I) and a vehicle, where the modified
CC peptide is capable of modulating NGF activity; (2) dimer or multimer of
CC (I); (3) modified peptide (III), its multimers or its salt, where the
CC peptide is capable of modulating NGF activity; (4) polynucleotide (IV)
CC encoding (I), (II) or (III); (5) expression vector (V) comprising (IV);
CC (6) host cell (VI) comprising (V); (7) a composition (VII) of matter and
CC a vehicle, where the composition of matter is capable of modulating NGF
CC activity; and (8) pharmaceutical composition comprising (I), (II) or
CC (III) and a diluent or carrier. (I) has analgesic activity, and can be
CC used as an inhibitor of NGF. (I) is useful for treating or preventing a
CC disease or disorder associated with NGF activity by administering (I) to
CC human or animal. The disease or disorder chosen from neurologic pain,
CC painful diabetic neuropathy, post-herpetic neuralgia, inflammatory pain,
CC migraine, asthma, hyperactive bladder, psoriasis, cancer, acute pain,
CC dental pain, pain from trauma, surgical pain, pain resulting from
CC amputation or abscess, causalgia, demyelinating diseases, trigeminal
CC neuralgia, chronic alcoholism, stroke, thalamic pain syndrome, diabetes,
CC acquired immuno deficiency syndrome (AIDS), toxins and chemotherapy,
CC general headache, cluster headache, mixed-vascular and non-vascular
CC syndromes, tension headache, general inflammation, arthritis, rheumatic
CC diseases, lupus, osteoarthritis, inflammatory bowel disorders,
CC inflammatory eye disorders, inflammatory or unstable bladder disorders,
CC skin complaints with inflammatory components, sunburn, carditis,
CC dermatitis, myositis, neuritis, collagen vascular diseases, chronic
CC inflammatory conditions, inflammatory pain associated hyperalgesia and
CC allodynia, neuropathic pain and associated hyperalgesia and allodynia,
CC diabetic neuropathy pain, sympathetically maintained pain,
CC deafferentation syndromes, epithelial tissue damage or dysfunction,
CC herpes simplex, post-herpetic neuralgia, disturbances of visceral
CC motility at respiratory, genitourinary, gastrointestinal or vascular
CC regions, wounds, burns, allergic skin reactions, pruritus, vitiligo,
CC general gastrointestinal disorders, colitis, gastric ulceration, duodenal
CC ulcers, vasomotor or allergic rhinitis, or bronchial disorders. (I) is
CC also useful for modulating pain or promoting analgesia by administering
CC (I) to human or animal. (I) is also useful in the manufacture of
CC medicament for the treatment of disease or disorder. The present sequence
CC is used in the exemplification of the present invention.
XX
SQ Sequence 777 BP; 202 A; 236 C; 206 G; 133 T; 0 U; 0 Other;

Query Match 58.4%; Score 662.4; DB 12; Length 777;
Best Local Similarity 97.7%; Pred. No. 9.9e-144;
Matches 672; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

```
Qy          1 CATATGGACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCG 60
              |||||||||||||||||||||||| ||||| || |||||||||||||||   || || |||
Db         36 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCG 95

Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         96 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 155

Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        156 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 215

Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        216 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 275

Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCT 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        276 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 335

Qy        301 TACGCATGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
              |||   |||  ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        336 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 395

Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        396 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 455

Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        456 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 515

Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        516 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 575

Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        576 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 635

Qy        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        636 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 695

Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
              |||||||||||||||||||||||||||||
Db        696 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 723
```

RESULT 12
AAA69444
ID AAA69444 standard; DNA; 794 BP.
XX
AC AAA69444;
XX
DT 31-OCT-2000 (first entry)
XX
DE Fc-TMP nucleotide sequence SEQ ID NO:5.
XX
KW Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
KW autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;
KW immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP;

```
KW   inhibitor; erythropoietin; thrombopoietin; interleukin 1;
KW   cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
KW   vascular endothelial growth factor; matrix metalloproteinase; asthma;
KW   thrombosis; pharmaceutical; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200024782-A2.
XX
PD   04-MAY-2000.
XX
PF   25-OCT-1999;   99WO-US025044.
XX
PR   23-OCT-1998;   98US-0105371P.
PR   22-OCT-1999;   99US-00428082.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Feige U,  Liu C,  Cheetham J,  Boone TC;
XX
DR   WPI; 2000-350702/30.
DR   P-PSDB; AAB16958.
XX
PT   Novel composition of matter comprising an Fc domain and pharmacologically
PT   active peptides, useful for treating cancer and autoimmune diseases.
XX
PS   Example 2; Page 178-179; 608pp; English.
XX
CC   The present invention describes composition of matter (I) comprising an
CC   Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
CC   (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
CC   independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-
CC   (L2)d-P2-(L3)e-P^3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2,
CC   P3, and P4 = are each independently sequences of pharmacologically active
CC   peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b,
CC   c, d, e, and f = are each independently 0 or 1, provided that at least 1
CC   of a and b is 1. The composition can have cytostatic, antiasthmatic,
CC   thrombolytic and immunosuppressive activities. DNAs, vectors and host
CC   cells from the present invention can be used for producing pharmaceutical
CC   compositions. The compositions are useful for treating cancer, asthma,
CC   thrombosis, or autoimmune diseases. The use of an Fc domain (rather than
CC   a Fab domain) can provide a longer half-life or incorporate functions
CC   such as Fc receptor binding, protein A binding, complement fixation, and
CC   possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to
CC   AAB18003 represent nucleotide and amino acid sequences used in the
CC   exemplification of the present invention
XX
SQ   Sequence 794 BP; 195 A; 242 C; 213 G; 144 T; 0 U; 0 Other;

  Query Match           58.4%;  Score 662.4;  DB 3;  Length 794;
  Best Local Similarity 97.7%;  Pred. No. 9.9e-144;
  Matches  672;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          1 CATATGGACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCG 60
              ||||||||||||||||||||||| ||||| || ||||||||||||||    || || |||
Db         36 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCG 95

Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         96 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 155

Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        156 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 215

Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        216 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 275

Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        276 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 335

Qy        301 TACGCATGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
              |||   |||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db        336 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 395

Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        396 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 455

Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        456 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 515

Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        516 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 575

Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        576 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 635

Qy        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        636 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 695

Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
              |||||||||||||||||||||||||||
Db        696 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 723


RESULT 13
ABL35761
ID   ABL35761 standard; DNA; 794 BP.
XX
AC   ABL35761;
XX
DT   05-APR-2002  (first entry)
XX
DE   Fc-TPO mimetic peptide (Fc-TMP) nucleic acid SEQ ID NO:5.
XX
KW   Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; IgG; EPO;
KW   erythropoietin; TPO; tumour necrosis factor alpha inhibitor;
KW   TNF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TMP;
KW   TPO mimetic peptide; EPO mimetic peptide; EMP; VEGF antagonist;
KW   MMP inhibitor; antiinflammatory; antitumour; immunosuppressive;
KW   cytostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological;
KW   antianaemic; anorectic; antiinfertility; haemostatic; dermatological;
KW   neuroprotective; inflammatory disease; autoimmune disease; tumour growth;
KW   cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity;
KW   sleep disorder; neurological degenerative disease; anaemia;
KW   thrombocytopaenia; metastatic tumour; systemic lupus erythematosus;
KW   Fanconi's syndrome; gene; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200183525-A2.
XX
PD   08-NOV-2001.
XX
PF   02-MAY-2001; 2001WO-US014310.
XX
PR   03-MAY-2000; 2000US-00563286.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Feige U,  Liu C,  Cheetham JC,  Boone TC,  Gudas JM;
XX
DR   WPI; 2002-130313/17.
DR   P-PSDB; ABB73411.
XX
PT   Novel vehicle-peptide molecule or its multimers useful for treating
PT   inflammatory and autoimmune diseases, cancer, rheumatoid arthritis,
```

PT diabetic retinopathy, obesity, sleep disorders and infertility.
XX
PS Example 2; Fig 7; 176pp; English.
XX
CC The present invention describes a vehicle-peptide molecule (I) or its
CC multimers. (I) can have antiinflammatory, antitumour, immunosuppressive,
CC cytostatic, antirheumatic, antiarthritic, antidiabetic, ophthalmological,
CC antianaemic, anorectic, antiinfertility, haemostatic, dermatological and
CC neuroprotective activities. (I) can be used as a therapeutic or
CC prophylactic agent as well as for screening purposes. (I) is useful for
CC diagnosing diseases characterised by dysfunction of their associated
CC protein of interest, for identifying normal or abnormal proteins of
CC interest, as a part of diagnostic kit to detect the presence of their
CC proteins of interest in a biological sample. Additionally, (I) is useful
CC for treating inflammatory and autoimmune diseases, tumour growth, cancer,
CC rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders,
CC infertility, and neurological degenerative diseases. (I), comprising EPO-
CC mimetic compounds are useful for treating disorders characterised by low
CC red blood cell levels such as anaemia. The TPO-mimetic comprising
CC compounds are useful for treating conditions that involve an existing
CC megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet
CC deficiency, such as thrombocytopaenia, aplastic anaemia, metastatic
CC tumour which result in thrombocytopaenia, systemic lupus erythematosus,
CC and Fanconi's syndrome. ABB72403 to ABB73426 and ABL35695 to ABL35777
CC represent amino acid and nucleic acid sequences used in the
CC exemplification of the present invention
XX
SQ Sequence 794 BP; 195 A; 242 C; 213 G; 144 T; 0 U; 0 Other;

Query Match 58.4%; Score 662.4; DB 6; Length 794;
Best Local Similarity 97.7%; Pred. No. 9.9e-144;
Matches 672; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

```
Qy          1 CATATGGACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCG 60
              |||||||||||||||||||||||| ||||| || ||||||||||||||   || || |||
Db         36 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCG 95

Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         96 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 155

Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        156 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 215

Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  .
Db        216 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 275

Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCT 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        276 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 335

Qy        301 TACGCATGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
              |||   |||  ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        336 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 395

Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        396 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 455

Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        456 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 515

Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        516 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 575

Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        576 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 635
```

```
Qy        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        636 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 695

Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
              |||||||||||||||||||||||||||
Db        696 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 723
```

RESULT 14
AAA69448
ID AAA69448 standard; DNA; 812 BP.
XX
AC AAA69448;
XX
DT 31-OCT-2000 (first entry)
XX
DE Fc-EMP nucleotide sequence SEQ ID NO:15.
XX
KW Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
KW autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;
KW immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP;
KW inhibitor; erythropoietin; thrombopoietin; interleukin 1;
KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
KW vascular endothelial growth factor; matrix metalloproteinase; asthma;
KW thrombosis; pharmaceutical; ds.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200024782-A2.
XX
PD 04-MAY-2000.
XX
PF 25-OCT-1999; 99WO-US025044.
XX
PR 23-OCT-1998; 98US-0105371P.
PR 22-OCT-1999; 99US-00428082.
XX
PA (AMGE-) AMGEN INC.
XX
PI Feige U, Liu C, Cheetham J, Boone TC;
XX
DR WPI; 2000-350702/30.
DR P-PSDB; AAB16964.
XX
PT Novel composition of matter comprising an Fc domain and pharmacologically
PT active peptides, useful for treating cancer and autoimmune diseases.
XX
PS Example 3; Page 190-191; 608pp; English.
XX
CC The present invention describes composition of matter (I) comprising an
CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
CC (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
CC independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-
CC (L2)d-P2-(L3)e-P^3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2,
CC P3, and P4 = are each independently sequences of pharmacologically active
CC peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b,
CC c, d, e, and f = are each independently 0 or 1, provided that at least 1
CC of a and b is 1. The composition can have cytostatic, antiasthmatic,
CC thrombolytic and immunosuppressive activities. DNAs, vectors and host
CC cells from the present invention can be used for producing pharmaceutical
CC compositions. The compositions are useful for treating cancer, asthma,
CC thrombosis, or autoimmune diseases. The use of an Fc domain (rather than
CC a Fab domain) can provide a longer half-life or incorporate functions
CC such as Fc receptor binding, protein A binding, complement fixation, and
CC possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to
CC AAB18003 represent nucleotide and amino acid sequences used in the
CC exemplification of the present invention
XX
SQ Sequence 812 BP; 198 A; 246 C; 218 G; 150 T; 0 U; 0 Other;

Query Match 58.4%; Score 662.4; DB 3; Length 812;

```
  Best Local Similarity   97.7%;  Pred. No. 1e-143;
  Matches  672;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          1 CATATGGACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCG 60
              |||||||||||||||||||||||| ||||| || ||||||||||||||    || || |||
Db         36 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCG 95

Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         96 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 155

Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        156 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 215

Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        216 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 275

Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCT 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        276 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 335

Qy        301 TACGCATGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
              |||   |||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db        336 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 395

Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        396 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 455

Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        456 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 515

Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        516 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 575

Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        576 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 635

Qy        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        636 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 695

Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
              ||||||||||||||||||||||||||||
Db        696 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 723


RESULT 15
ABL35765
ID   ABL35765 standard; DNA; 812 BP.
XX
AC   ABL35765;
XX
DT   05-APR-2002  (first entry)
XX
DE   Fc-EPO mimetic peptide (Fc-EMP) nucleic acid SEQ ID NO:15.
XX
KW   Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; IgG; EPO;
KW   erythropoietin; TPO; tumour necrosis factor alpha inhibitor;
KW   TNF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TMP;
KW   TPO mimetic peptide; EPO mimetic peptide; EMP; VEGF antagonist;
KW   MMP inhibitor; antiinflammatory; antitumour; immunosuppressive;
KW   cytostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological;
KW   antianaemic; anorectic; antiinfertility; haemostatic; dermatological;
KW   neuroprotective; inflammatory disease; autoimmune disease; tumour growth;
KW   cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity;
KW   sleep disorder; neurological degenerative disease; anaemia;
KW   thrombocytopaenia; metastatic tumour; systemic lupus erythematosus;
KW   Fanconi's syndrome; gene; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200183525-A2.
XX
PD   08-NOV-2001.
XX
PF   02-MAY-2001; 2001WO-US014310.
XX
PR   03-MAY-2000; 2000US-00563286.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Feige U,  Liu C,  Cheetham JC,  Boone TC,  Gudas JM;
XX
DR   WPI; 2002-130313/17.
DR   P-PSDB; ABB73415.
XX
PT   Novel vehicle-peptide molecule or its multimers useful for treating
PT   inflammatory and autoimmune diseases, cancer, rheumatoid arthritis,
PT   diabetic retinopathy, obesity, sleep disorders and infertility.
XX
PS   Example 3; Fig 13; 176pp; English.
XX
CC   The present invention describes a vehicle-peptide molecule (I) or its
CC   multimers. (I) can have antiinflammatory, antitumour, immunosuppressive,
CC   cytostatic, antirheumatic, antiarthritic, antidiabetic, ophthalmological,
CC   antianaemic, anorectic, antiinfertility, haemostatic, dermatological and
CC   neuroprotective activities. (I) can be used as a therapeutic or
CC   prophylactic agent as well as for screening purposes. (I) is useful for
CC   diagnosing diseases characterised by dysfunction of their associated
CC   protein of interest, for identifying normal or abnormal proteins of
CC   interest, as a part of diagnostic kit to detect the presence of their
CC   proteins of interest in a biological sample. Additionally, (I) is useful
CC   for treating inflammatory and autoimmune diseases, tumour growth, cancer,
CC   rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders,
CC   infertility, and neurological degenerative diseases. (I), comprising EPO-
CC   mimetic compounds are useful for treating disorders characterised by low
CC   red blood cell levels such as anaemia. The TPO-mimetic comprising
CC   compounds are useful for treating conditions that involve an existing
CC   megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet
CC   deficiency, such as thrombocytopaenia, aplastic anaemia, metastatic
CC   tumour which result in thrombocytopaenia, systemic lupus erythematosus,
CC   and Fanconi's syndrome. ABB72403 to ABB73426 and ABL35695 to ABL35777
CC   represent amino acid and nucleic acid sequences used in the
CC   exemplification of the present invention
XX
SQ   Sequence 812 BP; 198 A; 246 C; 218 G; 150 T; 0 U; 0 Other;

  Query Match           58.4%;  Score 662.4;  DB 6;  Length 812;
  Best Local Similarity   97.7%;  Pred. No. 1e-143;
  Matches  672;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          1 CATATGGACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCG 60
              |||||||||||||||||||||||| ||||| || ||||||||||||||    || || |||
Db         36 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCG 95

Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         96 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 155

Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        156 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 215

Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        216 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 275

Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCT 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
```

```
Db        276 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 335

Qy        301 TACGCATGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
              |||   |||  ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        336 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 395

Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        396 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 455

Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        456 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 515

Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        516 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 575

Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        576 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 635

Qy        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        636 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 695

Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
              ||||||||||||||||||||||||||||
Db        696 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 723
```

Search completed: October 17, 2004, 16:46:45
Job time : 591.736 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 17, 2004, 15:27:13 ; Search time 578.552 Seconds
(without alignments)
10035.691 Million cell updates/sec

Title: US-10-679-999-16
Perfect score: 1135
Sequence: 1 CATATGGACAAAACTCACAC.....TCCGGGTTGTTAATGGATCC 1135

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3403857 seqs, 2557783690 residues

Total number of hits satisfying chosen parameters: 6807714

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
18: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
19: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
20: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1135	100.0	1135	16	US-10-679-999-16	Sequence 16, Appl
2	1109.4	97.7	1135	16	US-10-679-999-13	Sequence 13, Appl
3	1105	97.4	1150	16	US-10-679-999-7	Sequence 7, Appli
4	1103.4	97.2	1150	16	US-10-679-999-10	Sequence 10, Appl
5	662.4	58.4	748	16	US-10-609-217-1067	Sequence 1067, Ap
6	662.4	58.4	748	16	US-10-632-388-1067	Sequence 1067, Ap
7	662.4	58.4	748	16	US-10-651-723-1067	Sequence 1067, Ap
8	662.4	58.4	748	16	US-10-645-761-1067	Sequence 1067, Ap
9	662.4	58.4	748	16	US-10-666-696-1067	Sequence 1067, Ap
10	662.4	58.4	748	16	US-10-653-048-1067	Sequence 1067, Ap
11	662.4	58.4	757	16	US-10-609-217-1055	Sequence 1055, Ap
12	662.4	58.4	757	16	US-10-632-388-1055	Sequence 1055, Ap
13	662.4	58.4	757	16	US-10-651-723-1055	Sequence 1055, Ap
14	662.4	58.4	757	16	US-10-645-761-1055	Sequence 1055, Ap
15	662.4	58.4	757	16	US-10-666-696-1055	Sequence 1055, Ap
16	662.4	58.4	757	16	US-10-653-048-1055	Sequence 1055, Ap
17	662.4	58.4	763	16	US-10-609-217-1059	Sequence 1059, Ap
18	662.4	58.4	763	16	US-10-632-388-1059	Sequence 1059, Ap
19	662.4	58.4	763	16	US-10-651-723-1059	Sequence 1059, Ap
20	662.4	58.4	763	16	US-10-645-761-1059	Sequence 1059, Ap
21	662.4	58.4	763	16	US-10-666-696-1059	Sequence 1059, Ap
22	662.4	58.4	763	16	US-10-653-048-1059	Sequence 1059, Ap
23	662.4	58.4	777	17	US-10-666-480-121	Sequence 121, App
24	662.4	58.4	794	16	US-10-609-217-5	Sequence 5, Appli
25	662.4	58.4	794	16	US-10-632-388-5	Sequence 5, Appli
26	662.4	58.4	794	16	US-10-651-723-5	Sequence 5, Appli
27	662.4	58.4	794	16	US-10-645-761-5	Sequence 5, Appli
28	662.4	58.4	794	16	US-10-666-696-5	Sequence 5, Appli
29	662.4	58.4	794	16	US-10-653-048-5	Sequence 5, Appli
30	662.4	58.4	812	16	US-10-609-217-15	Sequence 15, Appl
31	662.4	58.4	812	16	US-10-632-388-15	Sequence 15, Appl
32	662.4	58.4	812	16	US-10-651-723-15	Sequence 15, Appl
33	662.4	58.4	812	16	US-10-645-761-15	Sequence 15, Appl
34	662.4	58.4	812	16	US-10-666-696-15	Sequence 15, Appl
35	662.4	58.4	812	16	US-10-653-048-15	Sequence 15, Appl
36	662.4	58.4	837	15	US-10-269-806-151	Sequence 151, App
37	662.4	58.4	859	9	US-09-840-277-108	Sequence 108, App
38	662.4	58.4	861	16	US-10-609-217-7	Sequence 7, Appli
39	662.4	58.4	861	16	US-10-632-388-7	Sequence 7, Appli
40	662.4	58.4	861	16	US-10-651-723-7	Sequence 7, Appli
41	662.4	58.4	861	16	US-10-645-761-7	Sequence 7, Appli
42	662.4	58.4	861	16	US-10-666-696-7	Sequence 7, Appli
43	662.4	58.4	861	16	US-10-653-048-7	Sequence 7, Appli
44	660.8	58.2	773	16	US-10-609-217-1063	Sequence 1063, Ap
45	660.8	58.2	773	16	US-10-632-388-1063	Sequence 1063, Ap

ALIGNMENTS

```
RESULT 1
US-10-679-999-16
; Sequence 16, Application US/10679999
; Publication No. US20040067520A1
;  GENERAL INFORMATION:
;       APPLICANT: Mann, Michael B.
;                  Hecht, Randy I.
;       TITLE OF INVENTION: OB FUSION PROTEIN COMPOSITIONS AND
;                           METHODS
;       NUMBER OF SEQUENCES: 18
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Amgen Inc.
;            STREET: 1840 DeHavilland Drive
;            CITY: Thousand Oaks
;            STATE: CA
;            COUNTRY: USA
;            ZIP: 91320-1789
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/679,999
;            FILING DATE: 06-Oct-2003
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/09/568,528
;            FILING DATE: 09-May-2000
;            APPLICATION NUMBER: 09/267,517
;            FILING DATE: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Knight, Matthew W.
;            REGISTRATION NUMBER: 36,846
;            REFERENCE/DOCKET NUMBER: A-416
;  INFORMATION FOR SEQ ID NO: 16:
```

```
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1135 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        FEATURE:
;             NAME/KEY:  misc_feature
;             LOCATION:  4
;             OTHER INFORMATION:  /note= "Met = ATG"
;        SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-10-679-999-16

  Query Match             100.0%;  Score 1135;  DB 16;  Length 1135;
  Best Local Similarity   100.0%;  Pred. No. 6.3e-313;
  Matches 1135;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CATATGGACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CATATGGACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCG 60

Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120

Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180

Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240

Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCT 300

Qy        301 TACGCATGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TACGCATGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360

Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420

Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480

Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540

Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600

Qy        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660

Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTTCAGGACGACACCAAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTTCAGGACGACACCAAA 720

Qy        721 ACCTTAATTAAAACGATCGTTACGCGTATCAACGACATCAGTCACACCCAGTCGGTGAGC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ACCTTAATTAAAACGATCGTTACGCGTATCAACGACATCAGTCACACCCAGTCGGTGAGC 780

Qy        781 TCTAAACAGAAAGTTACAGGCCTGGACTTCATCCCGGGTCTGCACCCGATCCTGACCTTG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TCTAAACAGAAAGTTACAGGCCTGGACTTCATCCCGGGTCTGCACCCGATCCTGACCTTG 840

Qy        841 TCCAAAATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACCTCCATGCCGTCCCGT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TCCAAAATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACCTCCATGCCGTCCCGT 900

Qy        901 AACGTTATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTGCTGCACGTGCTGGCA 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 AACGTTATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTGCTGCACGTGCTGGCA 960

Qy        961 TTCTCCAAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACTCTGGACTCTCTGGGC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TTCTCCAAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACTCTGGACTCTCTGGGC 1020

Qy       1021 GGGGTCCTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTGTCCCGTCTGCAGGGT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GGGGTCCTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTGTCCCGTCTGCAGGGT 1080

Qy       1081 TCCCTTCAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGTTAATGGATCC 1135
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TCCCTTCAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGTTAATGGATCC 1135


RESULT 2
US-10-679-999-13
; Sequence 13, Application US/10679999
; Publication No. US20040067520A1
;   GENERAL INFORMATION:
;        APPLICANT: Mann, Michael B.
;                   Hecht, Randy I.
;        TITLE OF INVENTION: OB FUSION PROTEIN COMPOSITIONS AND
;                            METHODS
;        NUMBER OF SEQUENCES: 18
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Amgen Inc.
;             STREET: 1840 DeHavilland Drive
;             CITY: Thousand Oaks
;             STATE: CA
;             COUNTRY: USA
;             ZIP: 91320-1789
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/679,999
;             FILING DATE: 06-Oct-2003
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/568,528
;             FILING DATE: 09-May-2000
;             APPLICATION NUMBER: 09/267,517
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Knight, Matthew W.
;             REGISTRATION NUMBER: 36,846
;             REFERENCE/DOCKET NUMBER: A-416
;   INFORMATION FOR SEQ ID NO: 13:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1135 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        FEATURE:
;             NAME/KEY:  misc_feature
;             LOCATION:  4
;             OTHER INFORMATION:  /note= "Met = ATG"
;        SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-10-679-999-13

  Query Match             97.7%;  Score 1109.4;  DB 16;  Length 1135;
  Best Local Similarity   98.6%;  Pred. No. 1.2e-305;
  Matches 1119;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;
```

```
Qy          1 CATATGGACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCG 60
              |||||||||||||||||||||||| ||||| || ||||||||||||||    || |||||
Db          1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGTCCT 60

Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120

Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180

Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240

Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCT 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300

Qy        301 TACGCATGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
              |||   |||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360

Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420

Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480

Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540

Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600

Qy        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660

Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTTCAGGACGACACCAAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTTCAGGACGACACCAAA 720

Qy        721 ACCTTAATTAAAACGATCGTTACGCGTATCAACGACATCAGTCACACCCAGTCGGTGAGC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ACCTTAATTAAAACGATCGTTACGCGTATCAACGACATCAGTCACACCCAGTCGGTGAGC 780

Qy        781 TCTAAACAGAAAGTTACAGGCCTGGACTTCATCCCGGGTCTGCACCCGATCCTGACCTTG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TCTAAACAGAAAGTTACAGGCCTGGACTTCATCCCGGGTCTGCACCCGATCCTGACCTTG 840

Qy        841 TCCAAAATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACCTCCATGCCGTCCCGT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TCCAAAATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACCTCCATGCCGTCCCGT 900

Qy        901 AACGTTATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTGCTGCACGTGCTGGCA 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 AACGTTATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTGCTGCACGTGCTGGCA 960

Qy        961 TTCTCCAAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACTCTGGACTCTCTGGGC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TTCTCCAAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACTCTGGACTCTCTGGGC 1020

Qy       1021 GGGGTCCTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTGTCCCGTCTGCAGGGT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GGGGTCCTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTGTCCCGTCTGCAGGGT 1080

Qy       1081 TCCCTTCAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGTTAATGGATCC 1135
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TCCCTTCAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGTTAATGGATCC 1135
```

RESULT 3
US-10-679-999-7
; Sequence 7, Application US/10679999
; Publication No. US20040067520A1
; GENERAL INFORMATION:
; APPLICANT: Mann, Michael B.
; Hecht, Randy I.
; TITLE OF INVENTION: OB FUSION PROTEIN COMPOSITIONS AND
; METHODS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: CA
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/679,999
; FILING DATE: 06-Oct-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/568,528
; FILING DATE: 09-May-2000
; APPLICATION NUMBER: 09/267,517
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Knight, Matthew W.
; REGISTRATION NUMBER: 36,846
; REFERENCE/DOCKET NUMBER: A-416
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1150 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 4
; OTHER INFORMATION: /note= "Met = ATG"
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-679-999-7

Query Match 97.4%; Score 1105; DB 16; Length 1150;
Best Local Similarity 98.7%; Pred. No. 2.2e-304;
Matches 1114; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

```
Qy          7 GACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCGTCAGTC 66
              |||||||||||||||||||||||||||||||| || ||||||    || || |||||||||
Db         22 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC 81

Qy         67 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         82 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 141

Qy        127 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        142 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 201

Qy        187 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        202 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 261
```

```
Qy        247 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCTTACGCA 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |  |||
Db        262 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 321

Qy        307 TGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 366
              |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        322 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 381

Qy        367 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        382 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 441

Qy        427 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        442 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 501

Qy        487 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        502 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 561

Qy        547 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        562 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 621

Qy        607 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        622 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 681

Qy        667 CTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTTCAGGACGACACCAAAACCTTA 726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        682 CTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTTCAGGACGACACCAAAACCTTA 741

Qy        727 ATTAAAACGATCGTTACGCGTATCAACGACATCAGTCACACCCAGTCGGTGAGCTCTAAA 786
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        742 ATTAAAACGATCGTTACGCGTATCAACGACATCAGTCACACCCAGTCGGTGAGCTCTAAA 801

Qy        787 CAGAAAGTTACAGGCCTGGACTTCATCCCGGGTCTGCACCCGATCCTGACCTTGTCCAAA 846
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        802 CAGAAAGTTACAGGCCTGGACTTCATCCCGGGTCTGCACCCGATCCTGACCTTGTCCAAA 861

Qy        847 ATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACCTCCATGCCGTCCCGTAACGTT 906
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        862 ATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACCTCCATGCCGTCCCGTAACGTT 921

Qy        907 ATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTGCTGCACGTGCTGGCATTCTCC 966
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        922 ATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTGCTGCACGTGCTGGCATTCTCC 981

Qy        967 AAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACTCTGGACTCTCTGGGCGGGGTC 1026
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        982 AAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACTCTGGACTCTCTGGGCGGGGTC 1041

Qy       1027 CTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTGTCCCGTCTGCAGGGTTCCCTT 1086
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1042 CTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTGTCCCGTCTGCAGGGTTCCCTT 1101

Qy       1087 CAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGTTAATGGATCC 1135
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db       1102 CAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGTTAATGGATCC 1150
```

```
RESULT 4
US-10-679-999-10
; Sequence 10, Application US/10679999
; Publication No. US20040067520A1
;   GENERAL INFORMATION:
;        APPLICANT: Mann, Michael B.
;                   Hecht, Randy I.
;        TITLE OF INVENTION: OB FUSION PROTEIN COMPOSITIONS AND
;                            METHODS
;        NUMBER OF SEQUENCES: 18
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Amgen Inc.
;             STREET: 1840 DeHavilland Drive
;             CITY: Thousand Oaks
;             STATE: CA
;             COUNTRY: USA
;             ZIP: 91320-1789
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/679,999
;             FILING DATE: 06-Oct-2003
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/568,528
;             FILING DATE: 09-May-2000
;             APPLICATION NUMBER: 09/267,517
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Knight, Matthew W.
;             REGISTRATION NUMBER: 36,846
;             REFERENCE/DOCKET NUMBER: A-416
;   INFORMATION FOR SEQ ID NO: 10:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1150 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        FEATURE:
;             NAME/KEY:  misc_feature
;             LOCATION:  4
;             OTHER INFORMATION:  /note= "Met = ATG"
;        SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-679-999-10

  Query Match             97.2%;  Score 1103.4;  DB 16;  Length 1150;
  Best Local Similarity   98.6%;  Pred. No. 6.4e-304;
  Matches 1113;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          7 GACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCGTCAGTC 66
              |||||||||||||||| ||||| || ||||||||||||||   || ||||| ||||||
Db         22 GACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGTCCTTCAGTC 81

Qy         67 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         82 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 141

Qy        127 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        142 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 201

Qy        187 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        202 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 261

Qy        247 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCTTACGCA 306
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |  |||
Db        262 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 321

Qy        307 TGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 366
              |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        322 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 381

Qy        367 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        382 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 441

Qy        427 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        442 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 501
```

```
Qy        487 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        502 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 561

Qy        547 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        562 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 621

Qy        607 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        622 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 681

Qy        667 CTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTTCAGGACGACACCAAAACCTTA 726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        682 CTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTTCAGGACGACACCAAAACCTTA 741

Qy        727 ATTAAAACGATCGTTACGCGTATCAACGACATCAGTCACACCCAGTCGGTGAGCTCTAAA 786
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        742 ATTAAAACGATCGTTACGCGTATCAACGACATCAGTCACACCCAGTCGGTGAGCTCTAAA 801

Qy        787 CAGAAAGTTACAGGCCTGGACTTCATCCCGGGTCTGCACCCGATCCTGACCTTGTCCAAA 846
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        802 CAGAAAGTTACAGGCCTGGACTTCATCCCGGGTCTGCACCCGATCCTGACCTTGTCCAAA 861

Qy        847 ATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACCTCCATGCCGTCCCGTAACGTT 906
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        862 ATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACCTCCATGCCGTCCCGTAACGTT 921

Qy        907 ATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTGCTGCACGTGCTGGCATTCTCC 966
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        922 ATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTGCTGCACGTGCTGGCATTCTCC 981

Qy        967 AAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACTCTGGACTCTCTGGGCGGGGTC 1026
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        982 AAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACTCTGGACTCTCTGGGCGGGGTC 1041

Qy       1027 CTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTGTCCCGTCTGCAGGGTTCCCTT 1086
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1042 CTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTGTCCCGTCTGCAGGGTTCCCTT 1101

Qy       1087 CAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGTTAATGGATCC 1135
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1102 CAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGTTAATGGATCC 1150
```

RESULT 5
US-10-609-217-1067
; Sequence 1067, Application US/10609217
; Publication No. US20040044188A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/609,217
; CURRENT FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1067
; LENGTH: 748
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fc MMP INHIBITOR
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (4)..(732)
; OTHER INFORMATION:
US-10-609-217-1067

Query Match 58.4%; Score 662.4; DB 16; Length 748;
Best Local Similarity 97.7%; Pred. No. 2.4e-178;
Matches 672; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

```
Qy          1 CATATGGACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCG 60
              |||||||||||||||||||| ||||| || ||||||||||||||   || || |||
Db          1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCG 60

Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120

Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180

Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240

Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCT 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300

Qy        301 TACGCATGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
              |||   |||  ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360

Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420

Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480

Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540

Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600

Qy        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660

Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
              |||||||||||||||||||||||||||||
Db        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
```

RESULT 6
US-10-632-388-1067
; Sequence 1067, Application US/10632388
; Publication No. US20040053845A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/632,388
; CURRENT FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371

```
;  PRIOR FILING DATE: 1998-10-23
;  NUMBER OF SEQ ID NOS: 1133
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1067
;   LENGTH: 748
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Fc MMP INHIBITOR
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (4)..(732)
;   OTHER INFORMATION:
US-10-632-388-1067

  Query Match             58.4%;  Score 662.4;  DB 16;  Length 748;
  Best Local Similarity   97.7%;  Pred. No. 2.4e-178;
  Matches  672;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          1 CATATGGACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCG 60
              ||||||||||||||||||||||| ||||| || ||||||||||||||    || || |||
Db          1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCG 60

Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120

Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180

Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240

Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCT 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300

Qy        301 TACGCATGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
              |||   |||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360

Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420

Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480

Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540

Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600

Qy        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660

Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
              |||||||||||||||||||||||||||
Db        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688


RESULT 7
US-10-651-723-1067
; Sequence 1067, Application US/10651723
; Publication No. US20040057953A1
; GENERAL INFORMATION:
;  APPLICANT: FEIGE, ULRICH
;  APPLICANT:  LIU, CHUAN-FA
;  APPLICANT:  CHEETHAM, JANET C.
;  APPLICANT:  BOONE, THOMAS CHARLES
;  TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
;  FILE REFERENCE: A-527
;  CURRENT APPLICATION NUMBER: US/10/651,723
;  CURRENT FILING DATE:  2003-08-29
;  PRIOR APPLICATION NUMBER: US/09/428,082B
;  PRIOR FILING DATE: 1999-10-22
;  PRIOR APPLICATION NUMBER: 60/105,371
;  PRIOR FILING DATE: 1998-10-23
;  NUMBER OF SEQ ID NOS: 1133
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1067
;   LENGTH: 748
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Fc MMP INHIBITOR
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (4)..(732)
;   OTHER INFORMATION:
US-10-651-723-1067

  Query Match             58.4%;  Score 662.4;  DB 16;  Length 748;
  Best Local Similarity   97.7%;  Pred. No. 2.4e-178;
  Matches  672;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          1 CATATGGACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCG 60
              ||||||||||||||||||||||| ||||| || ||||||||||||||    || || |||
Db          1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCG 60

Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120

Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180

Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240

Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCT 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300

Qy        301 TACGCATGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
              |||   |||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360

Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420

Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480

Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540

Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600

Qy        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
```

```
Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
              ||||||||||||||||||||||||||||
Db        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
```

RESULT 8
US-10-645-761-1067
; Sequence 1067, Application US/10645761
; Publication No. US20040071712A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/645,761
; CURRENT FILING DATE: 2003-08-18
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1067
; LENGTH: 748
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fc MMP INHIBITOR
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (4)..(732)
; OTHER INFORMATION:
US-10-645-761-1067

Query Match 58.4%; Score 662.4; DB 16; Length 748;
Best Local Similarity 97.7%; Pred. No. 2.4e-178;
Matches 672; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

```
Qy          1 CATATGGACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCG 60
              |||||||||||||||||||||| ||||| || ||||||||||||||   || || |||
Db          1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCG 60

Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120

Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180

Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240

Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCT 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300

Qy        301 TACGCATGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
              ||| ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360

Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420

Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480

```
Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540

Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600

Qy        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660

Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
              ||||||||||||||||||||||||||||
Db        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
```

RESULT 9
US-10-666-696-1067
; Sequence 1067, Application US/10666696
; Publication No. US20040077022A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; APPLICANT: GUDAS, JEAN MARIE
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527A
; CURRENT APPLICATION NUMBER: US/10/666,696
; CURRENT FILING DATE: 2003-09-19
; PRIOR APPLICATION NUMBER: US/09/563,286C
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/428,082
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1157
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1067
; LENGTH: 748
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fc-MMP INHIBITOR
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (4)..(732)
; OTHER INFORMATION:
US-10-666-696-1067

Query Match 58.4%; Score 662.4; DB 16; Length 748;
Best Local Similarity 97.7%; Pred. No. 2.4e-178;
Matches 672; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

```
Qy          1 CATATGGACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCG 60
              |||||||||||||||||||||| ||||| || ||||||||||||||   || || |||
Db          1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCG 60

Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120

Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180

Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240

Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCT 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
```
```

```
Db        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300

Qy        301 TACGCATGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
              |||   |||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360

Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420

Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480

Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540

Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600

Qy        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660

Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
              |||||||||||||||||||||||||||
Db        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
```

RESULT 10
US-10-653-048-1067
; Sequence 1067, Application US/10653048
; Publication No. US20040087778A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/653,048
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1067
; LENGTH: 748
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fc MMP INHIBITOR
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (4)..(732)
; OTHER INFORMATION:
US-10-653-048-1067

Query Match 58.4%; Score 662.4; DB 16; Length 748;
Best Local Similarity 97.7%; Pred. No. 2.4e-178;
Matches 672; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

```
Qy          1 CATATGGACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCG 60
              |||||||||||||||||||||| ||||| || ||||||||||||||||    || || |||
Db          1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCG 60

Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120

Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180

Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240

Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCT 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300

Qy        301 TACGCATGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
              |||   |||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360

Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420

Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480

Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540

Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600

Qy        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660

Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
              |||||||||||||||||||||||||||
Db        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
```

RESULT 11
US-10-609-217-1055
; Sequence 1055, Application US/10609217
; Publication No. US20040044188A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/609,217
; CURRENT FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1055
; LENGTH: 757
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: FC-TNF-ALPA INHIBITORS
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (4)..(747)
; OTHER INFORMATION:
US-10-609-217-1055

```
  Query Match             58.4%;  Score 662.4;  DB 16;  Length 757;
  Best Local Similarity   97.7%;  Pred. No. 2.4e-178;
  Matches  672;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          1 CATATGGACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCG 60
              |||||||||||||||||||||||| ||||| || ||||||||||||||    || || |||
Db          1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCG 60

Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120

Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180

Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240

Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCT 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300

Qy        301 TACGCATGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
              |||   |||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360

Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420

Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480

Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540

Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600

Qy        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660

Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
              |||||||||||||||||||||||||||
Db        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688


RESULT 12
US-10-632-388-1055
; Sequence 1055, Application US/10632388
; Publication No. US20040053845A1
; GENERAL INFORMATION:
;  APPLICANT: FEIGE, ULRICH
;  APPLICANT:  LIU, CHUAN-FA
;  APPLICANT:  CHEETHAM, JANET C.
;  APPLICANT:  BOONE, THOMAS CHARLES
;  TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
;  FILE REFERENCE: A-527
;  CURRENT APPLICATION NUMBER: US/10/632,388
;  CURRENT FILING DATE:  2003-07-31
;  PRIOR APPLICATION NUMBER: US/09/428,082B
;  PRIOR FILING DATE: 1999-10-22
;  PRIOR APPLICATION NUMBER: 60/105,371
;  PRIOR FILING DATE: 1998-10-23
;  NUMBER OF SEQ ID NOS: 1133
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1055
;  LENGTH: 757
;  TYPE: DNA
;  ORGANISM: Artificial Sequence
;  FEATURE:
;  OTHER INFORMATION: FC-TNF-ALPA INHIBITORS
;  FEATURE:
;  NAME/KEY: CDS
;  LOCATION: (4)..(747)
;  OTHER INFORMATION:
US-10-632-388-1055

  Query Match             58.4%;  Score 662.4;  DB 16;  Length 757;
  Best Local Similarity   97.7%;  Pred. No. 2.4e-178;
  Matches  672;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          1 CATATGGACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCG 60
              |||||||||||||||||||||||| ||||| || ||||||||||||||    || || |||
Db          1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCG 60

Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120

Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180

Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240

Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCT 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300

Qy        301 TACGCATGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
              |||   |||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360

Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420

Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480

Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540

Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600

Qy        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660

Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
              |||||||||||||||||||||||||||
Db        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688


RESULT 13
US-10-651-723-1055
; Sequence 1055, Application US/10651723
; Publication No. US20040057953A1
; GENERAL INFORMATION:
;  APPLICANT: FEIGE, ULRICH
;  APPLICANT:  LIU, CHUAN-FA
;  APPLICANT:  CHEETHAM, JANET C.
;  APPLICANT:  BOONE, THOMAS CHARLES
```

```
;  TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
;  FILE REFERENCE: A-527
;  CURRENT APPLICATION NUMBER: US/10/651,723
;  CURRENT FILING DATE:  2003-08-29
;  PRIOR APPLICATION NUMBER: US/09/428,082B
;  PRIOR FILING DATE: 1999-10-22
;  PRIOR APPLICATION NUMBER: 60/105,371
;  PRIOR FILING DATE: 1998-10-23
;  NUMBER OF SEQ ID NOS: 1133
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1055
;   LENGTH: 757
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: FC-TNF-ALPA INHIBITORS
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (4)..(747)
;   OTHER INFORMATION:
US-10-651-723-1055

  Query Match             58.4%;  Score 662.4;  DB 16;  Length 757;
  Best Local Similarity   97.7%;  Pred. No. 2.4e-178;
  Matches  672;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          1 CATATGGACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCG 60
              |||||||||||||||||||||||| ||||| || ||||||||||||||   || || |||
Db          1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCG 60

Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120

Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180

Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240

Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCT 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300

Qy        301 TACGCATGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
              |||   |||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360

Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420

Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480

Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540

Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600

Qy        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660

Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
              |||||||||||||||||||||||||||
Db        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
```

```
RESULT 14
US-10-645-761-1055
; Sequence 1055, Application US/10645761
; Publication No. US20040071712A1
; GENERAL INFORMATION:
;  APPLICANT: FEIGE, ULRICH
;  APPLICANT:  LIU, CHUAN-FA
;  APPLICANT:  CHEETHAM, JANET C.
;  APPLICANT:  BOONE, THOMAS CHARLES
;  TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
;  FILE REFERENCE: A-527
;  CURRENT APPLICATION NUMBER: US/10/645,761
;  CURRENT FILING DATE:  2003-08-18
;  PRIOR APPLICATION NUMBER: US/09/428,082B
;  PRIOR FILING DATE: 1999-10-22
;  PRIOR APPLICATION NUMBER: 60/105,371
;  PRIOR FILING DATE: 1998-10-23
;  NUMBER OF SEQ ID NOS: 1133
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1055
;   LENGTH: 757
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: FC-TNF-ALPA INHIBITORS
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (4)..(747)
;   OTHER INFORMATION:
US-10-645-761-1055

  Query Match             58.4%;  Score 662.4;  DB 16;  Length 757;
  Best Local Similarity   97.7%;  Pred. No. 2.4e-178;
  Matches  672;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          1 CATATGGACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCG 60
              |||||||||||||||||||||||| ||||| || ||||||||||||||   || || |||
Db          1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCG 60

Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120

Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180

Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240

Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCT 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300

Qy        301 TACGCATGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
              |||   |||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360

Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420

Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480

Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
```

```
Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600

Qy        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660

Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
              ||||||||||||||||||||||||||||
Db        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688


RESULT 15
US-10-666-696-1055
; Sequence 1055, Application US/10666696
; Publication No. US20040077022A1
; GENERAL INFORMATION:
;  APPLICANT: FEIGE, ULRICH
;  APPLICANT:  LIU, CHUAN-FA
;  APPLICANT:  CHEETHAM, JANET C.
;  APPLICANT:  BOONE, THOMAS CHARLES
;  APPLICANT:  GUDAS, JEAN MARIE
;  TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
;  FILE REFERENCE: A-527A
;  CURRENT APPLICATION NUMBER: US/10/666,696
;  CURRENT FILING DATE:  2003-09-19
;  PRIOR APPLICATION NUMBER: US/09/563,286C
;  PRIOR FILING DATE: 2000-05-03
;  PRIOR APPLICATION NUMBER: 09/428,082
;  PRIOR FILING DATE: 1999-10-22
;  PRIOR APPLICATION NUMBER: 60/105,371
;  PRIOR FILING DATE: 1998-10-23
;  NUMBER OF SEQ ID NOS: 1157
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1055
;   LENGTH: 757
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Fc-TNF-ALPHA INHIBITORS
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (4)..(747)
;   OTHER INFORMATION:
US-10-666-696-1055

  Query Match           58.4%;  Score 662.4;  DB 16;  Length 757;
  Best Local Similarity  97.7%;  Pred. No. 2.4e-178;
  Matches  672;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          1 CATATGGACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCG 60
              |||||||||||||||||||||| ||||| || ||||||||||||||   || || |||
Db          1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCG 60

Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120

Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180

Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240

Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 300

Qy        301 TACGCATGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
              |||   |||  ||||||||||||||||||||||||||||||||||||||||||||||||

Db        301 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360

Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420

Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480

Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540

Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600

Qy        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660

Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
              ||||||||||||||||||||||||||||
Db        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688


Search completed: October 17, 2004, 18:18:54
Job time : 581.552 secs
```

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 17, 2004, 15:27:13 ; Search time 102.696 Seconds
(without alignments)
7855.635 Million cell updates/sec

Title: US-10-679-999-16
Perfect score: 1135
Sequence: 1 CATATGGACAAAACTCACAC.....TCCGGGTTGTTAATGGATCC 1135

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	662.4	58.4	748	4	US-09-428-082B-1067	Sequence 1067, Ap
2	662.4	58.4	757	4	US-09-428-082B-1055	Sequence 1055, Ap
3	662.4	58.4	763	4	US-09-428-082B-1059	Sequence 1059, Ap
4	662.4	58.4	794	4	US-09-428-082B-5	Sequence 5, Appli
5	662.4	58.4	812	4	US-09-428-082B-15	Sequence 15, Appl
6	662.4	58.4	861	4	US-09-428-082B-7	Sequence 7, Appli
7	660.8	58.2	773	4	US-09-428-082B-1063	Sequence 1063, Ap
8	658.6	58.0	1467	4	US-09-499-846-11	Sequence 11, Appl
9	658.6	58.0	1494	4	US-09-499-846-9	Sequence 9, Appli
10	658.6	58.0	1578	4	US-09-499-846-7	Sequence 7, Appli
11	658.4	58.0	684	4	US-09-428-082B-1	Sequence 1, Appli
12	658.4	58.0	684	4	US-09-847-249A-1	Sequence 1, Appli
13	658.4	58.0	684	4	US-09-840-669B-1	Sequence 1, Appli
14	658.4	58.0	684	4	US-09-843-221A-1	Sequence 1, Appli
15	657.8	58.0	1720	4	US-09-746-359A-52	Sequence 52, Appl
16	657.6	57.9	885	4	US-09-428-082B-21	Sequence 21, Appl
17	657.2	57.9	1050	1	US-07-940-861-42	Sequence 42, Appl
18	657.2	57.9	1050	1	US-08-459-512-42	Sequence 42, Appl
19	657.2	57.9	1050	2	US-08-459-657-42	Sequence 42, Appl
20	657.2	57.9	1050	2	US-08-460-132-42	Sequence 42, Appl
21	657.2	57.9	1050	3	US-08-466-465-7	Sequence 7, Appli
22	657.2	57.9	1050	4	US-09-730-465-7	Sequence 7, Appli
23	657.2	57.9	1050	5	PCT-US92-02050-42	Sequence 42, Appl
24	657.2	57.9	1446	3	US-09-189-129-1	Sequence 1, Appli
25	657.2	57.9	1446	4	US-09-824-286-1	Sequence 1, Appli
26	657.2	57.9	2043	3	US-08-227-496C-14	Sequence 14, Appl
27	657	57.9	705	4	US-09-023-655-1223	Sequence 1223, Ap
28	657	57.9	1019	3	US-09-178-869-1	Sequence 1, Appli
29	657	57.9	1019	4	US-09-761-413-1	Sequence 1, Appli
30	657	57.9	1080	3	US-09-180-100-14	Sequence 14, Appl
31	657	57.9	1182	3	US-09-180-100-18	Sequence 18, Appl
32	657	57.9	1272	5	PCT-US95-03866-11	Sequence 11, Appl
33	657	57.9	1272	5	PCT-US95-03866-13	Sequence 13, Appl
34	657	57.9	1428	1	US-08-488-376-19	Sequence 19, Appl
35	657	57.9	1428	2	US-08-634-223-19	Sequence 19, Appl
36	657	57.9	1428	2	US-08-634-224-19	Sequence 19, Appl
37	657	57.9	1428	2	US-08-634-400-19	Sequence 19, Appl
38	657	57.9	1428	2	US-08-635-878-19	Sequence 19, Appl
39	657	57.9	1428	2	US-08-770-057-19	Sequence 19, Appl
40	657	57.9	1428	3	US-09-335-697B-19	Sequence 19, Appl
41	657	57.9	1428	4	US-09-335-697B-19	Sequence 19, Appl
42	657	57.9	1428	4	US-09-740-002-19	Sequence 19, Appl
43	657	57.9	1431	3	US-08-487-550-3	Sequence 3, Appli
44	657	57.9	1431	3	US-08-487-550-11	Sequence 11, Appl
45	657	57.9	1431	4	US-09-526-098-3	Sequence 3, Appli

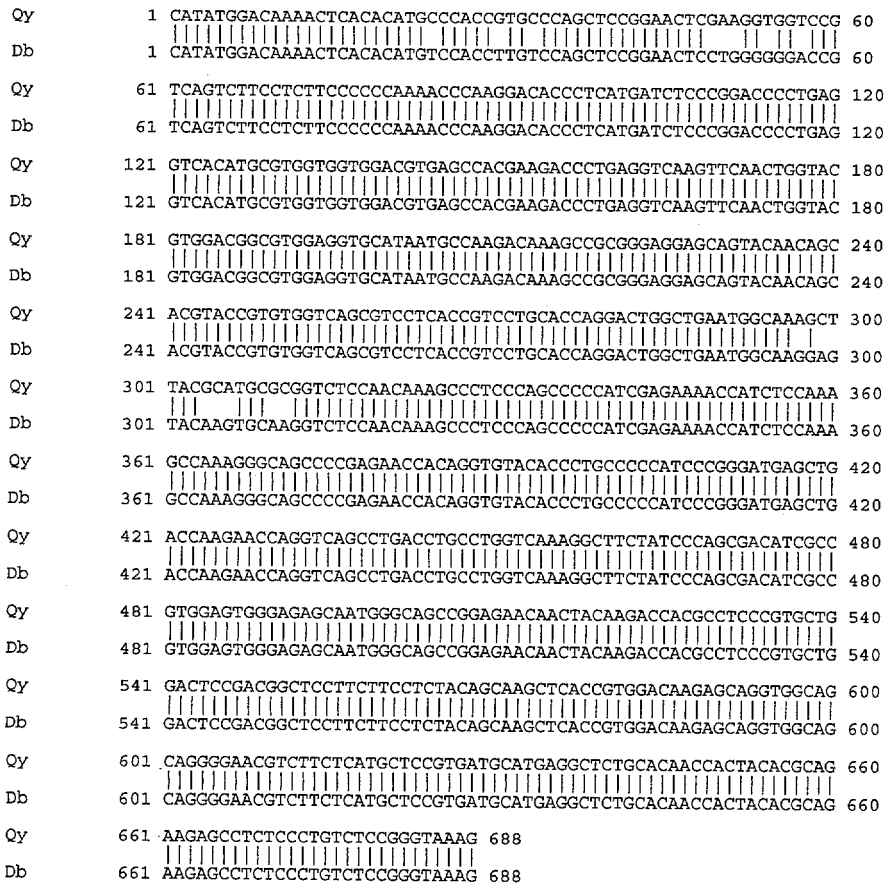
ALIGNMENTS

RESULT 1
US-09-428-082B-1067
; Sequence 1067, Application US/09428082B
; Patent No. 6660843
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/09/428,082B
; CURRENT FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1067
; LENGTH: 748
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fc MMP INHIBITOR
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (4)..(732)
; OTHER INFORMATION:
US-09-428-082B-1067

Query Match 58.4%; Score 662.4; DB 4; Length 748;
Best Local Similarity 97.7%; Pred. No. 3.5e-165;
Matches 672; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

```
Qy          1 CATATGGACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCG 60
              ||||||||||||||||||||||| ||||| || ||||||||||||||   || || |||
Db          1 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCG 60

Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120

Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180

Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240

Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCT 300
```

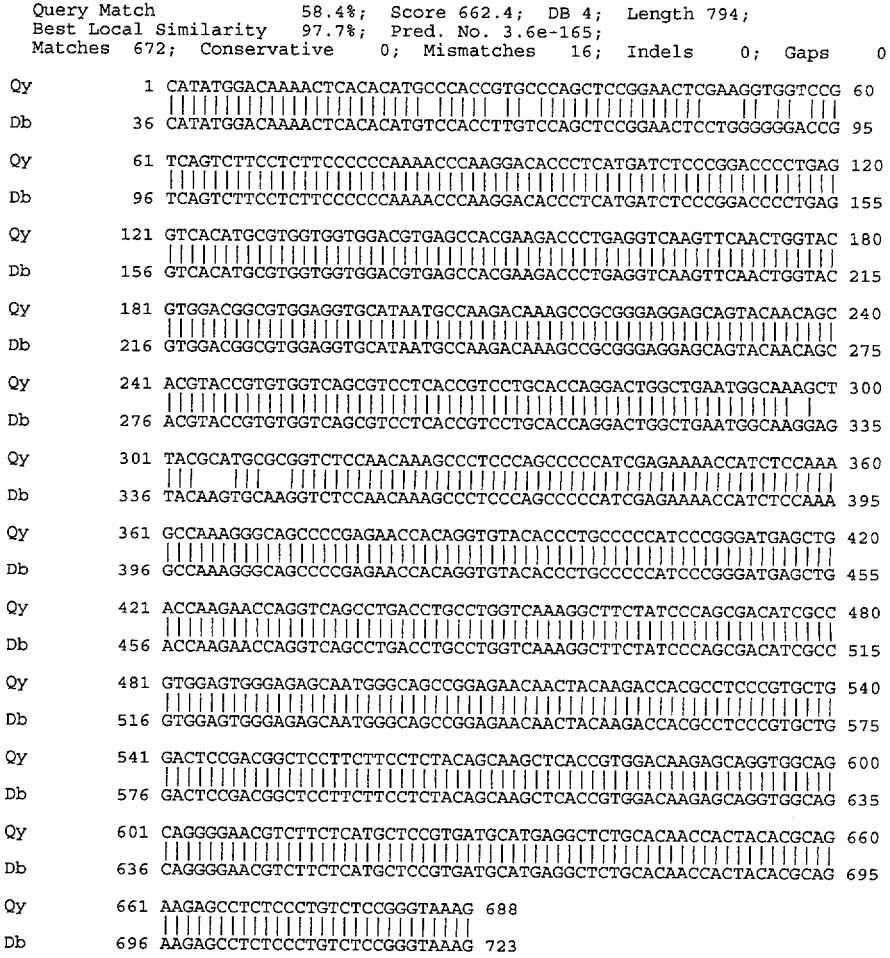
```
                    ||||||
```



RESULT 4
US-09-428-082B-5
; Sequence 5, Application US/09428082B
; Patent No. 6660843
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/09/428,082B
; CURRENT FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 794
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fc-TMP

; FEATURE:
; NAME/KEY: CDS
; LOCATION: (39)..(779)
; OTHER INFORMATION:
US-09-428-082B-5

Query Match 58.4%; Score 662.4; DB 4; Length 794;
Best Local Similarity 97.7%; Pred. No. 3.6e-165;
Matches 672; Conservative 0; Mismatches 16; Indels 0; Gaps 0;



RESULT 5
US-09-428-082B-15
; Sequence 15, Application US/09428082B
; Patent No. 6660843
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/09/428,082B
; CURRENT FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371

```
;  PRIOR FILING DATE: 1998-10-23
;  NUMBER OF SEQ ID NOS: 1133
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
;   LENGTH: 812
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Fc-EMP
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (39)..(797)
;   OTHER INFORMATION:
US-09-428-082B-15

  Query Match           58.4%;  Score 662.4;  DB 4;  Length 812;
  Best Local Similarity  97.7%;  Pred. No. 3.7e-165;
  Matches  672;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          1 CATATGGACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCG 60
              ||||||||||||||||||||||| ||||| || ||||||||||||||   || || |||
Db         36 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCG 95

Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         96 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 155

Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        156 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 215

Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        216 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 275

Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCT 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        276 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 335

Qy        301 TACGCATGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
              |||   |||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db        336 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 395

Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        396 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 455

Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        456 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 515

Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        516 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 575

Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        576 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 635

Qy        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        636 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 695

Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
              |||||||||||||||||||||||||||
Db        696 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 723


RESULT 6
US-09-428-082B-7
; Sequence 7, Application US/09428082B
; Patent No. 6660843
; GENERAL INFORMATION:
;  APPLICANT: FEIGE, ULRICH
;  APPLICANT:  LIU, CHUAN-FA
;  APPLICANT:  CHEETHAM, JANET C.
;  APPLICANT:  BOONE, THOMAS CHARLES
;  TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
;  FILE REFERENCE: A-527
;  CURRENT APPLICATION NUMBER: US/09/428,082B
;  CURRENT FILING DATE:  1999-10-22
;  PRIOR APPLICATION NUMBER: 60/105,371
;  PRIOR FILING DATE: 1998-10-23
;  NUMBER OF SEQ ID NOS: 1133
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
;   LENGTH: 861
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Fc-TMP-TMP
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (39)..(842)
;   OTHER INFORMATION:
US-09-428-082B-7

  Query Match           58.4%;  Score 662.4;  DB 4;  Length 861;
  Best Local Similarity  97.7%;  Pred. No. 3.7e-165;
  Matches  672;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          1 CATATGGACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCG 60
              ||||||||||||||||||||||| ||||| || ||||||||||||||   || || |||
Db         36 CATATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCG 95

Qy         61 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         96 TCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG 155

Qy        121 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        156 GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC 215

Qy        181 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        216 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGC 275

Qy        241 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCT 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        276 ACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAG 335

Qy        301 TACGCATGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 360
              |||   |||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db        336 TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAA 395

Qy        361 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        396 GCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTG 455

Qy        421 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        456 ACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC 515

Qy        481 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        516 GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTG 575

Qy        541 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        576 GACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG 635

Qy        601 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        636 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAG 695

Qy        661 AAGAGCCTCTCCCTGTCTCCGGGTAAAG 688
```

```
                                                
```

```
Db       1264 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 1323

Qy        547 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1324 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 1383

Qy        607 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1384 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 1443

Qy        667 CTCTCCCTGTCTCCGGGTAAA 687
              |||||||||||||||||||||
Db       1444 CTCTCCCTGTCTCCGGGTAAA 1464


RESULT 9
US-09-499-846-9
; Sequence 9, Application US/09499846
; Patent No. 6656728
; GENERAL INFORMATION:
;  APPLICANT: Kavanaugh et al.
;  TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR
;  TITLE OF INVENTION:  RECEPTOR-IMMUNOGLOBULIN FUSION
;  FILE REFERENCE: 035784/195012 (5784-
;  CURRENT APPLICATION NUMBER: US/09/499,846
;  CURRENT FILING DATE:  2000-02-07
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 9
;   LENGTH: 1494
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)...(1494)
US-09-499-846-9

  Query Match            58.0%;  Score 658.6;  DB 4;  Length 1494;
  Best Local Similarity  97.9%;  Pred. No. 4.6e-164;
  Matches  667;  Conservative    0;  Mismatches   14;  Indels    0;  Gaps    0;

Qy          7 GACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCGTCAGTC 66
              |||||||||||||||||||||||||||||||| || |||||||| || || |||||||||
Db        811 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCGAGGGGGGACCGTCAGTC 870

Qy         67 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 126
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        871 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 930

Qy        127 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 186
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        931 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 990

Qy        187 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 246
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        991 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 1050

Qy        247 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCTTACGCA 306
              |||||||||||||||||||||||||||||||||||||||||||||||||||| |  |||
Db       1051 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 1110

Qy        307 TGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 366
              |||  |||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db       1111 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCTCCATCGAGAAAACCATCTCCAAAGCCAAA 1170

Qy        367 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 426
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1171 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 1230

Qy        427 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 486
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1231 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 1290

Qy        487 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1291 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 1350

Qy        547 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1351 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 1410

Qy        607 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1411 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 1470

Qy        667 CTCTCCCTGTCTCCGGGTAAA 687
              |||||||||||||||||||||
Db       1471 CTCTCCCTGTCTCCGGGTAAA 1491


RESULT 10
US-09-499-846-7
; Sequence 7, Application US/09499846
; Patent No. 6656728
; GENERAL INFORMATION:
;  APPLICANT: Kavanaugh et al.
;  TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR
;  TITLE OF INVENTION:  RECEPTOR-IMMUNOGLOBULIN FUSION
;  FILE REFERENCE: 035784/195012 (5784-
;  CURRENT APPLICATION NUMBER: US/09/499,846
;  CURRENT FILING DATE:  2000-02-07
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 7
;   LENGTH: 1578
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)...(1578)
US-09-499-846-7

  Query Match            58.0%;  Score 658.6;  DB 4;  Length 1578;
  Best Local Similarity  97.9%;  Pred. No. 4.7e-164;
  Matches  667;  Conservative    0;  Mismatches   14;  Indels    0;  Gaps    0;

Qy          7 GACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCGTCAGTC 66
              |||||||||||||||||||||||||||||||| || |||||||| || || |||||||||
Db        895 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCGAGGGGGGACCGTCAGTC 954

Qy         67 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 126
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        955 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 1014

Qy        127 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 186
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1015 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 1074

Qy        187 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 246
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1075 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 1134

Qy        247 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCTTACGCA 306
              |||||||||||||||||||||||||||||||||||||||||||||||||||| |  |||
Db       1135 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 1194

Qy        307 TGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 366
              |||  |||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db       1195 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCTCCATCGAGAAAACCATCTCCAAAGCCAAA 1254

Qy        367 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 426
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1255 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 1314

Qy        427 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 486
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db       1315 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 1374

Qy        487 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1375 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 1434

Qy        547 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1435 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 1494

Qy        607 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1495 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 1554

Qy        667 CTCTCCCTGTCTCCGGGTAAA 687
              |||||||||||||||||||||
Db       1555 CTCTCCCTGTCTCCGGGTAAA 1575
```

RESULT 11
US-09-428-082B-1
; Sequence 1, Application US/09428082B
; Patent No. 6660843
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/09/428,082B
; CURRENT FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 684
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(684)
; OTHER INFORMATION:
US-09-428-082B-1

Query Match 58.0%; Score 658.4; DB 4; Length 684;
Best Local Similarity 97.7%; Pred. No. 3.9e-164;
Matches 668; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

```
Qy           4 ATGGACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCGTCA 63
               |||||||||||||||||||| ||||| || |||||||||||||||   || || ||||||
Db           1 ATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCGTCA 60

Qy          64 GTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTC 123
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 GTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTC 120

Qy         124 ACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTG 183
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 ACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTG 180

Qy         184 GACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACG 243
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 GACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACG 240

Qy         244 TACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCTTAC 303
               |||||||||||||||||||||||||||||||||||||||||||||||||||| | |||
Db         241 TACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTAC 300

Qy         304 GCATGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCC 363
               |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 AAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCC 360

Qy         364 AAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACC 423
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         361 AAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACC 420

Qy         424 AAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTG 483
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         421 AAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTG 480

Qy         484 GAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGAC 543
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         481 GAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGAC 540

Qy         544 TCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAG 603
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         541 TCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAG 600

Qy         604 GGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAG 663
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         601 GGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAG 660

Qy         664 AGCCTCTCCCTGTCTCCGGGTAAA 687
               |||||||||||||||||||||||||
Db         661 AGCCTCTCCCTGTCTCCGGGTAAA 684
```

RESULT 12
US-09-847-249A-1
; Sequence 1, Application US/09847249A
; Patent No. 6677136
; GENERAL INFORMATION:
; APPLICANT: MARSHALL, WILLIAM S.
; APPLICANT: STARK, KEVIN LEE
; TITLE OF INVENTION: GLUCAGON ANTAGONIST
; FILE REFERENCE: A-693
; CURRENT APPLICATION NUMBER: US/09/847,249A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,436
; PRIOR FILING DATE: 2000-05-03
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 684
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(684)
; OTHER INFORMATION:
US-09-847-249A-1

Query Match 58.0%; Score 658.4; DB 4; Length 684;
Best Local Similarity 97.7%; Pred. No. 3.9e-164;
Matches 668; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

```
Qy           4 ATGGACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCGTCA 63
               |||||||||||||||||||| ||||| || |||||||||||||||   || || ||||||
Db           1 ATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCGTCA 60

Qy          64 GTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTC 123
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 GTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTC 120

Qy         124 ACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTG 183
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 ACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTG 180

Qy         184 GACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACG 243
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 GACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACG 240

Qy         244 TACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCTTAC 303
               |||||||||||||||||||||||||||||||||||||||||||||||||||| | |||
```

```
Db        241 TACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTAC 300

Qy        304 GCATGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCC 363

Db        301 AAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCC 360

Qy        364 AAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACC 423

Db        361 AAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACC 420

Qy        424 AAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTG 483

Db        421 AAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTG 480

Qy        484 GAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGAC 543

Db        481 GAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGAC 540

Qy        544 TCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAG 603

Db        541 TCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAG 600

Qy        604 GGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAG 663

Db        601 GGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAG 660

Qy        664 AGCCTCTCCCTGTCTCCGGGTAAA 687

Db        661 AGCCTCTCCCTGTCTCCGGGTAAA 684
```

RESULT 13
US-09-840-669B-1
; Sequence 1, Application US/09840669B
; Patent No. 6743778
; GENERAL INFORMATION:
; APPLICANT: KOHNO, TADAHIKO
; TITLE OF INVENTION: APO-AI/AII PEPTIDE DERIVATIVES
; FILE REFERENCE: A-690
; CURRENT APPLICATION NUMBER: US/09/840,669B
; CURRENT FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: 60/198,920
; PRIOR FILING DATE: 2000-04-21
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 684
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(684)
; OTHER INFORMATION:
US-09-840-669B-1

Query Match 58.0%; Score 658.4; DB 4; Length 684;
Best Local Similarity 97.7%; Pred. No. 3.9e-164;
Matches 668; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

```
Qy          4 ATGGACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCGTCA 63

Db          1 ATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCGTCA 60

Qy         64 GTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTC 123

Db         61 GTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTC 120

Qy        124 ACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTG 183

Db        121 ACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTG 180

Qy        184 GACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACG 243

Db        181 GACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACG 240

Qy        244 TACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCTTAC 303

Db        241 TACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTAC 300

Qy        304 GCATGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCC 363

Db        301 AAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCC 360

Qy        364 AAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACC 423

Db        361 AAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACC 420

Qy        424 AAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTG 483

Db        421 AAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTG 480

Qy        484 GAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGAC 543

Db        481 GAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGAC 540

Qy        544 TCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAG 603

Db        541 TCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAG 600

Qy        604 GGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAG 663

Db        601 GGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAG 660

Qy        664 AGCCTCTCCCTGTCTCCGGGTAAA 687

Db        661 AGCCTCTCCCTGTCTCCGGGTAAA 684
```

RESULT 14
US-09-843-221A-1
; Sequence 1, Application US/09843221A
; Patent No. 6756480
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 684
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(684)
; OTHER INFORMATION:
US-09-843-221A-1

Query Match 58.0%; Score 658.4; DB 4; Length 684;
Best Local Similarity 97.7%; Pred. No. 3.9e-164;
Matches 668; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

```
Qy          4 ATGGACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCGTCA 63

Db          1 ATGGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGACCGTCA 60
```

```
Qy         64 GTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTC 123
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTC 120

Qy        124 ACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTG 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTG 180

Qy        184 GACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACG 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACG 240

Qy        244 TACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCTTAC 303
              |||||||||||||||||||||||||||||||||||||||||||||||| |  |||
Db        241 TACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTAC 300

Qy        304 GCATGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCC 363
                 |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCC 360

Qy        364 AAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACC 423
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACC 420

Qy        424 AAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTG 483
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTG 480

Qy        484 GAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGAC 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGAC 540

Qy        544 TCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAG 603
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAG 600

Qy        604 GGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAG 663
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAG 660

Qy        664 AGCCTCTCCCTGTCTCCGGGTAAA 687
              |||||||||||||||||||||||||
Db        661 AGCCTCTCCCTGTCTCCGGGTAAA 684
```

```
RESULT 15
US-09-746-359A-52
; Sequence 52, Application US/09746359A
; Patent No. 6610286
; GENERAL INFORMATION:
;  APPLICANT: Thompson, Penny
;  APPLICANT:  Foster, Donald C.
;  APPLICANT:  Xu, Wenfeng
;  APPLICANT:  Madden, Karen L.
;  APPLICANT:  Kelly, James D.
;  APPLICANT:  Sprecher, Cindy A.
;  APPLICANT:  Blumberg, Hal
;  APPLICANT:  Eagan, Maribeth A.
;  APPLICANT:  Jaspers, Stephen R.
;  APPLICANT:  Chandrasekher, Yasmin A.
;  APPLICANT:  No. 6610286ak, Julia E.
;  TITLE OF INVENTION: Method for Treating Inflammation
;  FILE REFERENCE: 99-108
;  CURRENT APPLICATION NUMBER: US/09/746,359A
;  CURRENT FILING DATE:  2001-05-21
;  PRIOR APPLICATION NUMBER: 60/171,969
;  PRIOR FILING DATE: 1999-12-23
;  PRIOR APPLICATION NUMBER: 60/213,341
;  PRIOR FILING DATE: 2000-06-22
;  NUMBER OF SEQ ID NOS: 72
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 52
;  LENGTH: 1720
;  TYPE: DNA
;  ORGANISM: Homo sapiens
;  FEATURE:
;  NAME/KEY: CDS
;  LOCATION: (1)...(1713)
US-09-746-359A-52

  Query Match             58.0%;  Score 657.8;  DB 4;  Length 1720;
  Best Local Similarity   97.5%;  Pred. No. 7.9e-164;
  Matches  668;  Conservative    0;  Mismatches   17;  Indels    0;  Gaps    0;
```

```
Qy          7 GACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCGTCAGTC 66
              |||||||||||||||||||||||||||||| || ||||||   || || |||||||||
Db       1033 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC 1092

Qy         67 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1093 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 1152

Qy        127 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1153 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 1212

Qy        187 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1213 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 1272

Qy        247 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCTTACGCA 306
              |||||||||||||||||||||||||||||||||||||||||||||||||||| |  |||
Db       1273 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 1332

Qy        307 TGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 366
              |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1333 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 1392

Qy        367 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1393 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 1452

Qy        427 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1453 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 1512

Qy        487 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1513 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 1572

Qy        547 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1573 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 1632

Qy        607 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1633 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 1692

Qy        667 CTCTCCCTGTCTCCGGGTAAAGTAC 691
              |||||||||||||||||||  ||
Db       1693 CTCTCCCTGTCTCCGGGTAAATGAC 1717
```

Search completed: October 17, 2004, 17:00:43
Job time : 104.696 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 17, 2004, 15:34:57 ; Search time 4354.1 Seconds
(without alignments)
11298.387 Million cell updates/sec

Title: US-10-679-999-17
Perfect score: 1135
Sequence: 1 GTATACCTGTTTTGAGTGTG.....AGGCCCAACAATTACCTAGG 1135

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1135	100.0	1135	6	BD056524	BD056524 OB fusion
2	1109.4	97.7	1135	6	BD056522	BD056522 OB fusion
3	1105	97.4	1150	6	BD056518	BD056518 OB fusion
4	1103.4	97.2	1150	6	BD056520	BD056520 OB fusion
5	662.4	58.4	861	6	BD263010	BD263010 Dimeric t
6	658.4	58.0	684	6	BD263000	BD263000 Dimeric t
7	638.4	56.2	1142	6	I27618	I27618 Sequence 9
8	440.8	38.8	454	6	BD004077	BD004077 Methods o
9	440.8	38.8	454	6	BD056516	BD056516 OB fusion
10	378.4	33.3	491	6	BD004075	BD004075 Methods o
11	378.4	33.3	491	6	BD056514	BD056514 OB fusion
12	361.6	31.9	1528	6	BD105735	BD105735 A method
13	361.6	31.9	1528	6	BD105743	BD105743 Immunoglo
14	60	5.3	2287	6	AR029004	AR029004 Sequence
15	60	5.3	2287	6	AR037308	AR037308 Sequence
16	60	5.3	2287	6	I90051	I90051 Sequence 1
17	60	5.3	2287	6	AR392155	AR392155 Sequence
18	60	5.3	2287	6	BD000539	BD000539 Antibody
c 19	51	4.5	125020	9	AF429315	AF429315 Homo sapi
c 20	49.8	4.4	232373	2	AC134805	AC134805 Rattus no
21	49.4	4.4	125020	9	AF429315	AF429315 Homo sapi
22	49.2	4.3	908	8	AB029092	AB029092 Cucumis s
23	49.2	4.3	1110	8	AB029147	AB029147 Cucumis s
c 24	48	4.2	234964	2	AC094679	AC094679 Rattus no
25	46.8	4.1	178323	2	AC126315	AC126315 Rattus no
26	46.2	4.1	178372	2	BX569797	BX569797 Danio rer
c 27	46.2	4.1	181047	5	AC139110	AC139110 Danio rer
28	46.2	4.1	191401	5	BX470130	BX470130 Zebrafish
c 29	44.6	3.9	109521	2	AP005551	AP005551 Oryza sat
c 30	44.6	3.9	127200	10	AC132580	AC132580 Mus muscu
c 31	44.4	3.9	174423	2	AC141189	AC141189 Rattus no
c 32	44.4	3.9	261604	2	AC119819	AC119819 Mus muscu
33	44	3.9	282995	2	AC131530	AC131530 Rattus no
c 34	43.8	3.9	2000	6	AX655393	AX655393 Sequence
35	43.4	3.8	174423	2	AC141189	AC141189 Rattus no
36	43.2	3.8	222797	2	AC126213	AC126213 Rattus no
c 37	43.2	3.8	236770	2	AC096493	AC096493 Rattus no
c 38	43.2	3.8	246199	2	AC119558	AC119558 Rattus no
c 39	43.2	3.8	253094	2	AC113774	AC113774 Rattus no
c 40	43.2	3.8	294769	2	AC098907	AC098907 Rattus no
41	43	3.8	468	6	I27620	I27620 Sequence 12
42	43	3.8	746	6	A51599	A51599 Sequence 9
c 43	43	3.8	216609	2	AC142133	AC142133 Rattus no
44	43	3.8	303774	2	AC105878	AC105878 Rattus no
c 45	42.8	3.8	175351	2	AC117900	AC117900 Rattus no

ALIGNMENTS

RESULT 1
BD056524
LOCUS BD056524 1135 bp DNA linear PAT 27-AUG-2002
DEFINITION OB fusion protein compositions and methods.
ACCESSION BD056524
VERSION BD056524.1 GI:22602130
KEYWORDS JP 2001512417-A/12.
SOURCE Aequorea victoria
ORGANISM Aequorea victoria
Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae; Aequorea.
REFERENCE 1 (bases 1 to 1135)
AUTHORS Mann,M.B. and Hecht,R.I.
TITLE OB fusion protein compositions and methods
JOURNAL Patent: JP 2001512417-A 12 21-AUG-2001;

```
            AMGEN INC
COMMENT     PN   JP 2001512417-A/12
            PD   21-AUG-2001
            PF   11-DEC-1997 JP 1998528896
            PR   20-DEC-1996 US    08/770973
            PI   MICHAEL BENJAMIN MANN,RANDY IRA HECHT
            PC   C07K14/575,A61K38/00,A61P3/04,A61P3/06,A61P3/10,A61P9/10, PC
            A61P43/00,
            PC   C12N15/09,C12N15/00,A61K37/02
            CC   Strandedness: Double;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers.
FEATURES              Location/Qualifiers
     source           1. .1135
                      /organism="Aequorea victoria"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:6100"
ORIGIN

  Query Match           100.0%;  Score 1135;  DB 6;  Length 1135;
  Best Local Similarity  100.0%;  Pred. No. 1.8e-266;
  Matches 1135;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTATACCTGTTTTGAGTGTGTACGGGTGGCACGGGTCGAGGCCTTGAGCTTCCACCAGGC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GTATACCTGTTTTGAGTGTGTACGGGTGGCACGGGTCGAGGCCTTGAGCTTCCACCAGGC 60

Qy         61 AGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTC 120

Qy        121 CAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATG 180

Qy        181 CACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCG 240

Qy        241 TGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTTCGA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTTCGA 300

Qy        301 ATGCGTACGCGCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATGCGTACGCGCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTT 360

Qy        361 CGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGAC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGAC 420

Qy        421 TGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGG 480

Qy        481 CACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGAC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGAC 540

Qy        541 CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTC 600

Qy        601 GTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTC 660

Qy        661 TTCTCGGAGAGGGACAGAGGCCCATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TTCTCGGAGAGGGACAGAGGCCCATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTT 720

Qy        721 TGGAATTAATTTTGCTAGCAATGCGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAATTAATTTTGCTAGCAATGCGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCG 780

Qy        781 AGATTTGTCTTTCAATGTCCGGACCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AGATTTGTCTTTCAATGTCCGGACCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAAC 840

Qy        841 AGGTTTTACCTGGTCTGGGACCGACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AGGTTTTACCTGGTCTGGGACCGACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCA 900

Qy        901 TTGCAATAGGTCTAGAGATTGCTGGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TTGCAATAGGTCTAGAGATTGCTGGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGT 960

Qy        961 AAGAGGTTTAGGACGGTGGACGGTACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AAGAGGTTTAGGACGGTGGACGGTACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCG 1020

Qy       1021 CCCCAGGACCTTCGTAGGCCAATGTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 CCCCAGGACCTTCGTAGGCCAATGTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCA 1080

Qy       1081 AGGGAAGTCCTGTACGAAACCGTCGACCTGGACAGAGGCCCAACAATTACCTAGG 1135
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 AGGGAAGTCCTGTACGAAACCGTCGACCTGGACAGAGGCCCAACAATTACCTAGG 1135


RESULT 2
BD056522
LOCUS       BD056522                1135 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  OB fusion protein compositions and methods.
ACCESSION   BD056522
VERSION     BD056522.1  GI:22602128
KEYWORDS    JP 2001512417-A/10.
SOURCE      Aequorea victoria
  ORGANISM  Aequorea victoria
            Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
            Aequoreidae; Aequorea.
REFERENCE   1  (bases 1 to 1135)
  AUTHORS   Mann,M.B. and Hecht,R.I.
  TITLE     OB fusion protein compositions and methods
  JOURNAL   Patent: JP 2001512417-A 10 21-AUG-2001;
            AMGEN INC
COMMENT     PN   JP 2001512417-A/10
            PD   21-AUG-2001
            PF   11-DEC-1997 JP 1998528896
            PR   20-DEC-1996 US    08/770973
            PI   MICHAEL BENJAMIN MANN,RANDY IRA HECHT
            PC   C07K14/575,A61K38/00,A61P3/04,A61P3/06,A61P3/10,A61P9/10, PC
            A61P43/00,
            PC   C12N15/09,C12N15/00,A61K37/02
            CC   Strandedness: Double;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers.
FEATURES              Location/Qualifiers
     source           1. .1135
                      /organism="Aequorea victoria"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:6100"
ORIGIN

  Query Match           97.7%;  Score 1109.4;  DB 6;  Length 1135;
  Best Local Similarity  98.6%;  Pred. No. 3.2e-260;
  Matches 1119;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          1 GTATACCTGTTTTGAGTGTGTACGGGTGGCACGGGTCGAGGCCTTGAGCTTCCACCAGGC 60
              |||||||||||||||||||| ||||| || ||||||||||||||    || |||||
Db          1 GTATACCTGTTTTGAGTGTGTACAGGTGGAACAGGTCGAGGCCTTGAGGACCCCCCAGGA 60

Qy         61 AGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTC 120
```

```
Qy       121 CAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATG 180
Db       121 CAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATG 180

Qy       181 CACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCG 240
Db       181 CACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCG 240

Qy       241 TGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTTCGA 300
Db       241 TGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTC 300

Qy       301 ATGCGTACGCGCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTT 360
Db       301 ATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTT 360

Qy       361 CGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGAC 420
Db       361 CGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGAC 420

Qy       421 TGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGG 480
Db       421 TGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGG 480

Qy       481 CACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGAC 540
Db       481 CACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGAC 540

Qy       541 CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTC 600
Db       541 CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTC 600

Qy       601 GTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTC 660
Db       601 GTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTC 660

Qy       661 TTCTCGGAGAGGGACAGAGGCCCATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTT 720
Db       661 TTCTCGGAGAGGGACAGAGGCCCATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTT 720

Qy       721 TGGAATTAATTTTGCTAGCAATGCGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCG 780
Db       721 TGGAATTAATTTTGCTAGCAATGCGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCG 780

Qy       781 AGATTTGTCTTTCAATGTCCGGACCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAAC 840
Db       781 AGATTTGTCTTTCAATGTCCGGACCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAAC 840

Qy       841 AGGTTTTACCTGGTCTGGGACCGACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCA 900
Db       841 AGGTTTTACCTGGTCTGGGACCGACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCA 900

Qy       901 TTGCAATAGGTCTAGAGATTGCTGGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGT 960
Db       901 TTGCAATAGGTCTAGAGATTGCTGGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGT 960

Qy       961 AAGAGGTTTAGGACGGTGGACGGTACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCG 1020
Db       961 AAGAGGTTTAGGACGGTGGACGGTACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCG 1020

Qy      1021 CCCCAGGACCTTCGTAGGCCAATGTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCA 1080
Db      1021 CCCCAGGACCTTCGTAGGCCAATGTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCA 1080

Qy      1081 AGGGAAGTCCTGTACGAAACCGTCGACCTGGACAGAGGCCCAACAATTACCTAGG 1135
Db      1081 AGGGAAGTCCTGTACGAAACCGTCGACCTGGACAGAGGCCCAACAATTACCTAGG 1135
```

RESULT 3
BD056518
LOCUS BD056518 1150 bp DNA linear PAT 27-AUG-2002
DEFINITION OB fusion protein compositions and methods.
ACCESSION BD056518
VERSION BD056518.1 GI:22602124
KEYWORDS JP 2001512417-A/6.
SOURCE Aequorea victoria
ORGANISM Aequorea victoria
Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae; Aequoreidae; Aequorea.
REFERENCE 1 (bases 1 to 1150)
AUTHORS Mann,M.B. and Hecht,R.I.
TITLE OB fusion protein compositions and methods
JOURNAL Patent: JP 2001512417-A 6 21-AUG-2001;
AMGEN INC
COMMENT PN JP 2001512417-A/6
PD 21-AUG-2001
PF 11-DEC-1997 JP 1998528896
PR 20-DEC-1996 US 08/770973
PI MICHAEL BENJAMIN MANN,RANDY IRA HECHT
PC C07K14/575,A61K38/00,A61P3/04,A61P3/06,A61P3/10,A61P9/10, PC A61P43/00,
PC C12N15/09,C12N15/00,A61K37/02
CC Strandedness: Double;
CC Topology: Linear;
FH Key Location/Qualifiers.
FEATURES Location/Qualifiers
source 1. .1150
/organism="Aequorea victoria"
/mol_type="genomic DNA"
/db_xref="taxon:6100"
ORIGIN

Query Match 97.4%; Score 1105; DB 6; Length 1150;
Best Local Similarity 98.7%; Pred. No. 3.8e-259;
Matches 1114; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

```
Qy         7 CTGTTTTGAGTGTGTACGGGTGGCACGGGTCGAGGCCTTGAGCTTCCACCAGGCAGTCAG 66
Db        22 CTGTTTTGAGTGTGTACGGGTGGCACGGGTCGTGGACTTGAGGACCCCCCTGGCAGTCAG 81

Qy        67 AAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGT 126
Db        82 AAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGT 141

Qy       127 ACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTG 186
Db       142 ACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTG 201

Qy       187 CCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATG 246
Db       202 CCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATG 261

Qy       247 GCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTTCGAATGCGT 306
Db       262 GCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATGTTC 321

Qy       307 ACGCGCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTT 366
Db       322 ACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTT 381

Qy       367 CCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTC 426
Db       382 CCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTC 441

Qy       427 TTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTC 486
Db       442 TTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTC 501

Qy       487 ACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGG 546
Db       502 ACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGG 561

Qy       547 CTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCC 606
Db       562 CTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCC 621
```

```
Qy        607 TTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCG 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        622 TTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCG 681

Qy        667 GAGAGGGACAGAGGCCCATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAAT 726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        682 GAGAGGGACAGAGGCCCATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAAT 741

Qy        727 TAATTTTGCTAGCAATGCGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTT 786
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        742 TAATTTTGCTAGCAATGCGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTT 801

Qy        787 GTCTTTCAATGTCCGGACCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTT 846
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        802 GTCTTTCAATGTCCGGACCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTT 861

Qy        847 TACCTGGTCTGGGACCGACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAA 906
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        862 TACCTGGTCTGGGACCGACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAA 921

Qy        907 TAGGTCTAGAGATTGCTGGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGG 966
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        922 TAGGTCTAGAGATTGCTGGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGG 981

Qy        967 TTTAGGACGGTGGACGGTACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAG 1026
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        982 TTTAGGACGGTGGACGGTACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAG 1041

Qy       1027 GACCTTCGTAGGCCAATGTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAA 1086
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1042 GACCTTCGTAGGCCAATGTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAA 1101

Qy       1087 GTCCTGTACGAAACCGTCGACCTGGACAGAGGCCCAACAATTACCTAGG 1135
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db       1102 GTCCTGTACGAAACCGTCGACCTGGACAGAGGCCCAACAATTACCTAGG 1150
```

```
RESULT 4
BD056520
LOCUS       BD056520                1150 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  OB fusion protein compositions and methods.
ACCESSION   BD056520
VERSION     BD056520.1  GI:22602126
KEYWORDS    JP 2001512417-A/8.
SOURCE      Aequorea victoria
  ORGANISM  Aequorea victoria
            Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
            Aequoreidae; Aequorea.
REFERENCE   1  (bases 1 to 1150)
  AUTHORS   Mann,M.B. and Hecht,R.I.
  TITLE     OB fusion protein compositions and methods
  JOURNAL   Patent: JP 2001512417-A 8 21-AUG-2001;
            AMGEN INC
COMMENT     PN   JP 2001512417-A/8
            PD   21-AUG-2001
            PF   11-DEC-1997 JP 1998528896
            PR   20-DEC-1996 US    08/770973
            PI   MICHAEL BENJAMIN MANN,RANDY IRA HECHT
            PC   C07K14/575,A61K38/00,A61P3/04,A61P3/06,A61P3/10,A61P9/10, PC
            A61P43/00,
            PC   C12N15/09,C12N15/00,A61K37/02
            CC   Strandedness: Double;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers.
FEATURES                Location/Qualifiers
     source             1. .1150
                        /organism="Aequorea victoria"
                        /mol_type="genomic DNA"
                        /db_xref="taxon:6100"

ORIGIN

  Query Match           97.2%;  Score 1103.4;  DB 6;  Length 1150;
```

```
  Best Local Similarity   98.6%;  Pred. No. 9.3e-259;
  Matches 1113;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          7 CTGTTTTGAGTGTGTACGGGTGGCACGGGTCGAGGCCTTGAGCTTCCACCAGGCAGTCAG 66
              |||||||||||||||| ||||| || ||||||||||||||    || ||||| ||||||
Db         22 CTGTTTTGAGTGTGTACAGGTGGAACAGGTCGAGGCCTTGAGGACCCCCCAGGAAGTCAG 81

Qy         67 AAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGT 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         82 AAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGT 141

Qy        127 ACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTG 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        142 ACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTG 201

Qy        187 CCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATG 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        202 CCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATG 261

Qy        247 GCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTTCGAATGCGT 306
              |||||||||||||||||||||||||||||||||||||||||||||||| | |||
Db        262 GCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATGTTC 321

Qy        307 ACGCGCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTT 366
              ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        322 ACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTT 381

Qy        367 CCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTC 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        382 CCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTC 441

Qy        427 TTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTC 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        442 TTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTC 501

Qy        487 ACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGG 546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        502 ACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGG 561

Qy        547 CTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCC 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        562 CTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCC 621

Qy        607 TTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCG 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        622 TTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCG 681

Qy        667 GAGAGGGACAGAGGCCCATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAAT 726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        682 GAGAGGGACAGAGGCCCATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAAT 741

Qy        727 TAATTTTGCTAGCAATGCGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTT 786
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        742 TAATTTTGCTAGCAATGCGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTT 801

Qy        787 GTCTTTCAATGTCCGGACCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTT 846
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        802 GTCTTTCAATGTCCGGACCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTT 861

Qy        847 TACCTGGTCTGGGACCGACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAA 906
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        862 TACCTGGTCTGGGACCGACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAA 921

Qy        907 TAGGTCTAGAGATTGCTGGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGG 966
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        922 TAGGTCTAGAGATTGCTGGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGG 981

Qy        967 TTTAGGACGGTGGACGGTACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAG 1026
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        982 TTTAGGACGGTGGACGGTACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAG 1041

Qy       1027 GACCTTCGTAGGCCAATGTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAA 1086
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db       1042 GACCTTCGTAGGCCAATGTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAA 1101

Qy       1087 GTCCTGTACGAAACCGTCGACCTGGACAGAGGCCCAACAATTACCTAGG 1135
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1102 GTCCTGTACGAAACCGTCGACCTGGACAGAGGCCCAACAATTACCTAGG 1150


RESULT 5
BD263010
LOCUS       BD263010                861 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Dimeric thrombopoietin peptide mimetics binding to MP1 receptor and
            having thrombopoietic activity.
ACCESSION   BD263010
VERSION     BD263010.1  GI:33072778
KEYWORDS    JP 2002536960-A/12.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 861)
  AUTHORS   Liu,C.F., Feige,U. and Cheetham,J.
  TITLE     Dimeric thrombopoietin peptide mimetics binding to MP1 receptor and
            having thrombopoietic activity
  JOURNAL   Patent: JP 2002536960-A 12 05-NOV-2002;
            AMGEN INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002536960-A/12
            PD   05-NOV-2002
            PF   22-OCT-1999 JP 2000578340
            PR   23-OCT-1998 US    60/105348
            PI   CHUAN FA LIU,ULRICH FEIGE,JANET CHEETHAM
            PC   C12N15/09,A61K38/00,A61P7/00,C07K14/52,C07K19/00,C12N1/15, PC
             C12N1/19,
            PC   C12N1/21,C12N5/10,C12P21/02,C12N15/00,C12N5/00,A61K37/02 CC
            Description of Artificial Sequence: oligonucleotide FH   Key
                Location/Qualifiers
            FT   source          1. .861
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .861
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
ORIGIN

  Query Match           58.4%;  Score 662.4;  DB 6;  Length 861;
  Best Local Similarity   97.7%;  Pred. No. 5.2e-151;
  Matches  672;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          1 GTATACCTGTTTTGAGTGTGTACGGGTGGCACGGGTCGAGGCCTTGAGCTTCCACCAGGC 60
              |||||||||||||||||||| ||||| || ||||||||||||||   || || |||
Db         36 GTATACCTGTTTTGAGTGTGTACAGGTGGAACAGGTCGAGGCCTTGAGGACCCCCCTGGC 95

Qy         61 AGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         96 AGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTC 155

Qy        121 CAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        156 CAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATG 215

Qy        181 CACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        216 CACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCG 275

Qy        241 TGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTTCGA 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        276 TGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTC 335

Qy        301 ATGCGTACGCGCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTT 360
              |||   ||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        336 ATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTT 395

Qy        361 CGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGAC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        396 CGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGAC 455

Qy        421 TGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        456 TGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGG 515

Qy        481 CACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGAC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        516 CACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGAC 575

Qy        541 CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        576 CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTC 635

Qy        601 GTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        636 GTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTC 695

Qy        661 TTCTCGGAGAGGGACAGAGGCCCATTTC 688
              ||||||||||||||||||||||||||||
Db        696 TTCTCGGAGAGGGACAGAGGCCCATTTC 723


RESULT 6
BD263000
LOCUS       BD263000                684 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Dimeric thrombopoietin peptide mimetics binding to MP1 receptor and
            having thrombopoietic activity.
ACCESSION   BD263000
VERSION     BD263000.1  GI:33072768
KEYWORDS    JP 2002536960-A/2.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 684)
  AUTHORS   Liu,C.F., Feige,U. and Cheetham,J.
  TITLE     Dimeric thrombopoietin peptide mimetics binding to MP1 receptor and
            having thrombopoietic activity
  JOURNAL   Patent: JP 2002536960-A 2 05-NOV-2002;
            AMGEN INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002536960-A/2
            PD   05-NOV-2002
            PF   22-OCT-1999 JP 2000578340
            PR   23-OCT-1998 US    60/105348
            PI   CHUAN FA LIU,ULRICH FEIGE,JANET CHEETHAM
            PC   C12N15/09,A61K38/00,A61P7/00,C07K14/52,C07K19/00,C12N1/15, PC
             C12N1/19,
            PC   C12N1/21,C12N5/10,C12P21/02,C12N15/00,C12N5/00,A61K37/02 CC
            Description of Artificial Sequence: oligonucleotide FH   Key
                Location/Qualifiers
            FT   source          1. .684
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .684
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
ORIGIN

  Query Match           58.0%;  Score 658.4;  DB 6;  Length 684;
  Best Local Similarity   97.7%;  Pred. No. 5e-150;
  Matches  668;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          4 TACCTGTTTTGAGTGTGTACGGGTGGCACGGGTCGAGGCCTTGAGCTTCCACCAGGCAGT 63
              |||||||||||||||||||| ||||| || ||||||||||||||   || || |||||||
Db          1 TACCTGTTTTGAGTGTGTACAGGTGGAACAGGTCGAGGCCTTGAGGACCCCCCTGGCAGT 60

Qy         64 CAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAG 123
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAG 120
```

```
Qy        124 TGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCAC 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCAC 180

Qy        184 CTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGC 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGC 240

Qy        244 ATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTTCGAATG 303
              |||||||||||||||||||||||||||||||||||||||||||||||||||||| |  |||
Db        241 ATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATG 300

Qy        304 CGTACGCGCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGG 363
              |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGG 360

Qy        364 TTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGG 423
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGG 420

Qy        424 TTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCAC 483
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCAC 480

Qy        484 CTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTG 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTG 540

Qy        544 AGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTC 603
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTC 600

Qy        604 CCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTC 663
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTC 660

Qy        664 TCGGAGAGGGACAGAGGCCCATTT 687
              |||||||||||||||||||||||||
Db        661 TCGGAGAGGGACAGAGGCCCATTT 684
```

```
RESULT 7
I27618
LOCUS       I27618                  1142 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 9 from patent US 5565335.
ACCESSION   I27618
VERSION     I27618.1  GI:1818394
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1142)
  AUTHORS   Capon,D.J. and Gregory,T.J.
  TITLE     Adhesion variants
  JOURNAL   Patent: US 5565335-A 9 15-OCT-1996;
FEATURES             Location/Qualifiers
     source          1. .1142
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             56.2%;  Score 638.4;  DB 6;  Length 1142;
  Best Local Similarity   96.7%;  Pred. No. 3.9e-145;
  Matches  665;  Conservative    0;  Mismatches   16;  Indels    7;  Gaps    1;

Qy          7 CTGTTTTGAGTGTGTACGGGTGGCACGGGTCGAGGCCTTGAGCTTCCACCAGGCAGTCAG 66
              |||||||||||||||||||||||||||||| || |||||   || || |||||||||
Db        440 CTGTTTTGAGTGTGTACGGGTGGCACGGGTCGTGGACTTGAGGACCCCCCTGGCAGTCAG 499

Qy         67 AAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGT 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        500 AAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGT 559
```

```
Qy        127 ACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTG 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        560 ACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTG 619

Qy        187 CCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATG 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        620 CCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATG 679

Qy        247 GCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTTCGAATGCGT 306
              || ||||||||||||||||||||||||||||||||||||||||||||||||| |  |||
Db        680 GCCCACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATGTTC 739

Qy        307 ACGCGCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTT 366
              |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        740 ACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTT 799

Qy        367 CCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTC 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        800 CCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTC 859

Qy        427 TTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTC 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        860 TTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTC 919

Qy        487 ACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGG 546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        920 ACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGG 979

Qy        547 CTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCC 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        980 CTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCC 1039

Qy        607 TTGCAGAAGAGTACGAGGC-------ACTACGTACTCCGAGACGTGTTGGTGATGTGCGT 659
              |||||||||||||||||||       ||||||||||||||||||||||||||||||||||||
Db       1040 TTGCAGAAGAGTACGAGGCACTACGTACTACGTACTCCGAGACGTGTTGGTGATGTGCGT 1099

Qy        660 CTTCTCGGAGAGGGACAGAGGCCCATTT 687
              ||||||||||||||||||||||||||||
Db       1100 CTTCTCGGAGAGGGACAGAGGCCCATTT 1127
```

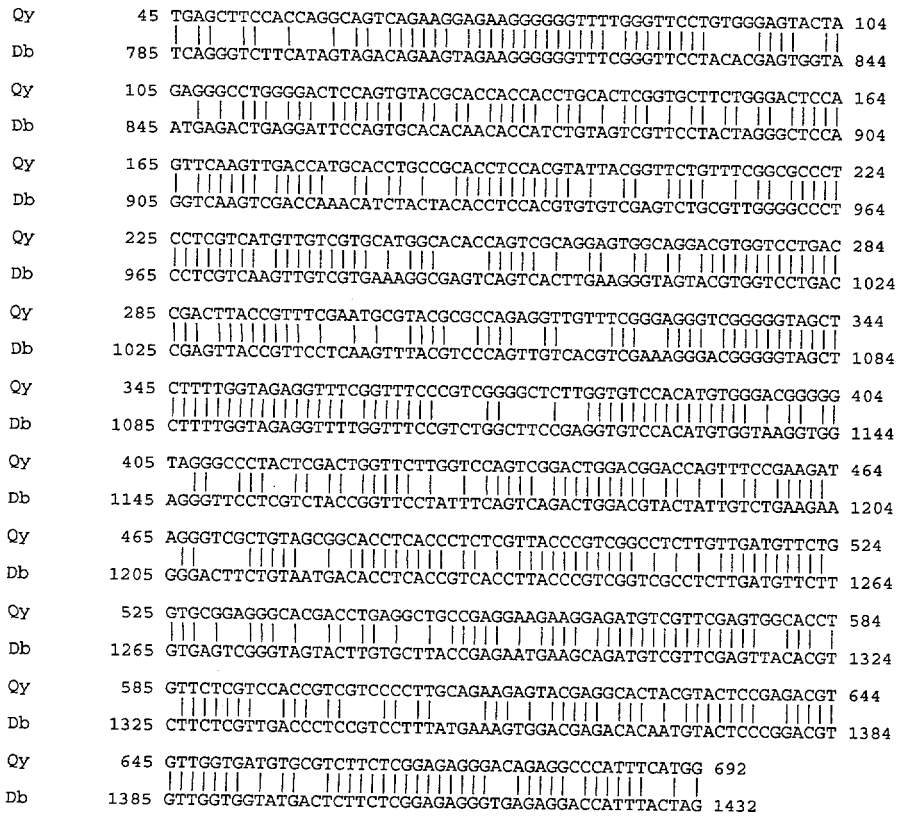
```
RESULT 8
BD004077
LOCUS       BD004077                454 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Methods of increasing sensitivity of an individual to OB protein by
            up-regulating OB protein receptor.
ACCESSION   BD004077
VERSION     BD004077.1  GI:18632038
KEYWORDS    JP 2001501177-A/4.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 454)
  AUTHORS   Pelleymounter,M.A.
  TITLE     Methods of increasing sensitivity of an individual to OB protein by
            up-regulating OB protein receptor
  JOURNAL   Patent: JP 2001501177-A 4 30-JAN-2001;
            AMGEN INC
COMMENT     OS   Unidentified
            PN   JP 2001501177-A/4
            PD   30-JAN-2001
            PF   26-AUG-1997 JP 1998511882
            PR   30-AUG-1996 US    08/705981
            PI   MARY ANN PELLEYMOUNTER
            PC   A61K38/00,A61K31/425,A61P1/16,A61P3/04,A61P3/06,A61P3/10, PC
            A61P9/10,
            PC   A61K37/02
            CC   Strandedness: Single;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers
            FT   source          1. .454
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
```

```
     source          1. .454
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
ORIGIN

  Query Match             38.8%;  Score 440.8;  DB 6;  Length 454;
  Best Local Similarity   98.5%;  Pred. No. 7.3e-97;
  Matches  445;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy        684 ATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATG 743
              ||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 ATACCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATG 62

Qy        744 CGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTTGTCTTTCAATGTCCGGA 803
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         63 CGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTTGTCGCACAATGTCCGGA 122

Qy        804 CCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCG 863
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 CCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCG 182

Qy        864 ACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAATAGGTCTAGAGATTGCT 923
              |||||||||||||||||||||||||||||||||||||||||| | ||||||||||||||
Db        183 ACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAAGAAGTCTAGAGATTGCT 242

Qy        924 GGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGG 983
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        243 GGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGG 302

Qy        984 TACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCAAT 1043
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        303 TACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCAAT 362

Qy       1044 GTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAAGTCCTGTACGAAACCGT 1103
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        363 GTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAAGTCCTGTACGAAACCGT 422

Qy       1104 CGACCTGGACAGAGGCCCAACAATTACCTAGG 1135
              ||||||||||||||||||||||||||||||
Db        423 CGACCTGGACAGAGGCCCAACAATTACCTAGG 454


RESULT 9
BD056516
LOCUS       BD056516                454 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  OB fusion protein compositions and methods.
ACCESSION   BD056516
VERSION     BD056516.1  GI:22602122
KEYWORDS    JP 2001512417-A/4.
SOURCE      Aequorea victoria
  ORGANISM  Aequorea victoria
            Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
            Aequoreidae; Aequorea.
REFERENCE   1  (bases 1 to 454)
  AUTHORS   Mann,M.B. and Hecht,R.I.
  TITLE     OB fusion protein compositions and methods
  JOURNAL   Patent: JP 2001512417-A 4 21-AUG-2001;
            AMGEN INC
COMMENT     PN   JP 2001512417-A/4
            PD   21-AUG-2001
            PF   11-DEC-1997 JP 1998528896
            PR   20-DEC-1996 US    08/770973
            PI   MICHAEL BENJAMIN MANN,RANDY IRA HECHT
            PC   C07K14/575,A61K38/00,A61P3/04,A61P3/06,A61P3/10,A61P9/10, PC
            A61P43/00,
            PC   C12N15/09,C12N15/00,A61K37/02
            CC   Strandedness: Double;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers.
FEATURES            Location/Qualifiers
     source         1. .454
                    /organism="Aequorea victoria"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:6100"
ORIGIN

  Query Match             38.8%;  Score 440.8;  DB 6;  Length 454;
  Best Local Similarity   98.5%;  Pred. No. 7.3e-97;
  Matches  445;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy        684 ATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATG 743
              ||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 ATACCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATG 62

Qy        744 CGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTTGTCTTTCAATGTCCGGA 803
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         63 CGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTTGTCGCACAATGTCCGGA 122

Qy        804 CCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCG 863
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 CCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCG 182

Qy        864 ACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAATAGGTCTAGAGATTGCT 923
              |||||||||||||||||||||||||||||||||||||||||| | ||||||||||||||
Db        183 ACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAAGAAGTCTAGAGATTGCT 242

Qy        924 GGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGG 983
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        243 GGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGG 302

Qy        984 TACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCAAT 1043
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        303 TACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCAAT 362

Qy       1044 GTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAAGTCCTGTACGAAACCGT 1103
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        363 GTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAAGTCCTGTACGAAACCGT 422

Qy       1104 CGACCTGGACAGAGGCCCAACAATTACCTAGG 1135
              ||||||||||||||||||||||||||||||
Db        423 CGACCTGGACAGAGGCCCAACAATTACCTAGG 454


RESULT 10
BD004075
LOCUS       BD004075                491 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Methods of increasing sensitivity of an individual to OB protein by
            up-regulating OB protein receptor.
ACCESSION   BD004075
VERSION     BD004075.1  GI:18632036
KEYWORDS    JP 2001501177-A/2.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 491)
  AUTHORS   Pelleymounter,M.A.
  TITLE     Methods of increasing sensitivity of an individual to OB protein by
            up-regulating OB protein receptor
  JOURNAL   Patent: JP 2001501177-A 2 30-JAN-2001;
            AMGEN INC
COMMENT     OS   Unidentified
            PN   JP 2001501177-A/2
            PD   30-JAN-2001
            PF   26-AUG-1997 JP 1998511882
            PR   30-AUG-1996 US    08/705981
            PI   MARY ANN PELLEYMOUNTER
            PC   A61K38/00,A61K31/425,A61P1/16,A61P3/04,A61P3/06,A61P3/10, PC
            A61P9/10,
            PC   A61K37/02
            CC   Strandedness: Single;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers
            FT   source          1. .491
            FT                   /organism='Unidentified'.
FEATURES            Location/Qualifiers
```

```
    source          1. .491
                    /organism="unidentified"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:32644"
ORIGIN

  Query Match             33.3%;  Score 378.4;  DB 6;  Length 491;
  Best Local Similarity   89.8%;  Pred. No. 1.3e-81;
  Matches  406;  Conservative    0;  Mismatches   46;  Indels    0;  Gaps    0;

Qy        684 ATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATG 743
              ||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         40 ATACCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATG 99

Qy        744 CGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTTGTCTTTCAATGTCCGGA 803
              ||||||||||||||||||||||||||||||||||    | ||||||||   |||||  || ||
Db        100 CGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCAGAGGCGATTTGTCGCACAATGGCCAGA 159

Qy        804 CCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCG 863
              |||||||||||||||||||||||||||||| | ||||||||||||||||||||||||||
Db        160 CCTGAAGTAGGGCCCAGACGTGGGCTAGGATTCGAACAGGTTTTACCTGGTCTGGGACCG 219

Qy        864 ACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAATAGGTCTAGAGATTGCT 923
              ||||||||||||  | |||||||||  |||||| | ||||||  |||||||
Db        220 ACATATGGTCGTCCACAATTGGAGGGACGGCAGGGTCTTGCAAGAAGTCTAGCGATTGCT 279

Qy        924 GGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGG 983
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||  ||||||
Db        280 GGAGCTCTTGGAAGCGCTGGACGACGTGGACGACCGTAAGAGGTTTAGGACGAGGGACGG 339

Qy        984 TACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCAAT 1043
                | | |||||||||  |||   |  |||  ||  ||||  ||||||||||||||||||    ||
Db        340 CGTCTGGAGTCCAGAAGTCTTTGGCCTTAGGGACCTGCCCCAGGACCTTCGTAGGGACAT 399

Qy        1044 GTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAAGTCCTGTACGAAACCGT 1103
               ||||||||||||||||||||||||||||||||||||||||||||||||||||  |||  |||
Db         400 GTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAAGTCCTGTAGGAAGTCGT 459

Qy        1104 CGACCTGGACAGAGGCCCAACAATTACCTAGG 1135
               |||||||  |||||||  ||||||||||||||
Db         460 CGACCTGCAAAGAGGCCTTACAATTACCTAGG 491


RESULT 11
BD056514
LOCUS       BD056514                491 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  OB fusion protein compositions and methods.
ACCESSION   BD056514
VERSION     BD056514.1  GI:22602120
KEYWORDS    JP 2001512417-A/2.
SOURCE      Aequorea victoria
  ORGANISM  Aequorea victoria
            Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
            Aequoreidae; Aequorea.
REFERENCE   1  (bases 1 to 491)
  AUTHORS   Mann,M.B. and Hecht,R.I.
  TITLE     OB fusion protein compositions and methods
  JOURNAL   Patent: JP 2001512417-A 2 21-AUG-2001;
            AMGEN INC
COMMENT     PN   JP 2001512417-A/2
            PD   21-AUG-2001
            PF   11-DEC-1997 JP 1998528896
            PR   20-DEC-1996 US    08/770973
            PI   MICHAEL BENJAMIN MANN,RANDY IRA HECHT
            PC   C07K14/575,A61K38/00,A61P3/04,A61P3/06,A61P3/10,A61P9/10, PC
            A61P43/00,
            PC   C12N15/09,C12N15/00,A61K37/02
            CC   Strandedness: Double;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers.
FEATURES                Location/Qualifiers
     source             1. .491
                        /organism="Aequorea victoria"
                        /mol_type="genomic DNA"
                        /db_xref="taxon:6100"
ORIGIN

  Query Match             33.3%;  Score 378.4;  DB 6;  Length 491;
  Best Local Similarity   89.8%;  Pred. No. 1.3e-81;
  Matches  406;  Conservative    0;  Mismatches   46;  Indels    0;  Gaps    0;

Qy        684 ATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATG 743
              ||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         40 ATACCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATG 99

Qy        744 CGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTTGTCTTTCAATGTCCGGA 803
              ||||||||||||||||||||||||||||||||||    | ||||||||   |||||  || ||
Db        100 CGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCAGAGGCGATTTGTCGCACAATGGCCAGA 159

Qy        804 CCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCG 863
              |||||||||||||||||||||||||||||| | ||||||||||||||||||||||||||
Db        160 CCTGAAGTAGGGCCCAGACGTGGGCTAGGATTCGAACAGGTTTTACCTGGTCTGGGACCG 219

Qy        864 ACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAATAGGTCTAGAGATTGCT 923
              ||||||||||||  | |||||||||  |||||| | ||||||  |||||||
Db        220 ACATATGGTCGTCCACAATTGGAGGGACGGCAGGGTCTTGCAAGAAGTCTAGCGATTGCT 279

Qy        924 GGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGG 983
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||  ||||||
Db        280 GGAGCTCTTGGAAGCGCTGGACGACGTGGACGACCGTAAGAGGTTTAGGACGAGGGACGG 339

Qy        984 TACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCAAT 1043
                | | |||||||||  |||   |  |||  ||  ||||  ||||||||||||||||||    ||
Db        340 CGTCTGGAGTCCAGAAGTCTTTGGCCTTAGGGACCTGCCCCAGGACCTTCGTAGGGACAT 399

Qy        1044 GTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAAGTCCTGTACGAAACCGT 1103
               ||||||||||||||||||||||||||||||||||||||||||||||||||||  |||  |||
Db         400 GTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAAGTCCTGTAGGAAGTCGT 459

Qy        1104 CGACCTGGACAGAGGCCCAACAATTACCTAGG 1135
               |||||||  |||||||  ||||||||||||||
Db         460 CGACCTGCAAAGAGGCCTTACAATTACCTAGG 491


RESULT 12
BD105735
LOCUS       BD105735                1528 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  A method for preparing a recombinant immunoglobulin.
ACCESSION   BD105735
VERSION     BD105735.1  GI:22651309
KEYWORDS    JP 2001346591-A/7.
SOURCE      Mus sp.
  ORGANISM  Mus sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 1528)
  AUTHORS   Cabilly,S., Heyneker,H.L., Holmes,W.E., Riggs,A.D. and Wetzel,R.B.
  TITLE     A method for preparing a recombinant immunoglobulin
  JOURNAL   Patent: JP 2001346591-A 7 18-DEC-2001;
            GENENTECH INC,CITY OF HOPE
COMMENT     OS   Mus sp. (mouse)
            PN   JP 2001346591-A/7
            PD   18-DEC-2001
            PF   03-APR-2001 JP 2001104856
            PR   08-APR-1983 US       483457
            PI   SHMUEL CABILLY,HERBERT L HEYNEKER,WILLIAM E HOLMES,ARTHUR D
            PI   RIGGS,
            PI   RONALD B WETZEL
            PC   C12N15/09,C07K16/00,C07K19/00,C12N1/21,C12P21/02//G01N33/531,
            PC   (C12N1/21,C12R1:19),C12N15/00
            CC   A method for preparing a recombinant immunoglobulin FH   Key
                      Location/Qualifiers
            FT   source          1. .1528
            FT                   /organism='Mus sp. (mouse)'.
FEATURES                Location/Qualifiers
     source             1. .1528
```

/organism="Mus sp."
/mol_type="genomic DNA"
/db_xref="taxon:10095"

ORIGIN



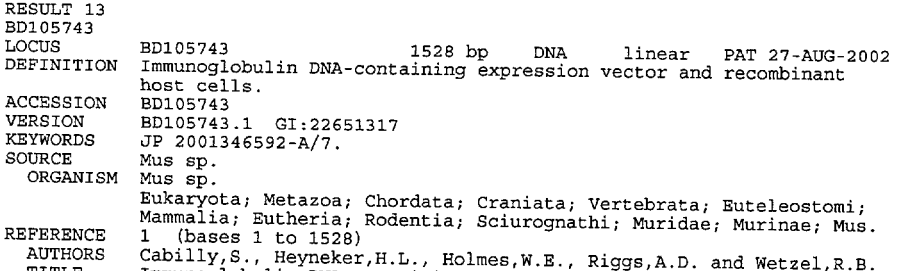
Query Match 31.9%; Score 361.6; DB 6; Length 1528;
Best Local Similarity 72.4%; Pred. No. 1.7e-77;
Matches 469; Conservative 0; Mismatches 179; Indels 0; Gaps 0;

RESULT 13
BD105743
LOCUS BD105743 1528 bp DNA linear PAT 27-AUG-2002
DEFINITION Immunoglobulin DNA-containing expression vector and recombinant host cells.
ACCESSION BD105743
VERSION BD105743.1 GI:22651317
KEYWORDS JP 2001346592-A/7.
SOURCE Mus sp.
ORGANISM Mus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1528)
AUTHORS Cabilly,S., Heyneker,H.L., Holmes,W.E., Riggs,A.D. and Wetzel,R.B.
TITLE Immunoglobulin DNA-containing expression vector and recombinant host cells
JOURNAL Patent: JP 2001346592-A 7 18-DEC-2001;
GENENTECH INC,CITY OF HOPE
COMMENT OS Mus sp. (mouse)

PN JP 2001346592-A/7
PD 18-DEC-2001
PF 03-APR-2001 JP 2001104857
PR 08-APR-1983 US 483457
PI SHMUEL CABILLY,HERBERT L HEYNEKER,WILLIAM E HOLMES,ARTHUR D
PI RIGGS,
PI RONALD B WETZEL
PC C12N15/09,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N15/00,C12N5/
PC 00
CC Immunoglobulin DNA-containing expression vector and recombinant host cells
FH Key Location/Qualifiers
FT source 1. .1528
FT /organism='Mus sp. (mouse)'.

FEATURES Location/Qualifiers
source 1. .1528
/organism="Mus sp."
/mol_type="genomic DNA"
/db_xref="taxon:10095"

ORIGIN



Query Match 31.9%; Score 361.6; DB 6; Length 1528;
Best Local Similarity 72.4%; Pred. No. 1.7e-77;
Matches 469; Conservative 0; Mismatches 179; Indels 0; Gaps 0;

RESULT 14
AR029004
LOCUS AR029004 2287 bp DNA linear PAT 29-SEP-1999

```
DEFINITION  Sequence 1 from patent US 5858983.
ACCESSION   AR029004
VERSION     AR029004.1  GI:5940977
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2287)
  AUTHORS   Seed,B. and Walz,G.
  TITLE     Inhibition of cell adhesion protein-carbohydrate interactions
  JOURNAL   Patent: US 5858983-A 1 12-JAN-1999;
FEATURES             Location/Qualifiers
     source          1. .2287
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             5.3%;  Score 60;  DB 6;  Length 2287;
  Best Local Similarity   100.0%;  Pred. No. 0.00083;
  Matches   60;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         74 AGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGCACC 133
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 AGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGCACC 1620


RESULT 15
AR037308
LOCUS       AR037308                2287 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 1 from patent US 5801044.
ACCESSION   AR037308
VERSION     AR037308.1  GI:5955164
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2287)
  AUTHORS   Seed,B. and Walz,G.
  TITLE     Nucleic acid encoding an antibody that inhibits cell adhesion
            protein-carbohydrate interactions
  JOURNAL   Patent: US 5801044-A 1 01-SEP-1998;
FEATURES             Location/Qualifiers
     source          1. .2287
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             5.3%;  Score 60;  DB 6;  Length 2287;
  Best Local Similarity   100.0%;  Pred. No. 0.00083;
  Matches   60;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         74 AGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGCACC 133
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 AGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGCACC 1620


Search completed: October 18, 2004, 01:19:59
Job time : 4357.1 secs
```

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 17, 2004, 15:27:13 ; Search time 3993.73 Seconds
(without alignments)
10355.995 Million cell updates/sec

Title: US-10-679-999-17
Perfect score: 1135
Sequence: 1 GTATACCTGTTTTGAGTGTG.....AGGCCCAACAATTACCTAGG 1135

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	50	4.4	714	6	CD781337	CD781337 EST652698
2	43.6	3.8	1039	6	CA128348	CA128348 SCJLLR200
c 3	43.2	3.8	486	1	AI869699	AI869699 wm02f07.x
4	43.2	3.8	910	9	CNS006ON	AL065629 Drosophil
c 5	43	3.8	1203	7	CK206445	CK206445 FGAS01803
c 6	42.8	3.8	509	2	BF593096	BF593096 7o56e02.x
c 7	42.8	3.8	552	6	CA686322	CA686322 wlm96.pk0
8	42.4	3.7	645	9	CNS012I3	AL101589 Drosophil
c 9	42.4	3.7	1101	9	CNS017SY	AL108460 Drosophil
c 10	42.2	3.7	512	1	AI289506	AI289506 qw28e11.x
c 11	42.2	3.7	586	1	AI687271	AI687271 tp94e04.x
12	41.8	3.7	343	1	AA330793	AA330793 EST34531
13	41.6	3.7	337	6	CB047414	CB047414 NISC_gg02
14	41.6	3.7	340	1	AA302570	AA302570 EST15740
c 15	41.6	3.7	408	6	CA720412	CA720412 wkm2n.pk0
c 16	41.6	3.7	414	4	BJ248630	BJ248630 BJ248630
c 17	41.6	3.7	439	2	BE488609	BE488609 WHE1051_G
c 18	41.6	3.7	442	6	CA719617	CA719617 wkm2n.pk0
c 19	41.6	3.7	443	1	AI582641	AI582641 tn47h04.x
c 20	41.6	3.7	443	6	CA656554	CA656554 wlm0.pk00
c 21	41.6	3.7	447	6	CA687517	CA687517 wlm96.pk0
c 22	41.6	3.7	448	6	CA692819	CA692819 wlm96.pk0
c 23	41.6	3.7	451	1	AI083954	AI083954 oz53b09.x
c 24	41.6	3.7	451	2	AW276084	AW276084 xq45c08.x
c 25	41.6	3.7	455	2	AW590575	AW590575 hg46c10.x
c 26	41.6	3.7	458	2	AW088852	AW088852 xd31e06.x
c 27	41.6	3.7	463	2	BF056551	BF056551 7k06g10.x
28	41.6	3.7	466	2	AW673691	AW673691 ba56g10.y
c 29	41.6	3.7	467	1	AI752976	AI752976 cr03b09.x
c 30	41.6	3.7	467	1	AI879509	AI879509 au53d05.x
c 31	41.6	3.7	469	1	AI088760	AI088760 qa16h11.x
c 32	41.6	3.7	472	6	CA448944	CA448944 UI-H-EI1-
c 33	41.6	3.7	479	1	AW002017	AW002017 wt83b12.x
34	41.6	3.7	480	2	BE873734	BE873734 601483878
c 35	41.6	3.7	481	1	AI347031	AI347031 qp54h02.x
c 36	41.6	3.7	481	2	AW069813	AW069813 cr50h12.x
c 37	41.6	3.7	489	4	BM673482	BM673482 UI-E-CR1-
c 38	41.6	3.7	492	2	AW402830	AW402830 UI-HF-BK0
c 39	41.6	3.7	493	6	CA688601	CA688601 wlm96.pk0
c 40	41.6	3.7	500	1	AI149427	AI149427 qc72f02.x
c 41	41.6	3.7	506	6	CA661058	CA661058 wlm1.pk00
c 42	41.6	3.7	511	6	CA679280	CA679280 wlm4.pk00
c 43	41.6	3.7	514	6	CA701633	CA701633 wkm2c.pk0
c 44	41.6	3.7	520	6	CA698728	CA698728 wlk8.pk00
c 45	41.6	3.7	526	1	AJ611898	AJ611898 AJ611898

ALIGNMENTS

RESULT 1
CD781337
LOCUS CD781337 714 bp mRNA linear EST 01-JUL-2004
DEFINITION EST652698 RAA Rhipicephalus appendiculatus cDNA clone RAAAT27 5' end, mRNA sequence.
ACCESSION CD781337
VERSION CD781337.1 GI:49537010
KEYWORDS EST.
SOURCE Rhipicephalus appendiculatus
ORGANISM Rhipicephalus appendiculatus
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari; Parasitiformes; Ixodida; Ixodidae; Rhipicephalus.
REFERENCE 1 (bases 1 to 714)
AUTHORS Nene,V., Lee,Y., Skilton,R., Mwaura,S., Quackenbush,J., Gardner,M. and Bishop,R.
TITLE An index of genes transcribed in the salivary glands of Rhipicephalus appendiculatus
JOURNAL Unpublished (2003)
COMMENT Other_ESTs: EST652697
Contact: Vishvanath Nene
Parasite Genomics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-610-5968
Fax: 301-838-0208
Email: nene@tigr.org
Seq primer: M13 reverse.
FEATURES Location/Qualifiers
source 1. .714
/organism="Rhipicephalus appendiculatus"
/mol_type="mRNA"
/strain="Muguga"
/db_xref="taxon:34631"
/clone="RAAAT27"
/dev_stage="Adult"
/lab_host="E. coli strain DH10B-TonA"
/clone_lib="RAA"
/note="Organ: Salivary glands; Vector: pCMVSport6.0.ccdb; Salivary glands were dissected on day four after initiation of feeding. Total RNA was prepared using acid guanidium thiocyanate-phenol-chloroform extraction. The cDNA library was custom prepared by Invitrogen Corporation. Briefly, first strand cDNA was primed using oligo(dT) containing a NotI site. Size fractionated double stranded cDNA was ligated to EcoRV-NotI cleaved vector and electroporated into E.coli. Library RAA was made from uninfected ticks."

ORIGIN

Query Match 4.4%; Score 50; DB 6; Length 714;
Best Local Similarity 55.1%; Pred. No. 0.014;
Matches 98; Conservative 0; Mismatches 80; Indels 0; Gaps 0;

```
Qy        432 CCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCACCCT 491
              | ||||  |  |||  |||      | |||| ||  |||  |  | || ||| |||
Db        253 CAAGTCCATCACGACACTCCAAGGCGAAGACATAGTGTTCCTGGCGACGGACATCAACCT 312

Qy        492 CTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGGCTGCC 551
                |     |||||| |    || |||||   | ||||  ||||||  || | | ||||
Db        313 GCCCGGCGCCGTCGACTGGGTGATGATGCAGTCGTGCTTTGGGCACCACTTCATGCTGGT 372

Qy        552 GAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCCTTG 609
              |  | |||||  |   |  || |||  | ||||      |  |   ||||||  |  |||
Db        373 GCTGGAGAAGCAAGAGAAGTACGACGGCCACCAACAGTTCTTTGCCGTCGTGCAGTTG 430
```

RESULT 2
CA128348
LOCUS CA128348 1039 bp mRNA linear EST 24-SEP-2003
DEFINITION SCJLLR2006A05.g LR2 Saccharum officinarum cDNA clone SCJLLR2006A05 5', mRNA sequence.
ACCESSION CA128348
VERSION CA128348.1 GI:35009126
KEYWORDS EST.
SOURCE Saccharum officinarum
ORGANISM Saccharum officinarum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum complex.
REFERENCE 1 (bases 1 to 1039)
AUTHORS Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.
TITLE The libraries that made SUCEST
JOURNAL Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
COMMENT Contact: Arruda P
Centro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
Email: parruda@unicamp.br
Clone distribution: clone distribution information can be found through the Brazilian Clone Collection Center (BCCC) at http://www.bcccenter.fcav.unesp.br
Plate: 006 row: A column: 05
Seq primer: T7 Promoter Primer.
FEATURES Location/Qualifiers
source 1. .1039
/organism="Saccharum officinarum"
/mol_type="mRNA"
/db_xref="taxon:4547"
/clone="SCJLLR2006A05"
/lab_host="DH10B"
/clone_lib="LR2"
/note="Organ: Leaf roll from field grown adult plants (small insert library); Vector: pSport1; Site_1: SalI; Site_2: NotI; An unidirectional cDNA library generated from [Leaf roll from field grown adult plants (small insert library)]. cDNA was prepared from polyA+ mRNA using SuperScript Plasmid System Kit (Invitrogen). The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 Kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at http://sucest.lad.ic.unicamp.br/public"

ORIGIN

Query Match 3.8%; Score 43.6; DB 6; Length 1039;
Best Local Similarity 45.6%; Pred. No. 0.93;
Matches 154; Conservative 0; Mismatches 184; Indels 0; Gaps 0;

```
Qy        427 TTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTC 486
              | |||  ||  ||  ||  ||   ||   ||   |  | |  |  | || | | || ||
Db        303 TCGGTGGAGACGTACAAGATCTACATCTTCAAGGTGCTGAAGCAGGTGCACCCGGACATC 362

Qy        487 ACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGG 546
                | ||||||     | |     | |  |||  ||||    |    |   |  ||  | ||
Db        363 TGCATCTCGTCCAAGGCCATGTCCATCATGAACTTCTTCATCAACGACATCTTCCATAAG 422

Qy        547 CTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCC 606
              |||  ||  |  ||  ||  |     |     |  ||  |    |  |||  |    || |
Db        423 CTGGCGGCGGAGGCGGCCAAACTGGCGCGCTACAACAAGAAGCCCACCATCACGTGCCGC 482

Qy        607 TTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCG 666
                |   |||  |     |  |  |||  ||||  |  ||  |  |  |   |  || |||||
Db        483 GAGATCCAGACTTTCGTCCGCCTCGTCCTCCCCGGCGAGCTCGCCAAGCACGCCTTCTTC 542

Qy        667 GAGAGGGACAGAGGCCCATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAAT 726
              |||  | ||  |||||  |  ||  |   |  | | |  |  ||  |||     |  |
Db        543 GAGGTGCACCAAGGCCGTTACCAAGTTCACCAGCTCCTATGCGAGCGATGGGACCTGCCT 602

Qy        727 TAATTTTGCTAGCAATGCGCATAGTTGCTGTAGTCAGT 764
              || ||| | |    | |  |     || ||| ||  ||
Db        603 TAGTTTCGTTCATGAAGTACTAGTGTGTTGTCGTGTGT 640
```

RESULT 3
AI869699/c
LOCUS AI869699 486 bp mRNA linear EST 07-MAR-2000
DEFINITION wm02f07.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2433253 3' similar to gb:J05016 PROTEIN DISULFIDE ISOMERASE-RELATED PROTEIN PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION AI869699
VERSION AI869699.1 GI:5543667
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 486)
AUTHORS NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index
JOURNAL Unpublished (1998)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 751 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 282.
FEATURES Location/Qualifiers
source 1. .486
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2433253"
/tissue_type="anaplastic oligodendroglioma"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Brn25"
/note="Organ: brain; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGGAGCGGCCGCATAGGTTTTTTTTTTTTTTTTTTTTTTTT 3']; double-stranded cDNA was ligated to Eco RI

adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized, and was constructed by Bento Soares and M.Fatima Bonaldo."

ORIGIN

Query Match 3.8%; Score 43.2; DB 1; Length 486;
Best Local Similarity 54.4%; Pred. No. 1;
Matches 87; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

```
Qy        914 AGAGATTGCTGGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGA 973
              | |||   |||||||  |||     | |    || |  || | |   ||   |  ||||
Db        430 ACAGAGATCTGGAGCATTTGAGCAAGTTTATAGAAGAACATGCCACAAAACTGAGCAGGA 371

Qy        974 CGGTGGACGGTACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTC 1033
              |   ||| |       |||| || ||  |||| ||   | | ||   | |  | | ||| |
Db        370 CCAAGGAAGAGCTTTGAAGGCCTGAGGTCTGCGAAAGGTGGGAGGAGGCAGACGCCCTGC 311

Qy       1034 GTAGGCCAATGTCGTGGCTTCAACAACGAGACAGGGCAGA 1073
              || | |||  |||| ||| || ||  |||| | ||  | |
Db        310 GTGGCCCATGGTCGGGGCGTCCACGCCGAGGCCGGCAACA 271
```

RESULT 4
CNS006ON
LOCUS CNS006ON 910 bp DNA linear GSS 03-JUN-1999
DEFINITION Drosophila melanogaster genome survey sequence T7 end of BAC # BACR14J21 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
ACCESSION AL065629
VERSION AL065629.1 GI:4944698
KEYWORDS GSS.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 910)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES Location/Qualifiers
source 1. .910
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACR14J21"
/clone_lib="RPCI-98"
/note="end : T7"

ORIGIN

Query Match 3.8%; Score 43.2; DB 9; Length 910;
Best Local Similarity 19.2%; Pred. No. 1.2;
Matches 81; Conservative 159; Mismatches 180; Indels 2; Gaps 1;

```
Qy        315 GAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTTCCCGTCGG 374
              | ||: |  : ||| ||| :|||||  | | |:|: |  : ||    |:   :::: |
Db        468 GGGGKGGGGKGGGGGGGGGHGGGGGSGGGTDTKTWTGGKSTGGGGGGGSSGGSSSKGGGC 527

Qy        375 GGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTCTTGGTCCA 434
              |:  :  || |:       : ||| :::| :  :::::::  :  : ::| : :   | |:
Db        528 GSGSYGGGGGGYGGTGSGSGGGGSSSSGCSSSSSSSSSSSSCGSSSBGCBSSCGCGSCSY 587

Qy        435 GTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCACCCTCTC 494
              : ::  :||:   | :: :   ::      | :::|:||    : ::: :| : : : :|
Db        588 SSSSTGSTGSCGCGSSSSSSSSSSCSSTSTSSSSTSGCGYSSSGSBSSSCSSTBTSSSTT 647

Qy        495 GTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGGCTGCCGAG 554
              :|:  : :|:: ::|:|  ||: |:|::: ::|::: : :: ::  : : ::: :::  :
Db        648 BTBTKBTSTYSTSYTST--TTSTTSTBSBTSYGSBBKSTSSTSSSTSSSTSSSSSSSTSS 705

Qy        555 GAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCCTTGCAGAA 614
              : : :::::||:   |: : ::|  |:: ::   : :    : : :| : :
Db        706 CTSTKBYSTSTBSYSBTTBTBTTSTSTBBTTSTBYTBBTTBYTKSTTSMTSTYTTBBSTS 765

Qy        615 GAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCGGAGAGGGA 674
              : :|  : :::  |  :| :|  :  : :: : |:    |: ::::: :|: :   : :
Db        766 KBSTBTSTBKSTGTKTBTSBTTSCTSSSSSBSTSYSYSTSCBSSBSBSSTSYSBCTSTST 825

Qy        675 CAGAGGCCCATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTG 734
              : : :::::    :   ::| ::|:||    :| |: :||:::: |  :  ||  || |
Db        826 STSSBBSSBSSSSSCGTSBTSSSTSTTTSTCTSTTCKTSTGBSSYGTGTSTYTTBTTTATT 885

Qy        735 CT 736
              :|
Db        886 ST 887
```

RESULT 5
CK206445/c
LOCUS CK206445 1203 bp mRNA linear EST 08-DEC-2003
DEFINITION FGAS018038 Triticum aestivum FGAS: Library 5 GATE 7 Triticum aestivum cDNA, mRNA sequence.
ACCESSION CK206445
VERSION CK206445.1 GI:39568835
KEYWORDS EST.
SOURCE Triticum aestivum (bread wheat)
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Triticum.
REFERENCE 1 (bases 1 to 1203)
AUTHORS Allard,F., Crosby,W.L., Danyluk,J., Eudes,F., Frick,M., Gaudet,D., Genswein,B., Graf,R., Gulick,P., Hrycan,L.D., Laroche,A., Links,M.G., McCarthy,E.L., Monroy,A., Muzak,I., Nilson,D., Penniket,C., Roach,J.L. and Sarhan,F.
TITLE Functional Genomics of Abiotic Stress In Wheat and Canola Crops
JOURNAL Unpublished (2003)
COMMENT Contact: Wm L Crosby
Bioinformatics
University of Saskatchewan, Department of Computer Science
1C101 Engineering Building, 57 Campus Drive, Saskatoon, Saskatchewan, S7N 5A9, Canada
Tel: 306 966 1769
Fax: 306 966 2033
Email: fgas_ests@cs.usask.ca
This sequence is the direct result of the Base calling software Phred (default parameters). It is the raw base calls. To aid in the identification of the high quality insert the software Lucy (default parameters) has been run on this sequence. Lucy identified the region [1,533].
Plate: L5B007 row: H column: 02.
FEATURES Location/Qualifiers
source 1. .1203
/organism="Triticum aestivum"
/mol_type="mRNA"
/db_xref="taxon:4565"
/clone_lib="Triticum aestivum FGAS: Library 5 GATE 7"
/note="Vector: pCMV.SPORT6; Crown and developmental stages

of spike formation in wheat cultivar Norstar. 4 mRNA populations were combined before constructing the library. The first mRNA population is from 1cm crown sections after 30 days of cold acclimation. The second is from 1cm crown sections after 11 days of deacclimation (before deacclimation plants were fully vernalized for 49 days). The third is from different developmental stages of spike formation (5 to 50mm) that still have not emerged from the leaf (dissection required). The last is from different developmental stages of spike and seed formation after having emerged from the leaf (visible). First strand synthesis in this library was done in the presence of methylated dCTP thereby protecting from internal cleavage with NotI."

ORIGIN

Query Match 3.8%; Score 43; DB 7; Length 1203;
Best Local Similarity 48.6%; Pred. No. 1.4;
Matches 118; Conservative 0; Mismatches 125; Indels 0; Gaps 0;

```
Qy        402 GGGTAGGGCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAA 461
              |||||| | | ||| |||          || ||||  || | || | |  |||| ||| |
Db        315 GGGTAGAGGCGTACGCGATCACCCAGAGGCCCAGCGGGGCGGGCCTGTTCAGTGGCCGCA 256

Qy        462 GATAGGGTCGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTT 521
              | |  || | || ||  ||| ||  | |       || | | |        ||| |    |
Db        255 GGTGCAGTTGGTGCAGGTGCAGCTGGCGCCGCACTTGCACTTGCCGTCGTTCTCCGCGGC 196

Qy        522 CTGGTGCGGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCA 581
              ||  |||      | |    ||      |  |  ||  | |  |||| |||      || ||
Db        195 CTCCTGCACCTCGAAGTGGCTCTTCTCGGTGTCGACCATGACGATGCCGTAGCCGTCGCC 136

Qy        582 CCTGTTCTCGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGA 641
              | | ||| ||  | || || |   |    ||||  |      |  |||||  |  ||  |
Db        135 CTTCTTCACGCACCCCCTCTTGTCGGCGCAGTCGCAGTTGCCGCACTTCTCACCCATGGC 76

Qy        642 CGT 644
                ||
Db         75 GGT 73
```

RESULT 6
BF593096/c
LOCUS BF593096 509 bp mRNA linear EST 12-DEC-2000
DEFINITION 7o56e02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3578187 3' similar to TR:Q29305 Q29305 DISULFIDE ISOMERASE-RELATED PROTEIN ;, mRNA sequence.
ACCESSION BF593096
VERSION BF593096.1 GI:11685420
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 509)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL, send email to: info@image.llnl.gov
Seq primer: -40UP from Gibco
High quality sequence stop: 405.
FEATURES Location/Qualifiers
source 1. .509
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3578187"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Kid11"
/note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA from the normalized library NCI_CGAP_Kid3 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1322376-1323911, 1456007-1456775, and 1500552-1502855). Subtraction by Bento Soares and M. Fatima Bonaldo. "

ORIGIN

Query Match 3.8%; Score 42.8; DB 2; Length 509;
Best Local Similarity 54.4%; Pred. No. 1.3;
Matches 86; Conservative 0; Mismatches 72; Indels 0; Gaps 0;

```
Qy        916 AGATTGCTGGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGACG 975
              |||   |||||||  |||      | |    || |  || | |  ||   |  |||||
Db        425 AGAAATCTGGAGCATTTGAGCAAGTTTATAGAAGAACATGCCACAAAACTGAGCAGGACC 366

Qy        976 GTGGACGGTACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTCGT 1035
                ||| |      |||| || ||  |||| |    | | ||   | |  | | ||| |||
Db        365 AAGGAAGAGCTTTGAAGGCCTGAGGTCTGCGGAAGGTGGGAGGAGGCAGACGCCCTGCGT 306

Qy       1036 AGGCCAATGTCGTGGCTTCAACAACGAGACAGGGCAGA 1073
                | |||  |||| ||| || ||| |||| | ||  | |
Db        305 GGCCCATGGTCGGGGCGTCCACACCGAGGCCGGCAACA 268
```

RESULT 7
CA686322/c
LOCUS CA686322 552 bp mRNA linear EST 25-NOV-2002
DEFINITION wlm96.pk032.g24 wlm96 Triticum aestivum cDNA clone wlm96.pk032.g24 5' end, mRNA sequence.
ACCESSION CA686322
VERSION CA686322.1 GI:25275677
KEYWORDS EST.
SOURCE Triticum aestivum (bread wheat)
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Triticum.
REFERENCE 1 (bases 1 to 552)
AUTHORS Tingey,S.V., Powell,W., Wolters,P., Dolan,M., Hainey,C., Yuan,Z., Miao,G., Caraher,N. and Hanafey,M.K.
TITLE DuPont Wheat cDNA Sequence
JOURNAL Unpublished (2002)
COMMENT Contact: Scott V. Tingey
Crop Genetics
E. I. DuPont de Nemours and Company
1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA
Tel: 302-631-2602
Fax: 302-631-2607
Email: Scott.V.Tingey@USA.dupont.com
Seq primer: M13.
FEATURES Location/Qualifiers
source 1. .552
/organism="Triticum aestivum"
/mol_type="mRNA"
/cultivar="Stephens"
/db_xref="taxon:4565"
/clone="wlm96.pk032.g24"
/tissue_type="leaf"
/clone_lib="wlm96"
/note="Vector: pBluescript SK+; Site_1: EcoRI; Site_2: XhoI; Wheat (Triticum aestivum L.) seedlings 96 hr after inoculation w/ E. graminis"

ORIGIN

Query Match 3.8%; Score 42.8; DB 6; Length 552;
Best Local Similarity 48.0%; Pred. No. 1.4;
Matches 119; Conservative 0; Mismatches 129; Indels 0; Gaps 0;

```
Qy        402 GGGTAGGGCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAA 461
Db        347 GGGTAGAGGCGTACGCGATGACCGAGAGGCCCAGCGGGGCGGGCCTGTTCAGTGGCCGCA 288

Qy        462 GATAGGGTCGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTT 521
Db        287 GGTGCAGTTGGTGCAGGTGCAGCTGGCGCCGCACTTGCACTTGCCGTCGTTCTCCGCGGC 228

Qy        522 CTGGTGCGGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCA 581
Db        227 CTCCTGCACCTCGAAGTGNCTCTTNTCGGTGTCGACCATGACGATGCCGTAGCCGTCGCC 168

Qy        582 CCTGTTCTCGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGA 641
Db        167 CTTCTTCACGCACTGGGTCTTGTCGGCGCAGTCGCAGTTGCCGCACTTGTCAGCCATGGC 108

Qy        642 CGTGTTGG 649
Db        107 GGTCTTGG 100
```

RESULT 8
CNS012I3
LOCUS CNS012I3 645 bp DNA linear GSS 26-JUL-1999
DEFINITION Drosophila melanogaster genome survey sequence T7 end of BAC BACN08C07 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.
ACCESSION AL101589
VERSION AL101589.1 GI:5613200
KEYWORDS GSS.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 645)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBeloBAC11.
FEATURES Location/Qualifiers
source 1. .645
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACN08C07"
/clone_lib="DrosBAC"
/plasmid="pBeloBAC11"
/note="end : T7"
ORIGIN

Query Match 3.7%; Score 42.4; DB 9; Length 645;
Best Local Similarity 14.0%; Pred. No. 1.8;
Matches 73; Conservative 117; Mismatches 330; Indels 2; Gaps 1;

```
Qy         14 GAGTGTGTACGGGTGGCACGGGTCGAGGCCTTGAGCTTCCACCAGGCAGTCAGAAGGAGA 73
Db         73 GNGNNNNNNNTGGTNNTNNTNNNGGTCKKGCGNNGNNNNNNNNGGGCCNNNTNGGKKKGG 132

Qy         74 AGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGCACC 133
Db        133 NGGGNNNGTNGTGGTNGNNGGGGGGGGNNNNNGGNNNTTNNTNGGTTTNNNGGNNNNNSC 192

Qy        134 ACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGCACC 193
Db        193 CCSNCTNCNNNNTNTTNSSSSSSNSNNNTNNNNNSNNSNNNSNNNNSSSGSSSNNNNSGG 252

Qy        194 TCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATGGCACACC 253
Db        253 SSSNNSNSNNGSGSSSSSNSNTSSNNNSNNTNSNNNSSNNNNSSTNSNNSNNSSSSTSTT 312

Qy        254 AGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTTCGAATGCGTACGCGCC 313
Db        313 NTSNSTSSNNSATGSSSSNSSSGGTTBSGSSSSSSSNSSSNNNNNNASNNSBT--SNSNN 370

Qy        314 AGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTTCCCGTCG 373
Db        371 SNSATTSSTNGSSGSSSSSSSSSSTSSNTSTSSTSNSSNSNTSSTTSSSSTTNSTSTSSS 430

Qy        374 GGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTCTTGGTCC 433
Db        431 SSNSTGSSSSTTTTNSSASSNNNSNNNNGNSSSSNAANSTSTTNSSNTTTSSNNSNSSCN 490

Qy        434 AGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCACCCTCT 493
Db        491 TTSANNTSSTNTTNTAGNNNNATSSSNSNNNSSNNNSNNNSNSGSGTSSGNTSSSSCTGT 550

Qy        494 CGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGC 535
Db        551 BSSGNSNSSNNNSCNGSNNSCTGNSSNSSSTTTGSSSSSNSS 592
```

RESULT 9
CNS017SY/c
LOCUS CNS017SY 1101 bp DNA linear GSS 26-JUL-1999
DEFINITION Drosophila melanogaster genome survey sequence SP6 end of BAC BACN37L08 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.
ACCESSION AL108460
VERSION AL108460.1 GI:5628764
KEYWORDS GSS.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 1101)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBeloBAC11.
FEATURES Location/Qualifiers
source 1. .1101
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACN37L08"
/clone_lib="DrosBAC"
/plasmid="pBeloBAC11"
/note="end : SP6"
ORIGIN

```
  Query Match             3.7%;  Score 42.4;  DB 9;  Length 1101;
  Best Local Similarity   18.2%;  Pred. No. 2;
  Matches   48;  Conservative  112;  Mismatches  104;  Indels    0;  Gaps    0;

Qy         16 GTGTGTACGGGTGGCACGGGTCGAGGCCTTGAGCTTCCACCAGGCAGTCAGAAGGAGAAG 75
              ::::   ::::|:::|:::: :: ::::|   ::| :: :  ::: | : :  :: :  :
Db        968 SKSBTSBSSBSTSSSASBSSSSSSSBSSTSTTBSTSBBBSTSSSSSGSSSSSBBSTBSBS 909

Qy         76 GGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGCACCAC 135
              :: : ||||: : |::|: ::  :|    : ::::: :::: :|   : :| ::: :: :
Db        908 SBTBTTTTTBTKSTSSTSSSSTSBTTTSBBSSSSSSSBSSSBSTTTSBSSTBSSYGSSSB 849

Qy        136 CACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGCACCTC 195
                :: : :|:|:|:  |: ::: :|:: ::|:  :: | :|   : :: :::   :  :
Db        848 TCTSKCSTBTSGSTBTSTBMSKBSSTSSTSBTSGSSBCGGSCGSTSGSSCSSBCGKSTSS 789

Qy        196 CACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATGGCACACCAG 255
                :  ||  :     |   | |:|||||:||||:     : :|||: :: | : ::
Db        788 GSTSSGTTCGBCSSTGGCSCCCYCSCCCTCSTCGTSTCCSCSCSGTGSSBKCCYSTSSSA 729

Qy        256 TCGCAGGAGTGGCAGGACGTGGTC 279
                |:  : :|::: ||   ||| |
Db        728 STGSSCSSSTSSSSGGTKMTGGCC 705


RESULT 10
AI289506/c
LOCUS       AI289506                512 bp    mRNA    linear   EST 21-DEC-1998
DEFINITION  qw28e11.x1 NCI_CGAP_Ut4 Homo sapiens cDNA clone IMAGE:1992428 3'
            similar to gb:J05016 PROTEIN DISULFIDE ISOMERASE-RELATED PROTEIN
            PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION   AI289506
VERSION     AI289506.1  GI:3932686
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 512)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Insert Length: 2198   Std Error: 0.00
            Seq primer: -40UP from Gibco
            High quality sequence stop: 307.
FEATURES             Location/Qualifiers
     source          1. .512
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1992428"
                     /tissue_type="serous papillary carcinoma, high grade, 2
                     pooled tumors"
                     /lab_host="DH10B"
                     /clone_lib="NCI_CGAP_Ut4"
                     /note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.48 kb. Life Technologies catalog #:
                     11542-016"
ORIGIN

  Query Match             3.7%;  Score 42.2;  DB 1;  Length 512;
  Best Local Similarity   53.8%;  Pred. No. 2;
  Matches   86;  Conservative    0;  Mismatches   74;  Indels    0;  Gaps    0;

Qy        914 AGAGATTGCTGGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGA 973
              | |||   |||||||  |||      | |    || |  || | |   ||   |   ||||
Db        435 ACAGAGATCTGGAGCATTTGAGCAAGTTTATAGAAGAACATGCCACAAAACTGAGCAGGA 376

Qy        974 CGGTGGACGGTACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTC 1033
              |   ||| |       |||| || ||  |||| |     | | ||   | |  | | ||| |
Db        375 CCAAGGAAGAGCTTTGAAGGCCTGAGGTCTGCGGAAGGTGGGAGGAGGCANACGCCCTGC 316

Qy       1034 GTAGGCCAATGTCGTGGCTTCAACAACGAGACAGGGCAGA 1073
              || | |||  |||| ||| || ||  |||| | ||  | |
Db        315 GTGGCCCATGGTCGGGGCGTCCACGCCGAGGCCGGCAACA 276


RESULT 11
AI687271/c
LOCUS       AI687271                586 bp    mRNA    linear   EST 14-DEC-1999
DEFINITION  tp94e04.x1 NCI_CGAP_Ut3 Homo sapiens cDNA clone IMAGE:2206974 3'
            similar to gb:J05016 PROTEIN DISULFIDE ISOMERASE-RELATED PROTEIN
            PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION   AI687271
VERSION     AI687271.1  GI:4898565
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 586)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Insert Length: 2159   Std Error: 0.00
            Seq primer: -40UP from Gibco
            High quality sequence stop: 399.
FEATURES             Location/Qualifiers
     source          1. .586
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2206974"
                     /tissue_type="poorly-differentiated endometrial
                     adenocarcinoma, 2 pooled tumors"
                     /lab_host="DH10B"
                     /clone_lib="NCI_CGAP_Ut3"
                     /note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.45 kb. Life Technologies catalog #:
                     11541-018"
ORIGIN

  Query Match             3.7%;  Score 42.2;  DB 1;  Length 586;
  Best Local Similarity   53.8%;  Pred. No. 2;
  Matches   86;  Conservative    0;  Mismatches   74;  Indels    0;  Gaps    0;

Qy        914 AGAGATTGCTGGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGA 973
              | |||   |||||||  |||      | |    || |  || | |   ||   |   ||||
Db        423 ACAGAGATCTGGAGCATTTGAGCAAGTTTATAGAAGAACATGCCACAAAACTGAGCAGGA 364

Qy        974 CGGTGGACGGTACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTC 1033
              |   ||| |       |||| || ||  |||| |     | | ||   | |  | | ||| |
```

```
Db        363 CCAAGGAAGAGCTTTGAAGGCCTGAGGTCTGCGGAAGGTGGGAGGAGGCANACGCCCTGC 304

Qy       1034 GTAGGCCAATGTCGTGGCTTCAACAACGAGACAGGGCAGA 1073
              || | |||  |||| ||| || ||  |||| | ||  | |
Db        303 GTGGCCCATGGTCGGGGCGTCCACGCCGAGGCCGGCAACA 264


RESULT 12
AA330793
LOCUS       AA330793               343 bp    mRNA    linear   EST 21-APR-1997
DEFINITION  EST34531 Embryo, 6 week I Homo sapiens cDNA 5' end similar to
            protein disulfide isomerase related protein, mRNA sequence.
ACCESSION   AA330793
VERSION     AA330793.1  GI:1983035
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 343)
  AUTHORS   Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
            Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
            White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,
            Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
            Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,
            Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr.,
            Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
            Moreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
            Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
            Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
            Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
            Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A.,
            He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
            Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H.,
            Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M.,
            Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
            Fraser,C.M. and Venter,J.C.
  TITLE     Initial assessment of human gene diversity and expression patterns
            based upon 83 million nucleotides of cDNA sequence
  JOURNAL   Nature 377 (6547 Suppl), 3-174 (1995)
  MEDLINE   96026280
   PUBMED   7566098
COMMENT     Other_ESTs: THC189915
            Contact: Kerlavage, AR
            Bioinformatics
            The Institute for Genomic Research
            9712 Medical Center Drive, Rockville, MD 20850 USA
            Tel: 3018699056
            Fax: 3018699423
            Email: arkerlav@tigr.org
            For clone availability, additional sequence and expression
            information related to this EST, please check the TIGR Human Gene
            Index (http://www.tigr.org/tdb/hgi/hgi.html)
            Seq primer: M13 Reverse.
FEATURES             Location/Qualifiers
     source          1. .343
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="ATCC (inhost):132414"
                     /db_xref="taxon:9606"
                     /dev_stage="embryo, 6 wks"
                     /clone_lib="Embryo, 6 week I"
                     /note="Organ: embryo; Vector: pBluescript SK-; Site_1:
                     EcoRI; Site_2: XhoI"
ORIGIN

  Query Match             3.7%;  Score 41.8;  DB 1;  Length 343;
  Best Local Similarity   53.1%;  Pred. No. 2.3;
  Matches   85;  Conservative    0;  Mismatches   75;  Indels    0;  Gaps    0;

Qy        914 AGAGATTGCTGGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGA 973
              | |||   |||||||  |||     | |     || |  || | |   ||   |   ||||
Db        161 ACAGAGATCTGGAGCATTTGAGCAAGTTTATAGAAGAACATGCCACAAAACTGAGCAGGA 220

Qy        974 CGGTGGACGGTACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTC 1033
              |   ||| |      |||| || ||  |||| |    | | ||   | |  | | |||| |
Db        221 CCAAGGAAGAGCTTTGAAGGCCTGAGGTCTGCGGAAGGTGGGAGGAGGCAGACGNCCTGC 280

Qy       1034 GTAGGCCAATGTCGTGGCTTCAACAACGAGACAGGGCAGA 1073
              || | |||  |||| ||| |  ||  |||| | ||  | |
Db        281 GTGGCCCATGGTCGGGGCGTNCACGNCGAGGCCGGCAACA 320


RESULT 13
CB047414
LOCUS       CB047414               337 bp    mRNA    linear   EST 17-JAN-2003
DEFINITION  NISC_gg02g05.y1 NCI_CGAP_Kid11 Homo sapiens cDNA clone
            IMAGE:3253425 5', mRNA sequence.
ACCESSION   CB047414
VERSION     CB047414.1  GI:27785701
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 337)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            cDNA Library Preparation:
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL
             DNA Sequencing by: National Institutes of Health Intramural
            Sequencing Center (NISC)
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            info@image.llnl.gov
            Plate: LLAM7961  row: M  column: 10
            Seq primer: M13RP1 reverse primer (ABI).
FEATURES             Location/Qualifiers
     source          1. .337
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3253425"
                     /lab_host="DH10B"
                     /clone_lib="NCI_CGAP_Kid11"
                     /note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with
                     a modified polylinker; Site_1: Not I; Site_2: Eco RI;
                     Plasmid DNA from the normalized library NCI_CGAP_Kid3 was
                     prepared, and ss circles were made in vitro. Following HAP
                     purification, this DNA was used as tracer in a subtractive
                     hybridization reaction. The driver was PCR-amplified cDNAs
                     from a pool of 5,000 clones made from the same library
                     (cloneIDs 1322376-1323911, 1456007-1456775, and
                     1500552-1502855). Subtraction by Bento Soares and M.
                     Fatima Bonaldo.  "
ORIGIN

  Query Match             3.7%;  Score 41.6;  DB 6;  Length 337;
  Best Local Similarity   53.8%;  Pred. No. 2.6;
  Matches   86;  Conservative    0;  Mismatches   74;  Indels    0;  Gaps    0;

Qy        914 AGAGATTGCTGGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGA 973
              | |||   |||||||  |||     | |     || |  || | |   ||   |   ||||
Db         16 ACAGAGATCTGGAGCATTTGAGCAAGTTTATAGAAGAACATGCCACAAAACTGAGCAGGA 75

Qy        974 CGGTGGACGGTACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTC 1033
              |   ||| |      |||| || ||  |||| |    | | ||   | |  | | |||| |
Db         76 CCAAGGAAGAGCTTTGAAGGCCTGAGGTCTGCGGAAGGTGGGAGGAGGCAGACGCCCTGC 135

Qy       1034 GTAGGCCAATGTCGTGGCTTCAACAACGAGACAGGGCAGA 1073
              || | |||  |||| ||| || ||  |||| | ||  | |
Db        136 GTGGCCCATGGTCGGGGCGTCCACGCCGAGGCCGGCAACA 175
```

```
RESULT 14
AA302570
LOCUS       AA302570                340 bp    mRNA    linear   EST 18-APR-1997
DEFINITION  EST15740 Aorta endothelial cells Homo sapiens cDNA 5' end similar
            to protein disulfide isomerase related protein, mRNA sequence.
ACCESSION   AA302570
VERSION     AA302570.1  GI:1954902
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 340)
  AUTHORS   Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
            Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
            White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,
            Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
            Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,
            Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr.,
            Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
            Moreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
            Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
            Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
            Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
            Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A.,
            He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
            Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H.,
            Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M.,
            Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
            Fraser,C.M. and Venter,J.C.
  TITLE     Initial assessment of human gene diversity and expression patterns
            based upon 83 million nucleotides of cDNA sequence
  JOURNAL   Nature 377 (6547 Suppl), 3-174 (1995)
  MEDLINE   96026280
   PUBMED   7566098
COMMENT     Other_ESTs: THC189915
            Contact: Kerlavage, AR
            Bioinformatics
            The Institute for Genomic Research
            9712 Medical Center Drive, Rockville, MD 20850 USA
            Tel: 3018699056
            Fax: 3018699423
            Email: arkerlav@tigr.org
            For clone availability, additional sequence and expression
            information related to this EST, please check the TIGR Human Gene
            Index (http://www.tigr.org/tdb/hgi/hgi.html)
            Seq primer: M13 Reverse.
FEATURES             Location/Qualifiers
     source          1. .340
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="ATCC (inhost):114748"
                     /db_xref="taxon:9606"
                     /cell_type="endothelial cell"
                     /dev_stage="adult"
                     /clone_lib="Aorta endothelial cells"
                     /note="Organ: aorta; Vector: pBluescript SK-; Site_1:
                     EcoRI; Site_2: XhoI"
ORIGIN

  Query Match             3.7%;  Score 41.6;  DB 1;  Length 340;
  Best Local Similarity   53.8%;  Pred. No. 2.6;
  Matches   86;  Conservative    0;  Mismatches   74;  Indels    0;  Gaps    0;

Qy        914 AGAGATTGCTGGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGA 973
              | |||    |||||||  |||      | |     || |  || | |    ||    |    ||||
Db         61 ACAGAGATCTGGAGCATTTGAGCAAGTTTATAGAAGAACATGCCACAAAACTGAGCAGGA 120

Qy        974 CGGTGGACGGTACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTC 1033
              |   ||| |      |||| || ||  |||| |    | | ||  | |  | | ||| |
Db        121 CCAAGGAAGAGCTTTGAAGGCCTGAGGTCTGCGGAAGGTGGGAGGAGGCAGACGCCCTGC 180

Qy       1034 GTAGGCCAATGTCGTGGCTTCAACAACGAGACAGGGCAGA 1073
              || | |||  |||| ||| || ||  |||| | ||  | |
Db        181 GTGGCCCATGGTCGGGGCGTCCACGCCGAGGCCGGCAACA 220


RESULT 15
CA720412/c
LOCUS       CA720412                408 bp    mRNA    linear   EST 26-NOV-2002
DEFINITION  wkm2n.pk007.a4 wkm2n Triticum aestivum cDNA clone wkm2n.pk007.a4 5'
            end, mRNA sequence.
ACCESSION   CA720412
VERSION     CA720412.1  GI:25442205
KEYWORDS    EST.
SOURCE      Triticum aestivum (bread wheat)
  ORGANISM  Triticum aestivum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Pooideae; Triticeae; Triticum.
REFERENCE   1  (bases 1 to 408)
  AUTHORS   Tingey,S.V., Powell,W., Wolters,P., Dolan,M., Hainey,C., Yuan,Z.,
            Miao,G., Caraher,N. and Hanafey,M.K.
  TITLE     DuPont Wheat cDNA Sequence
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Scott V. Tingey
            Crop Genetics
            E. I. DuPont de Nemours and Company
            1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA
            Tel: 302-631-2602
            Fax: 302-631-2607
            Email: Scott.V.Tingey@USA.dupont.com
            Seq primer: M13.
FEATURES             Location/Qualifiers
     source          1. .408
                     /organism="Triticum aestivum"
                     /mol_type="mRNA"
                     /cultivar="Spring wheat"
                     /db_xref="taxon:4565"
                     /clone="wkm2n.pk007.a4"
                     /tissue_type="kernel"
                     /lab_host="DH10B"
                     /clone_lib="wkm2n"
                     /note="Vector: pBluescript SK+; Site_1: EcoRI; Site_2:
                     XhoI; Wheat (Triticum aestivum L.) kernel malted 175 hours
                     at 4 C, normalized"
ORIGIN

  Query Match             3.7%;  Score 41.6;  DB 6;  Length 408;
  Best Local Similarity   48.0%;  Pred. No. 2.7;
  Matches  119;  Conservative    0;  Mismatches  129;  Indels    0;  Gaps    0;

Qy        402 GGGTAGGGCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAA 461
              |||||| | | ||| |||          || ||||  || | || | |  ||||  ||| |
Db        302 GGGTAGAGGCGTACGCGATGACCGAGAGGCCCAGCGGGGCGGGCCTGTTCAGTGGCCGCA 243

Qy        462 GATAGGGTCGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTT 521
              | |   || | || ||  ||| ||  | |     || | | |      || |  /
Db        242 GGTGCAGTTGGTGCAGGTGCAGCTGGCGCCGCACTTGCACTTGCCGTCGTTCTCCGCGGC 183

Qy        522 CTGGTGCGGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCA 581
              ||  |||      | |    ||       |  |  ||  | |  |||| |||    || ||
Db        182 CTCCTGCACCTCGAAGTGGCTCTTCTCGGTGTCGACCATGACGATGCCGTAGCCGTCGCC 123

Qy        582 CCTGTTCTCGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGA 641
              | | ||| ||  |   ||| |  |  ||||  |    |  |||||    |  |   |
Db        122 CTTCTTCACGCACTGGGTCTTGTCGGCGCAGTCGCAGTTGCCGCACTTGTCAGCCATGGC 63

Qy        642 CGTGTTGG 649
              || ||||
Db         62 GGTCTTGG 55


Search completed: October 18, 2004, 03:14:43
```

Job time : 3996.86 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 17, 2004, 15:27:12 ; Search time 588.611 Seconds
(without alignments)
10122.301 Million cell updates/sec

Title: US-10-679-999-17
Perfect score: 1135
Sequence: 1 GTATACCTGTTTTGAGTGTG.....AGGCCCAACAATTACCTAGG 1135

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_23Sep04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	662.4	58.4	777	12	ADM17770	Adm17770 Fc C-term
	2	657	57.9	993	12	ADM68910	Adm68910 Human IgG
	3	656.8	57.9	780	12	ADM17710	Adm17710 Fc N-term
	4	598.4	52.7	7033	12	ADJ65025	Adj65025 Plasmid p
	5	63.2	5.6	2572	6	AAD24594	Aad24594 Human ery
	6	60	5.3	2287	10	ADH54467	Adh54467 Human imm
	7	53.6	4.7	138	8	AAL51057	Aal51057 Cyclic si
c	8	43.8	3.9	2000	8	ADA71938	Ada71938 Rice gene
	9	43	3.8	8874	12	ADJ65028	Adj65028 Plasmid p
	10	42	3.7	1161	11	ABD09099	Abd09099 Pseudomon
	11	42	3.7	1200	4	AAS51550	Aas51550 Pseudomon
	12	42	3.7	1200	8	ACA19541	Aca19541 Prokaryot
c	13	42	3.7	1287	11	ABD09256	Abd09256 Pseudomon
	14	42	3.7	1359	11	ABD09020	Abd09020 Pseudomon
c	15	41.8	3.7	1182	10	ADC16621	Adc16621 Secondary
c	16	41.8	3.7	135638	10	ABX34289	Abx34289 S. atrool
	17	41.6	3.7	2171	3	AAF16286	Aaf16286 Human pro
	18	41.6	3.7	2172	6	ABQ54963	Abq54963 Human ova
	19	41.6	3.7	2300	6	AAS62246	Aas62246 cDNA sequ
	20	41.6	3.7	2300	6	ABK34737	Abk34737 Human cDN
	21	41.4	3.6	2000	8	ADA71938	Ada71938 Rice gene
	22	40.6	3.6	268	2	AAT20112	Aat20112 Human gen
	23	40	3.5	2930	12	ADO19793	Ado19793 Human PRO
	24	39.8	3.5	774	12	ADO44398	Ado44398 Z. mays F
c	25	39.6	3.5	1425	11	ACH95714	Ach95714 Klebsiell
	26	39.6	3.5	2016	11	ACH95697	Ach95697 Klebsiell
c	27	39.4	3.5	5331	3	AAA30292	Aaa30292 DNA fragm
c	28	39.2	3.5	1482	8	AAL52125	Aal52125 Humanised
c	29	39	3.4	688	2	ADR02223	Adr02223 A. gossyp
c	30	38.8	3.4	1057	2	AAQ03405	Aaq03405 Streptomy
c	31	38.8	3.4	3042	4	ABL28445	Abl28445 Drosophil
	32	38.8	3.4	5215	4	ABL28444	Abl28444 Drosophil
c	33	38.6	3.4	1440	2	AAT73384	Aat73384 P. membra
c	34	38.6	3.4	1440	4	AAD03829	Aad03829 Pichia me
c	35	38.6	3.4	1440	4	AAD07040	Aad07040 Pichia me
c	36	38.6	3.4	3489	3	AAA30290	Aaa30290 Kaposi's
c	37	38.6	3.4	3489	4	AAF82901	Aaf82901 Nucleotid
c	38	38.6	3.4	3489	6	ABA93487	Aba93487 Kaposi's
c	39	38.6	3.4	3489	12	ADJ65095	Adj65095 HHV8 DNA
	40	38.6	3.4	32207	2	AAV73805	Aav73805 KSHV LUR
	41	38.6	3.4	137507	2	AAV19941	Aav19941 KSHV long
	42	38.6	3.4	137508	12	ADN12162	Adn12162 Human her
c	43	38.4	3.4	543	2	AAQ23092	Aaq23092 Antigen t
	44	38.2	3.4	304	12	ADP61909	Adp61909 Maize car
	45	37.8	3.3	1464	4	ABL25527	Abl25527 Drosophil

ALIGNMENTS

RESULT 1
ADM17770
ID ADM17770 standard; DNA; 777 BP.
XX
AC ADM17770;
XX
DT 17-JUN-2004 (first entry)
XX
DE Fc C-terminal vector related oligonucleotide SEQ ID NO:122.
XX
KW nerve growth factor modulator; NGF modulator; analgesic; NGF inhibitor;
KW nerve growth factor inhibitor; neurologic pain; diabetic neuropathy;
KW post-herpetic neuralgia; inflammatory pain; migraine; asthma;
KW hyperactive bladder; psoriasis; cancer; acute pain; dental pain;
KW surgical pain; pain; causalgia; demyelinating disease;
KW trigeminal neuralgia; chronic alcoholism; stroke; thalamic pain syndrome;
KW diabetes; acquired immuno deficiency syndrome; AIDS; headache;
KW inflammation; arthritis; rheumatic disease; lupus; osteoarthritis;
KW inflammatory bowel disorder; inflammatory eye disorder; sunburn;
KW carditis; dermatitis; myositis; neuritis; collagen vascular disease;
KW chronic inflammatory condition; neuropathic pain; genitourinary; wound;
KW burn; allergic skin reaction; pruritus; vitiligo;
KW gastrointestinal disorder; colitis; gastric ulceration; duodenal ulcer;
KW ss.
XX
OS Synthetic.
XX
PN WO2004026329-A1.
XX
PD 01-APR-2004.
XX
PF 19-SEP-2003; 2003WO-US029866.
XX
PR 19-SEP-2002; 2002US-0412524P.
PR 18-SEP-2003; 2003US-00666480.
XX
PA (AMGE-) AMGEN INC.
XX
PI Boone TC, Wild KD, Sitney KC, Min H, Kimmel B;
XX
DR WPI; 2004-283150/26.
XX
PT Novel peptide capable of modulating nerve growth factor activity, useful
PT for treating disease or disorder e.g., acute pain, dental pain, cancer,

PT migraine and collagen vascular disease.
XX
PS Example 2; SEQ ID NO 122; 267pp; English.
XX
CC The present invention describes a peptide (I) that is capable of
CC modulating nerve growth factor (NGF) activity. Also described: (1)
CC modified peptide (II) comprising (I) and a vehicle, where the modified
CC peptide is capable of modulating NGF activity; (2) dimer or multimer of
CC (I); (3) modified peptide (III), its multimers or its salt, where the
CC peptide is capable of modulating NGF activity; (4) polynucleotide (IV)
CC encoding (I), (II) or (III); (5) expression vector (V) comprising (IV);
CC (6) host cell (VI) comprising (V); (7) a composition (VII) of matter and
CC a vehicle, where the composition of matter is capable of modulating NGF
CC activity; and (8) pharmaceutical composition comprising (I), (II) or
CC (III) and a diluent or carrier. (I) has analgesic activity, and can be
CC used as an inhibitor of NGF. (I) is useful for treating or preventing a
CC disease or disorder associated with NGF activity by administering (I) to
CC human or animal. The disease or disorder chosen from neurologic pain,
CC painful diabetic neuropathy, post-herpetic neuralgia, inflammatory pain,
CC migraine, asthma, hyperactive bladder, psoriasis, cancer, acute pain,
CC dental pain, pain from trauma, surgical pain, pain resulting from
CC amputation or abscess, causalgia, demyelinating diseases, trigeminal
CC neuralgia, chronic alcoholism, stroke, thalamic pain syndrome, diabetes,
CC acquired immuno deficiency syndrome (AIDS), toxins and chemotherapy,
CC general headache, cluster headache, mixed-vascular and non-vascular
CC syndromes, tension headache, general inflammation, arthritis, rheumatic
CC diseases, lupus, osteoarthritis, inflammatory bowel disorders,
CC inflammatory eye disorders, inflammatory or unstable bladder disorders,
CC skin complaints with inflammatory components, sunburn, carditis,
CC dermatitis, myositis, neuritis, collagen vascular diseases, chronic
CC inflammatory conditions, inflammatory pain associated hyperalgesia and
CC allodynia, neuropathic pain and associated hyperalgesia and allodynia,
CC diabetic neuropathy pain, sympathetically maintained pain,
CC deafferentation syndromes, epithelial tissue damage or dysfunction,
CC herpes simplex, post-herpetic neuralgia, disturbances of visceral
CC motility at respiratory, genitourinary, gastrointestinal or vascular
CC regions, wounds, burns, allergic skin reactions, pruritus, vitiligo,
CC general gastrointestinal disorders, colitis, gastric ulceration, duodenal
CC ulcers, vasomotor or allergic rhinitis, or bronchial disorders. (I) is
CC also useful for modulating pain or promoting analgesia by administering
CC (I) to human or animal. (I) is also useful in the manufacture of
CC medicament for the treatment of disease or disorder. The present sequence
CC is used in the exemplification of the present invention.
XX
SQ Sequence 777 BP; 133 A; 206 C; 236 G; 202 T; 0 U; 0 Other;

Query Match 58.4%; Score 662.4; DB 12; Length 777;
Best Local Similarity 97.7%; Pred. No. 7.1e-178;
Matches 672; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

```
Qy          1 GTATACCTGTTTTGAGTGTGTACGGGTGGCACGGGTCGAGGCCTTGAGCTTCCACCAGGC 60
              |||||||||||||||||||||| ||||| || ||||||||||||||   || || |||
Db         36 GTATACCTGTTTTGAGTGTGTACAGGTGGAACAGGTCGAGGCCTTGAGGACCCCCCTGGC 95

Qy         61 AGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         96 AGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTC 155

Qy        121 CAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        156 CAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATG 215

Qy        181 CACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        216 CACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCG 275

Qy        241 TGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTTCGA 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        276 TGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTC 335

Qy        301 ATGCGTACGCGCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTT 360
              |||   |||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db        336 ATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTT 395

Qy        361 CGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGAC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        396 CGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGAC 455

Qy        421 TGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        456 TGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGG 515

Qy        481 CACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGAC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        516 CACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGAC 575

Qy        541 CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        576 CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTC 635

Qy        601 GTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        636 GTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTC 695

Qy        661 TTCTCGGAGAGGGACAGAGGCCCATTTC 688
              |||||||||||||||||||||||||||
Db        696 TTCTCGGAGAGGGACAGAGGCCCATTTC 723
```

RESULT 2
ADM68910
ID ADM68910 standard; DNA; 993 BP.
XX
AC ADM68910;
XX
DT 03-JUN-2004 (first entry)
XX
DE Human IgG1 heavy chain DNA non-coding strand.
XX
KW Human; batch reformatting vector; ligand screening; phagemid;
KW phage display vector; pBRV; pRRV; internal ribosome entry site; IRES;
KW rapid reformatting vector; IgG1; immunoglobulin; heavy chain; ss.
XX
OS Homo sapiens.
XX
PN US2003224408-A1.
XX
PD 04-DEC-2003.
XX
PF 07-MAR-2003; 2003US-00383902.
XX
PR 07-MAR-2002; 2002US-0362403P.
XX
PA (DYAX-) DYAX CORP.
XX
PI Hoogenboom HRJM, Mullberg J, Ladner RC;
XX
DR WPI; 2004-119700/12.
XX
PT Screening ligands, by providing initial nucleic acid cassettes, modifying
PT cassette in single reaction mixture, introducing modified cassette into
PT mammalian cell, expressing modified cassette in transfected cells.
XX
PS Disclosure; SEQ ID NO 5; 63pp; English.
XX
CC The invention relates to screening ligands, by providing several initial
CC nucleic acid cassettes, modifying each nucleic acid cassette in single
CC reaction mixture so that it is functional in a second expression system,
CC introducing each modified nucleic acid cassette into a mammalian cell to
CC produce a mixture of transfected cells, and expressing each modified
CC nucleic acid cassette in transfected cells. Also included are screening
CC nucleic acids (involving providing a number of first different nucleic
CC acids, each encoding a hetero oligomeric candidate ligand, selecting a
CC subset of a number of first different nucleic acids by contacting
CC candidate ligands encoded by the members of a number of first different
CC nucleic acids to a target, reformatting each nucleic acid of the subset

CC for mammalian cell expression, such that each nucleic acid encodes a
CC hetero-oligomeric protein that includes a first functional domain of one
CC subunit of the candidate ligand, a second functional domain of another
CC subunit of the candidate ligand and an effector domain not encoded by the
CC nucleic acids of a number of first different nucleic acids, introducing
CC members of the subset into a mammalian cell to form several expression
CC cells that can produce the protein that includes the functional domain
CC and the effector domain, and screening the expression cells to identify
CC cells that produce at least a threshold amount of a ligand-effector
CC domain fusion protein) and evaluating display library members (involving
CC providing several display library members, determining an assessment for
CC each library member with respect to a property, storing information about
CC the assessments of the library members in a computer database, filtering
CC the information to identify a subset of the library members, and
CC reformatting each member of the subset for expression in a mammalian cell
CC by a method that comprises disposing nucleic acid for each member of the
CC selected subset into a single container). The method is useful for
CC screening ligands. Bacterial and mammalian expression vectors
CC (reformatting vectors) were prepared that support the transfer
CC individually or en masse of Fab heavy and light chain genes from a
CC bacterial expression vector to a mammalian expression vector. Typically,
CC the display vector was a phagemid or phage display vector, which mediate
CC the expression of the Fab on the surface of the bacteriophage M13 or fd.
CC The Fab-encoding segment was transferred from the bacterial display
CC vector to the eukaryotic vector, e.g., pBRV or pRRV by restricting the
CC vector with ApaL1 and BstE2. This fragment was subcloned into ApaL1/BstE2
CC sites of pBRV (batch reformatting vector) or pRRV (rapid reformatting
CC vector). This vector contained a CMV eukaryotic promoter in place of the
CC first bacterial leader sequence. The VH-CH1 sequence was no longer fused
CC to gene III but was fused in-frame to a sequence encoding an
CC immunoglobulin Fc region, e.g., including Hinge-CH2-CH3. Two intervening
CC segments which were inserted between heavy and light chain coding
CC sequences were IrES between the EcoRI and XhaI site for internal ribosome
CC entry and translation of the second coding region. The present sequence
CC is the non-coding strand of a DNA used in the constructs of the method of
CC the invention.
XX
SQ Sequence 993 BP; 161 A; 257 C; 340 G; 235 T; 0 U; 0 Other;

Query Match 57.9%; Score 657; DB 12; Length 993;
Best Local Similarity 97.8%; Pred. No. 2.7e-176;
Matches 666; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

```
Qy          7 CTGTTTTGAGTGTGTACGGGTGGCACGGGTCGAGGCCTTGAGCTTCCACCAGGCAGTCAG 66
              |||||||||||||||||||||||||||||| || ||||||   || || |||||||||
Db        310 CTGTTTTGAGTGTGTACGGGTGGCACGGGTCGTGGACTTGAGGACCCCCCTGGCAGTCAG 369

Qy         67 AAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGT 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        370 AAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGT 429

Qy        127 ACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTG 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        430 ACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTG 489

Qy        187 CCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATG 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        490 CCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATG 549

Qy        247 GCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTTCGAATGCGT 306
              |||||||||||||||||||||||||||||||||||||||||||||||| |  |||
Db        550 GCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATGTTC 609

Qy        307 ACGCGCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTT 366
              |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        610 ACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTT 669

Qy        367 CCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTC 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        670 CCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTC 729

Qy        427 TTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTC 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        730 TTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTC 789

Qy        487 ACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGG 546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        790 ACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGG 849

Qy        547 CTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCC 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        850 CTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCC 909

Qy        607 TTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCG 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        910 TTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCG 969

Qy        667 GAGAGGGACAGAGGCCCATTT 687
              |||||||||||||||||||||
Db        970 GAGAGGGACAGAGGCCCATTT 990
```

RESULT 3
ADM17710
ID ADM17710 standard; DNA; 780 BP.
XX
AC ADM17710;
XX
DT 17-JUN-2004 (first entry)
XX
DE Fc N-terminal vector related oligonucleotide SEQ ID NO:62.
XX
KW nerve growth factor modulator; NGF modulator; analgesic; NGF inhibitor;
KW nerve growth factor inhibitor; neurologic pain; diabetic neuropathy;
KW post-herpetic neuralgia; inflammatory pain; migraine; asthma;
KW hyperactive bladder; psoriasis; cancer; acute pain; dental pain;
KW surgical pain; pain; causalgia; demyelinating disease;
KW trigeminal neuralgia; chronic alcoholism; stroke; thalamic pain syndrome;
KW diabetes; acquired immuno deficiency syndrome; AIDS; headache;
KW inflammation; arthritis; rheumatic disease; lupus; osteoarthritis;
KW inflammatory bowel disorder; inflammatory eye disorder; sunburn;
KW carditis; dermatitis; myositis; neuritis; collagen vascular disease;
KW chronic inflammatory condition; neuropathic pain; genitourinary; wound;
KW burn; allergic skin reaction; pruritus; vitiligo;
KW gastrointestinal disorder; colitis; gastric ulceration; duodenal ulcer;
KW ss.
XX
OS Synthetic.
XX
PN WO2004026329-A1.
XX
PD 01-APR-2004.
XX
PF 19-SEP-2003; 2003WO-US029866.
XX
PR 19-SEP-2002; 2002US-0412524P.
PR 18-SEP-2003; 2003US-00666480.
XX
PA (AMGE-) AMGEN INC.
XX
PI Boone TC, Wild KD, Sitney KC, Min H, Kimmel B;
XX
DR WPI; 2004-283150/26.
XX
PT Novel peptide capable of modulating nerve growth factor activity, useful
PT for treating disease or disorder e.g., acute pain, dental pain, cancer,
PT migraine and collagen vascular disease.
XX
PS Example 2; SEQ ID NO 62; 267pp; English.
XX
CC The present invention describes a peptide (I) that is capable of
CC modulating nerve growth factor (NGF) activity. Also described: (1)
CC modified peptide (II) comprising (I) and a vehicle, where the modified
CC peptide is capable of modulating NGF activity; (2) dimer or multimer of
CC (I); (3) modified peptide (III), its multimers or its salt, where the
CC peptide is capable of modulating NGF activity; (4) polynucleotide (IV)

```
CC   encoding (I), (II) or (III); (5) expression vector (V) comprising (IV);
CC   (6) host cell (VI) comprising (V); (7) a composition (VII) of matter and
CC   a vehicle, where the composition of matter is capable of modulating NGF
CC   activity; and (8) pharmaceutical composition comprising (I), (II) or
CC   (III) and a diluent or carrier. (I) has analgesic activity, and can be
CC   used as an inhibitor of NGF. (I) is useful for treating or preventing a
CC   disease or disorder associated with NGF activity by administering (I) to
CC   human or animal. The disease or disorder chosen from neurologic pain,
CC   painful diabetic neuropathy, post-herpetic neuralgia, inflammatory pain,
CC   migraine, asthma, hyperactive bladder, psoriasis, cancer, acute pain,
CC   dental pain, pain from trauma, surgical pain, pain resulting from
CC   amputation or abscess, causalgia, demyelinating diseases, trigeminal
CC   neuralgia, chronic alcoholism, stroke, thalamic pain syndrome, diabetes,
CC   acquired immuno deficiency syndrome (AIDS), toxins and chemotherapy,
CC   general headache, cluster headache, mixed-vascular and non-vascular
CC   syndromes, tension headache, general inflammation, arthritis, rheumatic
CC   diseases, lupus, osteoarthritis, inflammatory bowel disorders,
CC   inflammatory eye disorders, inflammatory or unstable bladder disorders,
CC   skin complaints with inflammatory components, sunburn, carditis,
CC   dermatitis, myositis, neuritis, collagen vascular diseases, chronic
CC   inflammatory conditions, inflammatory pain associated hyperalgesia and
CC   allodynia, neuropathic pain and associated hyperalgesia and allodynia,
CC   diabetic neuropathy pain, sympathetically maintained pain,
CC   deafferentation syndromes, epithelial tissue damage or dysfunction,
CC   herpes simplex, post-herpetic neuralgia, disturbances of visceral
CC   motility at respiratory, genitourinary, gastrointestinal or vascular
CC   regions, wounds, burns, allergic skin reactions, pruritus, vitiligo,
CC   general gastrointestinal disorders, colitis, gastric ulceration, duodenal
CC   ulcers, vasomotor or allergic rhinitis, or bronchial disorders. (I) is
CC   also useful for modulating pain or promoting analgesia by administering
CC   (I) to human or animal. (I) is also useful in the manufacture of
CC   medicament for the treatment of disease or disorder. The present sequence
CC   is used in the exemplification of the present invention.
XX
SQ   Sequence 780 BP; 132 A; 208 C; 237 G; 203 T; 0 U; 0 Other;

  Query Match             57.9%;  Score 656.8;  DB 12;  Length 780;
  Best Local Similarity   96.8%;  Pred. No. 2.8e-176;
  Matches  670;  Conservative    0;  Mismatches   22;  Indels    0;  Gaps    0;

Qy          6 CCTGTTTTGAGTGTGTACGGGTGGCACGGGTCGAGGCCTTGAGCTTCCACCAGGCAGTCA 65
              ||||||||||||||||||| ||||| |||||||| || ||||||   || || ||||||||
Db         89 CCTGTTTTGAGTGTGTACAGGTGGAACGGGTCGTGGACTTGAGGACCCCCCTGGCAGTCA 148

Qy         66 GAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTG 125
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        149 AAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTG 208

Qy        126 TACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCT 185
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        209 TACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCT 268

Qy        186 GCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCAT 245
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        269 GCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCAT 328

Qy        246 GGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTTCGAATGCG 305
              |||||||||||||||||||||||||||||||||||||||||||||||| |  |||
Db        329 GGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATGTT 388

Qy        306 TACGCGCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTT 365
              |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        389 CACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTT 448

Qy        366 TCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTT 425
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        449 TCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTT 508

Qy        426 CTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCT 485
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        509 CTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCT 568

Qy        486 CACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAG 545
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        569 CACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAG 628

Qy        546 GCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCC 605
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        629 GCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCC 688

Qy        606 CTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTCTC 665
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        689 CTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTCTC 748

Qy        666 GGAGAGGGACAGAGGCCCATTTCATGGCTAGG 697
              |||||||||||||||||||  |  |||||
Db        749 GGAGAGGGACAGAGGCCCATTTATTACCTAGG 780


RESULT 4
ADJ65025
ID   ADJ65025 standard; DNA; 7033 BP.
XX
AC   ADJ65025;
XX
DT   06-MAY-2004  (first entry)
XX
DE   Plasmid pD17-H39E3-2.h4a complemetary strand DNA sequence SEQ ID NO:4.
XX
KW   humanised antibody; human 4-1BB; human 4-1BB ligand; cancer; cytostatic;
KW   gene therapy; antibody; plasmid; pD17-H39E3-2.h4a; gene; ds.
XX
OS   Synthetic.
XX
PN   WO2004010947-A2.
XX
PD   05-FEB-2004.
XX
PF   30-JUL-2003; 2003WO-US023735.
XX
PR   30-JUL-2002; 2002US-0399646P.
XX
PA   (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX
PI   Jure-Kunkel M,  Ganguly S,  Abraham R,  Hollenbaugh DL,  Rillema J;
PI   Thorne B,  Shuford WW,  Mittler RS;
XX
DR   WPI; 2004-143726/14.
XX
PT   New humanized antibody that binds to human 4-1BB and allows binding of
PT   human 4-1BB to a human 4-1BB ligand, useful for preparing a composition
PT   for treating cancer.
XX
PS   Example; SEQ ID NO 4; 78pp; English.
XX
CC   The present invention describes a humanised antibody (I) that binds to
CC   human 4-1BB and allows binding of human 4-1BB to a human 4-1BB ligand.
CC   Also described: (1) a pharmaceutical composition comprising the antibody
CC   (I) and a carrier; (2) treating cancer in a subject; and (3) an isolated
CC   polynucleotide comprising nucleotides 693-2072 of the 7033-base pairs
CC   (bp) sequence (SEQ ID NO: 3, ADJ65024) or nucleotides 633-1034 or 1409-
CC   1726 of the 8874-bp sequence (SEQ ID NO: 6, ADJ65027). (I) has cytostatic
CC   activity, and can be used in gene therapy. The humanised antibody (I) can
CC   be used for preparing a composition for treating cancer. The present
CC   sequence represents the complementary strand of the plasmid pD17-H39E3-
CC   2.h4a nucleotide sequence, which is used in an example from the present
CC   invention.
XX
SQ   Sequence 7033 BP; 1789 A; 1687 C; 1766 G; 1791 T; 0 U; 0 Other;

  Query Match             52.7%;  Score 598.4;  DB 12;  Length 7033;
  Best Local Similarity   92.5%;  Pred. No. 2.9e-159;
  Matches  629;  Conservative    0;  Mismatches   51;  Indels    0;  Gaps    0;

Qy         15 AGTGTGTACGGGTGGCACGGGTCGAGGCCTTGAGCTTCCACCAGGCAGTCAGAAGGAGAA 74
                ||   | ||||||||| |||||||| || ||  ||   || || || ||||||||||| ||
```

```
Db       1400 AGGTGGAACGGGTGGAACGGGTCGTGGACTCAAGGACCCCCCTGGTAGTCAGAAGGACAA 1459

Qy         75 GGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGCACCA 134
              |||||||||||||||||||| |||||||||||||||||||||||||||| ||||||||
Db       1460 GGGGGGTTTTGGGTTCCTGTGAGAGTACTAGAGGGCCTGGGGACTCCAGTGCACGCACCA 1519

Qy        135 CCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGCACCT 194
              |||||||||||||||| |||||||| |||||| |||||||||||||||||||| ||||||||
Db       1520 CCACCTGCACTCGGTCCTTCTGGGGCTCCAGGTCAAGTTGACCATGCACCTACCGCACCT 1579

Qy        195 CCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATGGCACACCA 254
              |||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Db       1580 CCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCAAGTTGTCGTGCATGGCACACCA 1639

Qy        255 GTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTTCGAATGCGTACGCGCCA 314
              |||||||||||||||||||||||||||||||||||| ||||| |  |||   |||  |||
Db       1640 GTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTGCCGTTCCTCATGTTCACGTTCCA 1699

Qy        315 GAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTTCCCGTCGG 374
              |||||||||| |||||  || ||||||||||||||||||||||||||||||||||||||||
Db       1700 GAGGTTGTTTCCGGAGGGCAGGAGGTAGCTCTTTTGGTAGAGGTTTCGGTTTCCCGTCGG 1759

Qy        375 GGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTCTTGGTCCA 434
              |||||| |||||||||||||||||||||||||| ||| ||| ||||||||||||||||
Db       1760 GGCTCTCGGTGTCCACATGTGGGACGGGGGTAGGGTCCTCCTCTACTGGTTCTTGGTCCA 1819

Qy        435 GTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCACCCTCTC 494
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db       1820 GTCGGACTGGACGGACCAGTTTCCGAAGATGGGGTCGCTGTAGCGGCACCTCACCCTCTC 1879

Qy        495 GTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGGCTGCCGAG 554
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1880 GTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGGCTGCCGAG 1939

Qy        555 GAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCCTTGCAGAA 614
              |||||||||||||||| ||| |||||||||||||||||||||| ||||||| |||||
Db       1940 GAAGAAGGAGATGTCGTCCGATTGGCACCTGTTCTCGTCCACCGTCCTCCCCTTACAGAA 1999

Qy        615 GAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCGGAGAGGGA 674
              |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db       2000 GAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGTGTCTTCTCGGAGAGGGA 2059

Qy        675 CAGAGGCCCATTTCATGGCT 694
              ||||| |||||||  | | |
Db       2060 CAGAGACCCATTTACTAGAT 2079
```

RESULT 5
AAD24594
ID AAD24594 standard; DNA; 2572 BP.
XX
AC AAD24594;
XX
DT 09-APR-2002 (first entry)
XX
DE Human erythropoietin (Epo) related DNA.
XX
KW Human; erythropoietin; Epo; haematocrit; anaemia; kidney function;
KW cancer; myelosuppressive therapy; anti-viral drug; ds.
XX
OS Homo sapiens.
XX
PN WO200181405-A2.
XX
PD 01-NOV-2001.
XX
PF 19-APR-2001; 2001WO-US012836.
XX
PR 21-APR-2000; 2000US-00559001.
XX
PA (AMGE-) AMGEN INC.
XX
PI Egrie JC, Elliott SG, Browne JK, Sitney KC;
XX
DR WPI; 2002-034433/04.
XX
PT Increasing and maintaining hematocrit in mammal suffering from anemia,
PT comprising administering hyperglycosylated analog of erythropoietin less
PT frequently and at lower molar amount of recombinant human erythropoietin.
XX
PS Disclosure; Page 86-95; 95pp; English.
XX
CC The invention relates to a method for increasing and maintaining
CC haematocrit in a mammal. The method comprises administering a
CC hyperglycosylated analogue of erythropoietin (Epo) in a pharmaceutical
CC composition, less frequently than an equivalent molar amount of and at a
CC lower molar amount than recombinant human Epo (rHuEpo) to obtain a
CC comparable target haematocrit. Epo is a glycoprotein hormone necessary
CC for the maturation of erythroid progenitor cells into erythrocytes. Human
CC Epo analogue is useful for raising and maintaining haematocrit to a
CC comparable target haematocrit in a mammal suffering from anaemia
CC associated with a decline or loss of kidney function, myelosuppressive
CC therapy comprising chemotherapeutic or anti-viral drugs or associated
CC with excessive blood loss during surgical procedures, and in cancer
CC condition. The present sequence is human Epo related DNA. Note: The
CC present sequence is designated SEQ ID NO:26 in the sequence listing, but
CC does not correspond to the sequence designated SEQ ID NO: 26 in the
CC figure of the specification (AAE15348). The present sequence is not
CC further referred to in the specification, and has been represented in a
CC protein format in the sequence listing
XX
SQ Sequence 2572 BP; 529 A; 757 C; 757 G; 529 T; 0 U; 0 Other;

```
  Query Match             5.6%;  Score 63.2;  DB 6;  Length 2572;
  Best Local Similarity   89.5%;  Pred. No. 3.6e-07;
  Matches   68;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy        416 TCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGT 475
              ||| |  |   | || ||||||||||||||||||||||||||||||||||||||||||
Db       2085 TCGCCGTGGAGTGGGACCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGT 2144

Qy        476 AGCGGCACCTCACCCT 491
              ||||||||||||||||
Db       2145 AGCGGCACCTCACCCT 2160
```

RESULT 6
ADH54467
ID ADH54467 standard; DNA; 2287 BP.
XX
AC ADH54467;
XX
DT 25-MAR-2004 (first entry)
XX
DE Human immunoglobulin IgG1gene.
XX
KW Human; gene; ds; ELAM-1 protein; sialyl-Lex determinant; immune reaction;
KW inflammation; sepsis; organ damage; leukocyte extravasation;
KW adult respiratory distress syndrome; glomerular nephritis;
KW rheumatoid arthritis; gene therapy; antibody-based therapy; heart attack;
KW septic shock; septicaemia; rheumatoid arthritis; psoriasis;
KW immunoglobulin; IgG1.
XX
OS Homo sapiens.
XX

```
FH   Key             Location/Qualifiers
FT   CDS             1. .2270
FT                   /*tag= b
FT                   /product= "IgG1 protein"
FT                   /transl_except= (pos:1360. .1362, aa:Glu)
FT                   /transl_except= (pos:1363. .1365, aa:Pro)
FT                   /transl_except= (pos:1366. .1368, aa:Lys)
FT                   /transl_except= (pos:1369. .1371, aa:Ser)
FT                   /transl_except= (pos:1372. .1374, aa:Cys)
FT                   /transl_except= (pos:1375. .1377, aa:Asp)
FT                   /transl_except= (pos:1378. .1380, aa:Lys)
```

```
FT                   /transl_except= (pos:1381. .1383, aa:Thr)
FT                   /transl_except= (pos:1384. .1386, aa:His)
FT                   /transl_except= (pos:1387. .1389, aa:Thr)
FT                   /transl_except= (pos:1390. .1392, aa:Cys)
FT                   /transl_except= (pos:1396. .1398, aa:Pro)
FT                   /transl_except= (pos:1399. .1401, aa:Cys)
FT                   /transl_except= (pos:1560. .1562, aa:Phe)
FT                   /transl_except= (pos:1563. .1565, aa:Pro)
FT                   /transl_except= (pos:1566. .1568, aa:Pro)
FT                   /transl_except= (pos:1569. .1571, aa:Lys)
FT                   /transl_except= (pos:1572. .1574, aa:Pro)
FT                   /transl_except= (pos:1575. .1577, aa:Lys)
FT                   /transl_except= (pos:1578. .1580, aa:Asp)
FT                   /transl_except= (pos:1581. .1583, aa:Thr)
FT                   /transl_except= (pos:1584. .1586, aa:Lys)
FT                   /transl_except= (pos:1587. .1589, aa:Met)
FT                   /transl_except= (pos:1590. .1592, aa:Ile)
FT                   /transl_except= (pos:1593. .1595, aa:Ser)
FT                   /transl_except= (pos:1596. .1598, aa:Arg)
FT                   /transl_except= (pos:1599. .1601, aa:Thr)
FT                   /transl_except= (pos:1602. .1604, aa:Pro)
FT                   /transl_except= (pos:1605. .1607, aa:Glu)
FT                   /transl_except= (pos:1608. .1610, aa:Val)
FT                   /transl_except= (pos:1611. .1613, aa:Thr)
FT                   /transl_except= (pos:1614. .1616, aa:Cys)
FT                   /transl_except= (pos:1617. .1619, aa:Val)
FT                   /transl_except= (pos:1620. .1622, aa:Val)
FT   exon            1. .300
FT                   /*tag= a
FT   intron          301. .360
FT                   /*tag= c
FT   exon            361. .453
FT                   /*tag= d
FT   intron          454. .678
FT                   /*tag= e
FT   exon            679. .903
FT                   /*tag= f
FT   intron          904. .960
FT                   /*tag= g
FT   exon            961. .972
FT                   /*tag= h
FT   intron          973. .1359
FT                   /*tag= i
FT   exon            1360. .1404
FT                   /*tag= j
FT   intron          1405. .1523
FT                   /*tag= k
FT   exon            1524. .1853
FT                   /*tag= l
FT   intron          1854. .1949
FT                   /*tag= m
FT   exon            1950. .2270
FT                   /*tag= n
XX
PN   US6613746-B1.
XX
PD   02-SEP-2003.
XX
PF   07-JUN-1995;   95US-00472888.
XX
PR   23-NOV-1990;   90US-00618314.
XX
PA   (GEHO ) GEN HOSPITAL CORP.
XX
PI   Seed B,  Walz G;
XX
DR   WPI; 2003-895370/82.
DR   P-PSDB; ADH54473.
XX
PT   Inhibiting the binding of a cell bearing ELAM-1 protein to a cell bearing
PT   sialyl-Lex determinant, useful in treating inflammation, comprises
PT   contacting the ELAM-1 bearing cell with alpha 1-acid glycoprotein-
PT   antibody fusion protein.
XX
PS   Disclosure; SEQ ID NO 1; 40pp; English.
XX
CC   The invention relates to a method for inhibiting the binding of a cell
CC   bearing an ELAM-1 protein to a molecule or cell bearing a sialyl-Lex
CC   determinant. The method comprising contacting the ELAM-1 bearing cell
CC   with an alpha1 -acid glycoprotein (AGP)-antibody fusion protein bearing
CC   the sialyl-Lex determinant, where the inhibition of an ELAM-1-sialyl-Lex-
CC   based interaction treats an adverse immune reaction. The invention is
CC   useful in reducing inflammation in a human patient and protecting a
CC   mammal against any adverse immune reaction (including sepsis, organ
CC   damage attributable to inappropriate leukocyte extravasation, adult
CC   respiratory distress syndrome, glomerular nephritis or rheumatoid
CC   arthritis). The invention is useful in gene therapy. The method, as well
CC   as the AGP-antibody fusion protein, are useful in any antibody-based
CC   therapy, for e.g. to reduce inflammation or to treat heart attack, septic
CC   shock, septicaemia, rheumatoid arthritis or psoriasis. The present
CC   sequence is human immunoglobulin IgG1 gene.
XX
SQ   Sequence 2287 BP; 478 A; 739 C; 667 G; 403 T; 0 U; 0 Other;

  Query Match             5.3%;  Score 60;  DB 10;  Length 2287;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-06;
  Matches   60;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         74 AGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGCACC 133
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 AGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGCACC 1620


RESULT 7
AAL51057
ID   AAL51057 standard; DNA; 138 BP.
XX
AC   AAL51057;
XX
DT   20-FEB-2003  (first entry)
XX
DE   Cyclic single-strand anti-tumour antibody-related coding sequence #6.
XX
KW   Cyclic single-strand anti-tumour antibody; anti-tumour Fab; ds;
KW   anti-human Cd3 Fab; anti-human CD28 Fab; immunotherapy; tumour;
KW   ovarian cancer.
XX
OS   Unidentified.
XX
PN   WO200283738-A1.
XX
PD   24-OCT-2002.
XX
PF   10-APR-2002; 2002WO-CN000252.
XX
PR   11-APR-2001; 2001CN-00110554.
XX
PA   (GENE-) INST GENETICS CAS.
PA   (BEIJ-) BEIJING ABT GENETIC ENG TECHNOLOGY CO LT.
XX
PI   Huang H,  Cheng J,  Wang X,  Song L,  Zhang Z,  Lin Q,  Gu Y;
XX
DR   WPI; 2003-075525/07.
DR   P-PSDB; AAO16031.
XX
PT   Cyclic single-strand tri-specific antibody made from antitumor Fab,
PT   single-strand antibody and modified anti-human CD3 or CD28 Fab,
PT   applicable in early-stage diagnosis, and prevention or treatment of
PT   tumors e.g. ovarian cancer.
XX
PS   Disclosure; Fig 4A; 49pp; Chinese.
XX
CC   The invention comprises a cyclic single-strand anti-tumour antibody, the
CC   antibody of the invention is obtained by combining anti-tumour Fab and
CC   modified anti-human Cd3 or CD28 Fab. The antibody is useful in the
CC   immunotherapy of tumours - particularly ovarian cancer, including the
```

```
CC   sensitive early-stage diagnosis and post-operative eradication of
CC   disease. The present DNA sequence encodes a peptide which was used in the
CC   invention
XX
SQ   Sequence 138 BP; 35 A; 37 C; 39 G; 27 T; 0 U; 0 Other;

  Query Match             4.7%;  Score 53.6;  DB 8;  Length 138;
  Best Local Similarity   93.3%;  Pred. No. 5.8e-05;
  Matches   56;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        235 TTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCG 294
              ||||||||||||||| || || ||||||||||||||| |||||||||||||||||||||||
Db         61 TTGTCGTGCATGGCCCAACATTCGCAGGAGTGGCATGACGTGGTCCTGACCGACTTACCG 120


RESULT 8
ADA71938/c
ID   ADA71938 standard; DNA; 2000 BP.
XX
AC   ADA71938;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Rice gene, SEQ ID 5263.
XX
KW   Plant; bacterial infection; fungal infection; viral infection; rice;
KW   gene; ds.
XX
OS   Oryza sativa.
XX
PN   WO2003000898-A1.
XX
PD   03-JAN-2003.
XX
PF   22-JUN-2001; 2001WO-IB001105.
XX
PR   22-JUN-2001; 2001WO-IB001105.
XX
PA   (SYGN ) SYNGENTA PARTICIPATIONS AG.
XX
PI   Chang H,  Chen W,  Cooper B,  Glazebrook J,  Goff SA,  Hou Y;
PI   Katagiri F,  Quan S,  Tao Y,  Whitham S,  Xie Z,  Zhu T,  Zou G;
XX
DR   WPI; 2003-175290/17.
XX
PT   Identifying at least one gene involved in plant resistance or response to
PT   pathogenic infection for conferring resistance or tolerance to a plant to
PT   bacterial, fungal or viral infection by determining or detecting plant
PT   gene expression.
XX
PS   Claim 27; SEQ ID NO 5263; 899pp; English.
XX
CC   The present invention relates to a method (M1) for identifying genes
CC   involved in plant resistance or response to pathogenic infection. M1
CC   comprises identifying a gene whose expression is significantly altered in
CC   the incompatible interaction of plant gene expression relative to
CC   expression of the gene in an uninfected plant, in a mutant plant that
CC   does not express a gene associated with response to pathogenic infection,
CC   or in a corresponding incompatible or compatible interaction. (M1) is
CC   useful for conferring resistance to resistance or tolerance to a plant to
CC   bacterial, fungal or viral infection. The present sequence was used to
CC   illustrate the invention.
XX
SQ   Sequence 2000 BP; 336 A; 265 C; 284 G; 363 T; 0 U; 752 Other;

  Query Match             3.9%;  Score 43.8;  DB 8;  Length 2000;
  Best Local Similarity   9.0%;  Pred. No. 0.11;
  Matches   79;  Conservative  388;  Mismatches  400;  Indels    8;  Gaps    2;

Qy        178 ATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTG 237
              :|: |  :  | |:  :::| |:||::  ::|:: : :   |  | : : : :| :
Db        879 MTKWAWTWMTCMCMAKWYMATGWATWMWWRYTMYTYCYAMTCAKCKYKMAMTKWWTTWAC 820

Qy        238 TCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTT 297
              :  ::  : :  : :: ::: :   ::  :     |: :::  :   :: ::|   :::
Db        819 AWRATSWRWRAMAGMRWKRYKMKRAYWWRWWRCWKAGWARWMKSRYRWKWKKYATRYYWK 760

Qy        298 CGAATGCGTACGCGCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTT--TGGTAGA 355
              : |:|    : : :::: ::|  :  ::  :  ::    : ::|::  :|:  ::::: :
Db        759 MWAMTWWWSWRRWKSYRMWSGMGRMRWSAWRYCSRMKCAKTKYASSARWTKRAKRSYRYR 700

Qy        356 GGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTAC 415
              ::::: :: :|: ::: :: ::|    :::   | |  ::  :: :| : :  : ::
Db        699 RRWYWKRKGWTYRYRYWRSCRMTRARMSKRRKWAGASMKSCWMYWRGARSMWYSKYSCSA 640

Qy        416 TCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGT 475
              :|   |:  |: : :| : | :::    :: ::::::|: ||    ::: : : ::: ::
Db        639 KCCKKTRYMTSSYMSTGMYGMYSSYKSMSWTSKMSYMGKMTCTMYTSMKGSTRRSKMGRW 580

Qy        476 AGCGGC------ACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCG 529
              |::::       : :  :: ::: : |:  |  ::  :|::|   ::  :|   : ::
Db        579 SGMSRMYMRWWKKMRKRKYMRYMKWKCTWRRCMCYRWGYTMYTTSRSRMMYTGRYKARYT 520

Qy        530 GAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCT 589
              : :: ::::   : :  ::|::   : : : |  :| ::| : : ::   : ::  :: :
Db        519 SKRRYMWYKYRKYCWYYYYGMYMKCSYMMRYGYCKACKKCCYAMCWKAAYSGMMMYWYRK 460

Qy        590 CGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGG 649
              ::: :::: :: ::: :::          ||:  :| :   :  :|:: ::  :| ::::   :
Db        459 YSKWMRMSTKYMWSMWYKKCRSMKYGAKGCYGCKMWTYCSYGYMKWYTYMGSYKYSRCYK 400

Qy        650 TGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCATTTCATGGCTAGGTCTTTCAAGTCC 709
              : :      |::: :::: :    ::    ::   ::: :   :: |: ::::   :|:
Db        399 YMRMYMYKGWMYMMYYSAYSSMMTWYYYYAKYWKYWYKRRGTMSWYGKSYKKKYCTWWCY 340

Qy        710 TGCTGTGGTTTTGGAATTAATTTTGCTAGCAATGCGCATAGTTGCTGTAGTCAGTGTGGG 769
              :| :  :: :  :  |:  :  :          : | ::::|:::  : ::|  ::: ::
Db        339 MKCMRCYRWRKMMRKKTKYSKRCYCWRYATCYWCCCYRKRGWYSRRSMMRTAGKWKMRSW 280

Qy        770 TCAGCCACTCGAGATTTGTCTTTCAATGTCCGGACCTGAAGTAGGGCCCAGACGTGGGCT 829
              :  : :::::  : ::::::  :  :  ::| ::   | :| :| : :::|   :
Db        279 SRWCRSYSWYKMYKKMWKKSYYMSYGWARSSGTWSRSAAKRTYKGYSTSRRAKMMRACRM 220

Qy        830 AGGACTGGAACAGGTTTTACCTGGTCTGGGACCGACATATGGTCGTCTAGAATTGGAGGT 889
              :     :: :      :  : : :: ::: ::::    : : | ||: ||: ::   :
Db        219 YSACRRYSRTSYYCGCSYCGSSKWKYMSKSCSMRMTCSSWCSCCYTCYYGAMCWSCCMSM 160

Qy        890 ACGGCAGGGCATTGCAATAGGTCTAGAGATTGCTGGAGCTCTTGGAAGCGCTGGACGACG 949
              :: |: |   : :: : : :  |:   :  |:: :  |:: : :    : ::   |  :
Db        159 MYMGSCGCYTRGWKWRSKYSMCCKKYCSCCTKYCSYTGYYRYCKWYKYSYYKCYYCYCYW 100

Qy        950 TGCACGACCGTAAGAGGTTTAGGACGGTGGACGGTACCCGAAGTCCAGAACTCTGAGACC 1009
              : : :: ::: : :::   ::: |: :|:: ::   ::: |   :| :  ::  : :  :
Db         99 YMSYMRYMMKCMCSRSCSSWMSCAYCSTSSTSRWMSMYYAAKMGMCGSSGMYRMSKSCKM 40

Qy       1010 TGAGAGACCCGCCCCAGGACCTTCGTAGGCCAATG 1044
              ::   :  : |:  | :: ::: :   | ::: |:
Db         39 YSKYSSCKYTGSKKCTKRKYYYCYWSSGYSMWCTS 5


RESULT 9
ADJ65028
ID   ADJ65028 standard; DNA; 8874 BP.
XX
AC   ADJ65028;
XX
DT   06-MAY-2004  (first entry)
XX
DE   Plasmid pD16-H39E3.L1 complementary strand DNA sequence SEQ ID NO:7.
XX
KW   humanised antibody; human 4-1BB; human 4-1BB ligand; cancer; cytostatic;
KW   gene therapy; antibody; plasmid; pD16-H39E3.L1; gene; ds.
XX
OS   Synthetic.
XX
PN   WO2004010947-A2.
```

XX
PD 05-FEB-2004.
XX
PF 30-JUL-2003; 2003WO-US023735.
XX
PR 30-JUL-2002; 2002US-0399646P.
XX
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
XX
PI Jure-Kunkel M, Ganguly S, Abraham R, Hollenbaugh DL, Rillema J;
PI Thorne B, Shuford WW, Mittler RS;
XX
DR WPI; 2004-143726/14.
XX
PT New humanized antibody that binds to human 4-1BB and allows binding of
PT human 4-1BB to a human 4-1BB ligand, useful for preparing a composition
PT for treating cancer.
XX
PS Example; SEQ ID NO 7; 78pp; English.
XX
CC The present invention describes a humanised antibody (I) that binds to
CC human 4-1BB and allows binding of human 4-1BB to a human 4-1BB ligand.
CC Also described: (1) a pharmaceutical composition comprising the antibody
CC (I) and a carrier; (2) treating cancer in a subject; and (3) an isolated
CC polynucleotide comprising nucleotides 693-2072 of the 7033-base pairs
CC (bp) sequence (SEQ ID NO: 3, ADJ65024) or nucleotides 633-1034 or 1409-
CC 1726 of the 8874-bp sequence (SEQ ID NO: 6, ADJ65027). (I) has cytostatic
CC activity, and can be used in gene therapy. The humanised antibody (I) can
CC be used for preparing a composition for treating cancer. The present
CC sequence represents the complementary strand plasmid pD16-H39E3.L1
CC nucleotide sequence, which is used in an example from the present
CC invention.
XX
SQ Sequence 8874 BP; 2378 A; 1964 C; 2127 G; 2405 T; 0 U; 0 Other;

Query Match 3.8%; Score 43; DB 12; Length 8874;
Best Local Similarity 49.5%; Pred. No. 0.34;
Matches 143; Conservative 0; Mismatches 140; Indels 6; Gaps 1;

```
Qy        379 CTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTCTTGGTCCAGTCG 438
              | ||||   || | || | | | || |||||    ||  || |||           | |
Db       1418 CGTGGTAGACAGAAGTAGAAGGGCGGTAGACTACTCGTCAACTTTAGACCTTGACGGAGA 1477

Qy        439 GACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCAC------CCTC 492
              |    |||||| | ||   ||||||||||||| ||   |   ||  ||||      |||
Db       1478 CAACACACGGACGACTTATTGAAGATAGGGTCTCTCCGGTTTCATGTCACCTTCCACCTA 1537

Qy        493 TCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGGCTGCCG 552
              | |       ||  |||  |||  | |  |||       |       |      |  ||| ||
Db       1538 TTGCGGGAGGTTAGCCCATTGAGGGTCCTCTCACAGTGTCTCGTCCTGTCGTTCCTGTCG 1597

Qy        553 AGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCCTTGCAG 612
              |||  |  ||||  |||||  || ||  ||  |||       |   || |    || |||
Db       1598 TGGATGTCGGAGTCGTCGTGGGACTGCGACTCGTTTCGTCTGATGCTCTTTGTGTTTCAG 1657

Qy        613 AAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCT 661
              | | | |||   || |  ||| |||  |||  |  | |  |||  |||
Db       1658 ATGCGGACGCTTCAGTGGGTAGTCCCGGACTCGAGCGGGCAGTGTTTCT 1706
```

RESULT 10
ABD09099
ID ABD09099 standard; DNA; 1161 BP.
XX
AC ABD09099;
XX
DT 29-JUL-2004 (first entry)
XX
DE Pseudomonas aeruginosa polynucleotide #7703.
XX
KW Bacterial infection; gene; ds; Pseudomonas aeruginosa infection;
KW antibacterial.
XX
OS Pseudomonas aeruginosa.
XX
PN US6551795-B1.
XX
PD 22-APR-2003.
XX
PF 18-FEB-1999; 99US-00252991.
XX
PR 18-FEB-1998; 98US-0074788P.
PR 27-JUL-1998; 98US-0094190P.
XX
PA (GENO-) GENOME THERAPEUTICS CORP.
XX
PI Rubenfield MJ, Nolling J, Deloughery C, Bush D;
XX
DR WPI; 2003-615309/58.
DR P-PSDB; ABO75528.
XX
PT Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,
PT useful as molecular targets for diagnostics, prophylaxis and treatment of
PT pathological conditions resulting from bacterial infection.
XX
PS Disclosure; SEQ ID NO 7703; 455pp; English.
XX
CC The invention relates to Pseudomonas aeruginosa polypeptides and the
CC polynucleotides encoding them. The sequences are useful in diagnosis and
CC therapy of pathological conditions, as molecular targets for diagnostics,
CC prophylaxis and treatment of pathological conditions resulting from a
CC bacterial infection, for evaluating a compound, such as a polypeptide,
CC for the ability to bind a P. aeruginosa nucleic acid, as components of
CC effective antibacterial targets, as targets for antibacterial drugs,
CC including anti-P. aeruginosa drugs, as templates for recombinant
CC production of P. aeruginosa-derived peptides or polypeptides, as target
CC components for diagnosis and/or treatment of P. aeruginosa-caused
CC infection, and in detection of P. aeruginosa sequences or other sequences
CC of Pseudomonas species using biochip technology. Sequences ABD01397-
CC ABD17967 represent P. aeruginosa polynucleotides of the invention. Note:
CC The sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format from USPTO at
CC seqdata.uspto.gov/sequence.html
XX
SQ Sequence 1161 BP; 156 A; 367 C; 390 G; 248 T; 0 U; 0 Other;

Query Match 3.7%; Score 42; DB 11; Length 1161;
Best Local Similarity 47.1%; Pred. No. 0.28;
Matches 129; Conservative 0; Mismatches 145; Indels 0; Gaps 0;

```
Qy        119 TCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCA 178
              |||||  | || |  |  |  |  ||  ||| | |      |     | |  ||| |
Db        332 TCCAGCCTTCGGAGATCGCCAAGGTCTGCGTGGTGATCTTCATGGCCGGCTACCTGATCC 391

Qy        179 TGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGT 238
              | || || | |  ||| | |    || |  | |||  |  | | ||||  |||||
Db        392 GCCGCCAGCAGGAGGTCCGGGAAAGCTGGATGGGCTTCTTCAAGCCCTTCGTGGTGTTGC 451

Qy        239 CGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTTC 298
              |   |||||   || |  || |      || |||| | | |   ||||   ||  | |
Db        452 TGCCGATGGCCGGCCTGCTGCTGCGCGAGCCGGACTTCGGCGCCACCGTGGTAATGATGG 511

Qy        299 GAATGCGTACGCGCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGT 358
              |    ||  |  |||  |  | | ||   ||  ||  | |||  |   || |
Db        512 GCGCTGCCGCGGCCATGCTGTTCCTCGGCGGGGTGGGGCTGTTCCGCTTCGGCCTGATGG 571

Qy        359 TTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACAT 392
              | | | |  | ||||| ||  | |  | |  ||
Db        572 TGCTGCTGGCGGTCGGCGCGGTGGTCCTGCTGAT 605
```

RESULT 11
AAS51550
ID AAS51550 standard; DNA; 1200 BP.
XX
AC AAS51550;

XX
DT 13-FEB-2002 (first entry)
XX
DE Pseudomonas aeruginosa DNA for cellular proliferation protein #135.
XX
KW Antisense; ds; prokaryotic cellular proliferation gene; antibiotic;
KW antibacterial; drug design.
XX
OS Pseudomonas aeruginosa.
XX
PN WO200170955-A2.
XX
PD 27-SEP-2001.
XX
PF 21-MAR-2001; 2001WO-US009180.
XX
PR 21-MAR-2000; 2000US-0191078P.
PR 23-MAY-2000; 2000US-0206848P.
PR 26-MAY-2000; 2000US-0207727P.
PR 23-OCT-2000; 2000US-0242578P.
PR 27-NOV-2000; 2000US-0253625P.
PR 22-DEC-2000; 2000US-0257931P.
PR 16-FEB-2001; 2001US-0269308P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
PI Yamamoto RT, Xu HH;
XX
DR WPI; 2001-611495/70.
DR P-PSDB; AAU33691.
XX
PT New polynucleotides for the identification and development of
PT antibiotics, comprise sequences of antisense nucleic acids.
XX
PS Claim 27; SEQ ID NO 4132; 511pp; English.
XX
CC The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the genes,
CC their use in the discovery of novel antibiotics, the essential genes
CC themselves and the encoded proteins. The prokaryotes used are Escherichia
CC coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,
CC Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also
CC useful for the identification of potential new targets for antibiotic
CC development. The antisense nucleic acids can also be used to identify
CC proteins used in proliferation, to express these proteins, and to obtain
CC antibodies capable of binding to the expressed proteins. The proteins can
CC be used to screen compounds in rational drug discovery programmes. The
CC antisense nucleic acid sequence is also useful to screen for homologous
CC nucleic acids which are required for cell proliferation in a wide variety
CC of organisms. The present sequence encodes an essential prokaryotic
CC cellular proliferation protein. Note: The sequence data for this patent
CC did not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1200 BP; 157 A; 384 C; 402 G; 257 T; 0 U; 0 Other;

Query Match 3.7%; Score 42; DB 4; Length 1200;
Best Local Similarity 47.1%; Pred. No. 0.29;
Matches 129; Conservative 0; Mismatches 145; Indels 0; Gaps 0;

```
Qy        119 TCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCA 178
              ||||| | || |   |  |  |  ||  ||| |  |      |  | ||| |
Db        371 TCCAGCCTTCGGAGATCGCCAAGGTCTGCGTGGTGATCTTCATGGCCGGCTACCTGATCC 430

Qy        179 TGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGT 238
                | || || | |  |||  | |    || |  | |||  |   | | ||||  |||||
Db        431 GCCGCCAGCAGGAGGTCCGGGAAAGCTGGATGGGCTTCTTCAAGCCCTTCGTGGTGTTGC 490

Qy        239 CGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTTC 298
                |  |||||   || |  || |      || |||| | | |   ||||   ||  | |
Db        491 TGCCGATGGCCGGCCTGCTGCTGCGCGAGCCGGACTTCGGCGCCACCGTGGTAATGATGG 550

Qy        299 GAATGCGTACGCGCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGT 358
              |          || |  | ||| |  | | | ||   ||  ||  | |||  |   || |
Db        551 GCGCTGCCGCGGCCATGCTGTTCCTCGGCGGGGTGGGGCTGTTCCGCTTCGGCCTGATGG 610

Qy        359 TTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACAT 392
              | | | |  | |||||  ||  | |   | |  ||
Db        611 TGCTGCTGGCGGTCGGCGCGGTGGTCCTGCTGAT 644
```

RESULT 12
ACA19541
ID ACA19541 standard; DNA; 1200 BP.
XX
AC ACA19541;
XX
DT 19-JUN-2003 (first entry)
XX
DE Prokaryotic essential gene #1198.
XX
KW Antisense; ds; prokaryotic essential gene; cell proliferation;
KW drug design; gene.
XX
OS Pseudomonas aeruginosa.
XX
PN WO200277183-A2.
XX
PD 03-OCT-2002.
XX
PF 21-MAR-2002; 2002WO-US009107.
XX
PR 21-MAR-2001; 2001US-00815242.
PR 06-SEP-2001; 2001US-00948993.
PR 25-OCT-2001; 2001US-0342923P.
PR 08-FEB-2002; 2002US-00072851.
PR 06-MAR-2002; 2002US-0362699P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX
DR WPI; 2003-029926/02.
DR P-PSDB; ABU15671.
XX
PT New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX
PS Claim 14; SEQ ID NO 7411; 1766pp; English.
XX
CC The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide;(5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for

CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than S. aureus, S. typhimurium,
CC K. pneumoniae or P. aeruginosa. The present sequence is one of the target
CC prokaryotic essential genes. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1200 BP; 157 A; 384 C; 402 G; 257 T; 0 U; 0 Other;

Query Match 3.7%; Score 42; DB 8; Length 1200;
Best Local Similarity 47.1%; Pred. No. 0.29;
Matches 129; Conservative 0; Mismatches 145; Indels 0; Gaps 0;

Qy 119 TCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCA 178
Db 371 TCCAGCCTTCGGAGATCGCCAAGGTCTGCGTGGTGATCTTCATGGCCGGCTACCTGATCC 430

Qy 179 TGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGT 238
Db 431 GCCGCCAGCAGGAGGTCCGGGAAAGCTGGATGGGCTTCTTCAAGCCCTTCGTGGTGTTGC 490

Qy 239 CGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTTC 298
Db 491 TGCCGATGGCCGGCCTGCTGCTGCGCGAGCCGGACTTCGGCGCCACCGTGGTAATGATGG 550

Qy 299 GAATGCGTACGCGCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGT 358
Db 551 GCGCTGCCGCGGCCATGCTGTTCCTCGGCGGGGTGGGGCTGTTCCGCTTCGGCCTGATGG 610

Qy 359 TTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACAT 392
Db 611 TGCTGCTGGCGGTCGGCGCGGTGGTCCTGCTGAT 644

RESULT 13
ABD09256/c
ID ABD09256 standard; DNA; 1287 BP.
XX
AC ABD09256;
XX
DT 29-JUL-2004 (first entry)
XX
DE Pseudomonas aeruginosa polynucleotide #7860.
XX
KW Bacterial infection; gene; ds; Pseudomonas aeruginosa infection;
KW antibacterial.
XX
OS Pseudomonas aeruginosa.
XX
PN US6551795-B1.
XX
PD 22-APR-2003.
XX
PF 18-FEB-1999; 99US-00252991.
XX
PR 18-FEB-1998; 98US-0074788P.
PR 27-JUL-1998; 98US-0094190P.
XX
PA (GENO-) GENOME THERAPEUTICS CORP.
XX
PI Rubenfield MJ, Nolling J, Deloughery C, Bush D;
XX
DR WPI; 2003-615309/58.
DR P-PSDB; ABO75685.
XX
PT Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,
PT useful as molecular targets for diagnostics, prophylaxis and treatment of
PT pathological conditions resulting from bacterial infection.
XX
PS Disclosure; SEQ ID NO 7860; 455pp; English.
XX
CC The invention relates to Pseudomonas aeruginosa polypeptides and the
CC polynucleotides encoding them. The sequences are useful in diagnosis and
CC therapy of pathological conditions, as molecular targets for diagnostics,
CC prophylaxis and treatment of pathological conditions resulting from a
CC bacterial infection, for evaluating a compound, such as a polypeptide,
CC for the ability to bind a P. aeruginosa nucleic acid, as components of
CC effective antibacterial targets, as targets for antibacterial drugs,
CC including anti-P. aeruginosa drugs, as templates for recombinant
CC production of P. aeruginosa-derived peptides or polypeptides, as target
CC components for diagnosis and/or treatment of P. aeruginosa-caused
CC infection, and in detection of P. aeruginosa sequences or other sequences
CC of Pseudomonas species using biochip technology. Sequences ABD01397-
CC ABD17967 represent P. aeruginosa polynucleotides of the invention. Note:
CC The sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format from USPTO at
CC seqdata.uspto.gov/sequence.html
XX
SQ Sequence 1287 BP; 276 A; 437 C; 408 G; 166 T; 0 U; 0 Other;

Query Match 3.7%; Score 42; DB 11; Length 1287;
Best Local Similarity 47.1%; Pred. No. 0.29;
Matches 129; Conservative 0; Mismatches 145; Indels 0; Gaps 0;

Qy 119 TCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCA 178
Db 908 TCCAGCCTTCGGAGATCGCCAAGGTCTGCGTGGTGATCTTCATGGCCGGCTACCTGATCC 849

Qy 179 TGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGT 238
Db 848 GCCGCCAGCAGGAGGTCCGGGAAAGCTGGATGGGCTTCTTCAAGCCCTTCGTGGTGTTGC 789

Qy 239 CGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTTC 298
Db 788 TGCCGATGGCCGGCCTGCTGCTGCGCGAGCCGGACTTCGGCGCCACCGTGGTAATGATGG 729

Qy 299 GAATGCGTACGCGCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGT 358
Db 728 GCGCTGCCGCGGCCATGCTGTTCCTCGGCGGGGTGGGGCTGTTCCGCTTCGGCCTGATGG 669

Qy 359 TTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACAT 392
Db 668 TGCTGCTGGCGGTCGGCGCGGTGGTCCTGCTGAT 635

RESULT 14
ABD09020
ID ABD09020 standard; DNA; 1359 BP.
XX
AC ABD09020;
XX
DT 29-JUL-2004 (first entry)
XX
DE Pseudomonas aeruginosa polynucleotide #7624.
XX
KW Bacterial infection; gene; ds; Pseudomonas aeruginosa infection;
KW antibacterial.
XX
OS Pseudomonas aeruginosa.
XX
PN US6551795-B1.
XX
PD 22-APR-2003.
XX
PF 18-FEB-1999; 99US-00252991.
XX
PR 18-FEB-1998; 98US-0074788P.
PR 27-JUL-1998; 98US-0094190P.
XX
PA (GENO-) GENOME THERAPEUTICS CORP.
XX
PI Rubenfield MJ, Nolling J, Deloughery C, Bush D;
XX

DR WPI; 2003-615309/58.
DR P-PSDB; ABO75449.
XX
PT Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,
PT useful as molecular targets for diagnostics, prophylaxis and treatment of
PT pathological conditions resulting from bacterial infection.
XX
PS Disclosure; SEQ ID NO 7624; 455pp; English.
XX
CC The invention relates to Pseudomonas aeruginosa polypeptides and the
CC polynucleotides encoding them. The sequences are useful in diagnosis and
CC therapy of pathological conditions, as molecular targets for diagnostics,
CC prophylaxis and treatment of pathological conditions resulting from a
CC bacterial infection, for evaluating a compound, such as a polypeptide,
CC for the ability to bind a P. aeruginosa nucleic acid, as components of
CC effective antibacterial targets, as targets for antibacterial drugs,
CC including anti-P. aeruginosa drugs, as templates for recombinant
CC production of P. aeruginosa-derived peptides or polypeptides, as target
CC components for diagnosis and/or treatment of P. aeruginosa-caused
CC infection, and in detection of P. aeruginosa sequences or other sequences
CC of Pseudomonas species using biochip technology. Sequences ABD01397-
CC ABD17967 represent P. aeruginosa polynucleotides of the invention. Note:
CC The sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format from USPTO at
CC seqdata.uspto.gov/sequence.html
XX
SQ Sequence 1359 BP; 177 A; 438 C; 463 G; 281 T; 0 U; 0 Other;

Query Match 3.7%; Score 42; DB 11; Length 1359;
Best Local Similarity 47.1%; Pred. No. 0.3;
Matches 129; Conservative 0; Mismatches 145; Indels 0; Gaps 0;

Qy 119 TCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCA 178
Db 576 TCCAGCCTTCGGAGATCGCCAAGGTCTGCGTGGTGATCTTCATGGCCGGCTACCTGATCC 635

Qy 179 TGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGT 238
Db 636 GCCGCCAGCAGGAGGTCCGGGAAAGCTGGATGGGCTTCTTCAAGCCCTTCGTGGTGTTGC 695

Qy 239 CGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTTC 298
Db 696 TGCCGATGGCCGGCCTGCTGCTGCGCGAGCCGGACTTCGGCGCCACCGTGGTAATGATGG 755

Qy 299 GAATGCGTACGCGCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGT 358
Db 756 GCGCTGCCGCGGCCATGCTGTTCCTCGGCGGGGTGGGGCTGTTCCGCTTCGGCCTGATGG 815

Qy 359 TTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACAT 392
Db 816 TGCTGCTGGCGGTCGGCGCGGTGGTCCTGCTGAT 849

RESULT 15
ADC16621/c
ID ADC16621 standard; DNA; 1182 BP.
XX
AC ADC16621;
XX
DT 18-DEC-2003 (first entry)
XX
DE Secondary amylase partial DNA SeqID15 related to Cephalosporin C.
XX
KW amidase; secondary amylase; peptidase; protease; hydantoinase;
KW food flavour; bacterial killing; fungal killing;
KW fine chemical intermediate; peptide bond synthesis; chiral resolution;
KW Cephalosporin C hydrolysis; cephalosporin biosynthesis pathway;
KW cephalosporin-like antibiotic; bacteriocide; fungicide;
KW enzymatic decontamination; microbiological contamination; gene; ds.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT CDS 1. .1182
FT /*tag= a
FT /product= "Secondary amylase"
FT /partial
FT /note= "No start codon"
XX
PN WO2003064613-A2.
XX
PD 07-AUG-2003.
XX
PF 28-JAN-2003; 2003WO-US002694.
XX
PR 28-JAN-2002; 2002US-0352895P.
XX
PA (DIVE-) DIVERSA CORP.
XX
PI Barton NR, Weiner DP, Greenberg W, Luu S, Chang K, Waters E;
XX
DR WPI; 2003-636801/60.
DR P-PSDB; ADC16622.
XX
PT Novel isolated or recombinant nucleic acid encoding an amidase
PT polypeptide useful for hydrolysis of a penicillin or cephalosporin,
PT synthesis of a 7-aminocephalosporanic acid, cell wall hydrolysis.
XX
PS Claim 1; SEQ ID NO 15; 204pp; English.
XX
CC This invention relates to novel amidase proteins and the nucleic acid
CC sequences which encode them. In particular the invention relates to
CC secondary amylases which include a variety of useful enzymes such as
CC peptidases, proteases and hydantoinases. This class of enzymes can be
CC used in a range of commercial applications such as increasing flavour in
CC food, promoting bacterial and fungal killing, modifying and deprotecting
CC fine chemical intermediates, synthesising peptide bonds and carrying out
CC chiral resolutions. In particular, the specification identifies a need
CC for an enzyme capable of hydrolysing Cephalosporin C. Cephalosporin C is
CC the fermentation product of the cephalosporin biosynthesis pathway and
CC its major use is as a building block for cephalosporin-like antibiotics.
CC The present invention provides secondary amidase enzymes, capable of
CC hydrolysing cephalosporin C. The amidases may be useful as a
CC bacteriocide, a fungicide, on any surface or sample, solid or liquid, and
CC thus can be used in enzymatic decontamination of specimens as a means to
CC control and prevent microbiological contamination. The present sequence
CC is a DNA sequence encoding a secondary amylase enzyme of the invention.
XX
SQ Sequence 1182 BP; 188 A; 432 C; 391 G; 170 T; 0 U; 1 Other;

Query Match 3.7%; Score 41.8; DB 10; Length 1182;
Best Local Similarity 46.0%; Pred. No. 0.32;
Matches 142; Conservative 0; Mismatches 167; Indels 0; Gaps 0;

Qy 476 AGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGC 535
Db 422 AGCGACGCGGGATCGCCCGGCAAGCCGGCGAACGCCCGGTCCACGGCCTGGCCGGGGGTC 363

Qy 536 ACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCA 595
Db 362 ATGTGAGGAAGCTCTCCAGGCGGTCGAGGGCGACGTTCCAGCCGCGGCCGTGGTCGTCGC 303

Qy 596 CCGTCGTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGT 655
Db 302 GCGCCTTCTCGTCGAAGAACTGCTCGTGGGTCAGCGTCAGCATGGTGCCCTCGGTGACCG 243

Qy 656 GCGTCTTCTCGGAGAGGGACAGAGGCCCATTTCATGGCTAGGTCTTTCAAGTCCTGCTGT 715
Db 242 GGTTGAGCTCGATCGTCACCAGCGATTCGCGCTCGGGCGTGCTCTGCCAGGCCCACGAGA 183

Qy 716 GGTTTTGGAATTAATTTTGCTAGCAATGCGCATAGTTGCTGTAGTCAGTGTGGGTCAGCC 775
Db 182 AGGCGAGCTTCCGGTTGGGCACGACCTCCTTGTAGATGCCGCTGACGCTGTGATGCTCGT 123

Qy 776 ACTCGAGAT 784

Db 122 TCTTGGGAT 114

Search completed: October 17, 2004, 16:46:47
Job time : 590.736 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 17, 2004, 15:27:13 ; Search time 578.552 Seconds
(without alignments)
10035.691 Million cell updates/sec

Title: US-10-679-999-17
Perfect score: 1135
Sequence: 1 GTATACCTGTTTTGAGTGTG.....AGGCCCAACAATTACCTAGG 1135

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3403857 seqs, 2557783690 residues

Total number of hits satisfying chosen parameters: 6807714

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
18: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
19: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
20: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1135	100.0	1135	16	US-10-679-999-17	Sequence 17, Appl
2	1109.4	97.7	1135	16	US-10-679-999-14	Sequence 14, Appl
3	1105	97.4	1150	16	US-10-679-999-8	Sequence 8, Appli
4	1103.4	97.2	1150	16	US-10-679-999-11	Sequence 11, Appl
5	662.4	58.4	777	17	US-10-666-480-122	Sequence 122, App
6	656.8	57.9	780	17	US-10-666-480-62	Sequence 62, Appl
7	638.4	56.2	1142	15	US-10-157-408-9	Sequence 9, Appli
8	638.4	56.2	1142	15	US-10-097-044A-9	Sequence 9, Appli
9	638.4	56.2	1142	18	US-10-769-247-9	Sequence 9, Appli
10	598.4	52.7	7033	17	US-10-630-406-4	Sequence 4, Appli
11	476.6	42.0	2366	9	US-09-229-200A-12	Sequence 12, Appl
12	440.8	38.8	454	9	US-09-366-133-5	Sequence 5, Appli
13	440.8	38.8	454	14	US-10-214-037-5	Sequence 5, Appli
14	440.8	38.8	454	16	US-10-679-999-5	Sequence 5, Appli
15	378.4	33.3	491	9	US-09-366-133-2	Sequence 2, Appli
16	378.4	33.3	491	14	US-10-214-037-2	Sequence 2, Appli
17	378.4	33.3	491	16	US-10-679-999-2	Sequence 2, Appli
c 18	71	6.3	23770	14	US-10-035-637-8	Sequence 8, Appli
c 19	44.6	3.9	1188	17	US-10-437-963-65538	Sequence 65538, A
20	43	3.8	468	15	US-10-157-408-12	Sequence 12, Appl
21	43	3.8	468	15	US-10-097-044A-12	Sequence 12, Appl
22	43	3.8	468	18	US-10-769-247-12	Sequence 12, Appl
23	43	3.8	8874	17	US-10-630-406-7	Sequence 7, Appli
c 24	42.4	3.7	1116	15	US-10-156-761-6640	Sequence 6640, Ap
c 25	42.4	3.7	9025608	15	US-10-156-761-1	Sequence 1, Appli
26	42	3.7	1200	9	US-09-815-242-4132	Sequence 4132, Ap
27	42	3.7	1200	16	US-10-282-122A-7411	Sequence 7411, Ap
c 28	41.8	3.7	1182	16	US-10-354-437-15	Sequence 15, Appl
29	41.8	3.7	34460	13	US-10-087-192-115	Sequence 115, App
c 30	41.8	3.7	135638	15	US-10-314-657-1	Sequence 1, Appli
c 31	41.6	3.7	1986	17	US-10-441-949-47	Sequence 47, Appl
c 32	41.6	3.7	1986	17	US-10-441-949-51	Sequence 51, Appl
c 33	41.6	3.7	2034	17	US-10-441-949-49	Sequence 49, Appl
c 34	41.6	3.7	2034	17	US-10-441-949-50	Sequence 50, Appl
35	41.6	3.7	2171	9	US-09-925-300-721	Sequence 721, App
36	41.6	3.7	2172	16	US-10-264-049-843	Sequence 843, App
37	41.6	3.7	2300	9	US-09-823-245A-506	Sequence 506, App
38	41.6	3.7	2300	9	US-09-822-830A-33	Sequence 33, Appl
39	41.2	3.6	1049	14	US-10-123-155-358	Sequence 358, App
40	41.2	3.6	1049	15	US-10-146-731-358	Sequence 358, App
41	41.2	3.6	1049	15	US-10-140-472-358	Sequence 358, App
42	41.2	3.6	1049	15	US-10-141-761-358	Sequence 358, App
43	41.2	3.6	1049	15	US-10-142-885-358	Sequence 358, App
44	41.2	3.6	1049	15	US-10-158-790-358	Sequence 358, App
45	41.2	3.6	1049	15	US-10-137-871-358	Sequence 358, App

ALIGNMENTS

```
RESULT 1
US-10-679-999-17
; Sequence 17, Application US/10679999
; Publication No. US20040067520A1
;  GENERAL INFORMATION:
;       APPLICANT: Mann, Michael B.
;                  Hecht, Randy I.
;       TITLE OF INVENTION: OB FUSION PROTEIN COMPOSITIONS AND
;                           METHODS
;       NUMBER OF SEQUENCES: 18
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Amgen Inc.
;            STREET: 1840 DeHavilland Drive
;            CITY: Thousand Oaks
;            STATE: CA
;            COUNTRY: USA
;            ZIP: 91320-1789
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/679,999
;            FILING DATE: 06-Oct-2003
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/09/568,528
;            FILING DATE: 09-May-2000
;            APPLICATION NUMBER: 09/267,517
;            FILING DATE: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Knight, Matthew W.
;            REGISTRATION NUMBER: 36,846
;            REFERENCE/DOCKET NUMBER: A-416
;  INFORMATION FOR SEQ ID NO: 17:
```

```
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 1135 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: double
;            TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-10-679-999-17

  Query Match            100.0%;  Score 1135;  DB 16;  Length 1135;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1135;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTATACCTGTTTTGAGTGTGTACGGGTGGCACGGGTCGAGGCCTTGAGCTTCCACCAGGC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GTATACCTGTTTTGAGTGTGTACGGGTGGCACGGGTCGAGGCCTTGAGCTTCCACCAGGC 60

Qy         61 AGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTC 120

Qy        121 CAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATG 180

Qy        181 CACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCG 240

Qy        241 TGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTTCGA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTTCGA 300

Qy        301 ATGCGTACGCGCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATGCGTACGCGCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTT 360

Qy        361 CGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGAC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGAC 420

Qy        421 TGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGG 480

Qy        481 CACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGAC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGAC 540

Qy        541 CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTC 600

Qy        601 GTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTC 660

Qy        661 TTCTCGGAGAGGGACAGAGGCCCATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TTCTCGGAGAGGGACAGAGGCCCATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTT 720

Qy        721 TGGAATTAATTTTGCTAGCAATGCGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAATTAATTTTGCTAGCAATGCGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCG 780

Qy        781 AGATTTGTCTTTCAATGTCCGGACCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AGATTTGTCTTTCAATGTCCGGACCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAAC 840

Qy        841 AGGTTTTACCTGGTCTGGGACCGACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AGGTTTTACCTGGTCTGGGACCGACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCA 900

Qy        901 TTGCAATAGGTCTAGAGATTGCTGGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TTGCAATAGGTCTAGAGATTGCTGGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGT 960

Qy        961 AAGAGGTTTAGGACGGTGGACGGTACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AAGAGGTTTAGGACGGTGGACGGTACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCG 1020

Qy       1021 CCCCAGGACCTTCGTAGGCCAATGTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 CCCCAGGACCTTCGTAGGCCAATGTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCA 1080

Qy       1081 AGGGAAGTCCTGTACGAAACCGTCGACCTGGACAGAGGCCCAACAATTACCTAGG 1135
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 AGGGAAGTCCTGTACGAAACCGTCGACCTGGACAGAGGCCCAACAATTACCTAGG 1135


RESULT 2
US-10-679-999-14
; Sequence 14, Application US/10679999
; Publication No. US20040067520A1
;   GENERAL INFORMATION:
;        APPLICANT: Mann, Michael B.
;                   Hecht, Randy I.
;        TITLE OF INVENTION: OB FUSION PROTEIN COMPOSITIONS AND
;                            METHODS
;        NUMBER OF SEQUENCES: 18
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Amgen Inc.
;             STREET: 1840 DeHavilland Drive
;             CITY: Thousand Oaks
;             STATE: CA
;             COUNTRY: USA
;             ZIP: 91320-1789
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/679,999
;             FILING DATE: 06-Oct-2003
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/568,528
;             FILING DATE: 09-May-2000
;             APPLICATION NUMBER: 09/267,517
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Knight, Matthew W.
;             REGISTRATION NUMBER: 36,846
;             REFERENCE/DOCKET NUMBER: A-416
;   INFORMATION FOR SEQ ID NO: 14:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1135 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-10-679-999-14

  Query Match            97.7%;  Score 1109.4;  DB 16;  Length 1135;
  Best Local Similarity  98.6%;  Pred. No. 0;
  Matches 1119;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          1 GTATACCTGTTTTGAGTGTGTACGGGTGGCACGGGTCGAGGCCTTGAGCTTCCACCAGGC 60
              |||||||||||||||||||| ||||| || ||||||||||||||    || ||||||
Db          1 GTATACCTGTTTTGAGTGTGTACAGGTGGAACAGGTCGAGGCCTTGAGGACCCCCCAGGA 60

Qy         61 AGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTC 120
```

```
Qy       121 CAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATG 180
Db       121 CAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATG 180

Qy       181 CACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCG 240
Db       181 CACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCG 240

Qy       241 TGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTTCGA 300
Db       241 TGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTC 300

Qy       301 ATGCGTACGCGCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTT 360
Db       301 ATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTT 360

Qy       361 CGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGAC 420
Db       361 CGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGAC 420

Qy       421 TGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGG 480
Db       421 TGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGG 480

Qy       481 CACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGAC 540
Db       481 CACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGAC 540

Qy       541 CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTC 600
Db       541 CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTC 600

Qy       601 GTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTC 660
Db       601 GTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTC 660

Qy       661 TTCTCGGAGAGGGACAGAGGCCCATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTT 720
Db       661 TTCTCGGAGAGGGACAGAGGCCCATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTT 720

Qy       721 TGGAATTAATTTTGCTAGCAATGCGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCG 780
Db       721 TGGAATTAATTTTGCTAGCAATGCGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCG 780

Qy       781 AGATTTGTCTTTCAATGTCCGGACCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAAC 840
Db       781 AGATTTGTCTTTCAATGTCCGGACCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAAC 840

Qy       841 AGGTTTTACCTGGTCTGGGACCGACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCA 900
Db       841 AGGTTTTACCTGGTCTGGGACCGACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCA 900

Qy       901 TTGCAATAGGTCTAGAGATTGCTGGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGT 960
Db       901 TTGCAATAGGTCTAGAGATTGCTGGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGT 960

Qy       961 AAGAGGTTTAGGACGGTGGACGGTACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCG 1020
Db       961 AAGAGGTTTAGGACGGTGGACGGTACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCG 1020

Qy      1021 CCCCAGGACCTTCGTAGGCCAATGTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCA 1080
Db      1021 CCCCAGGACCTTCGTAGGCCAATGTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCA 1080

Qy      1081 AGGGAAGTCCTGTACGAAACCGTCGACCTGGACAGAGGCCCAACAATTACCTAGG 1135
Db      1081 AGGGAAGTCCTGTACGAAACCGTCGACCTGGACAGAGGCCCAACAATTACCTAGG 1135

RESULT 3
US-10-679-999-8
; Sequence 8, Application US/10679999
; Publication No. US20040067520A1
;  GENERAL INFORMATION:
;       APPLICANT: Mann, Michael B.
;                  Hecht, Randy I.
;       TITLE OF INVENTION: OB FUSION PROTEIN COMPOSITIONS AND
;                           METHODS
;       NUMBER OF SEQUENCES: 18
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Amgen Inc.
;            STREET: 1840 DeHavilland Drive
;            CITY: Thousand Oaks
;            STATE: CA
;            COUNTRY: USA
;            ZIP: 91320-1789
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/679,999
;            FILING DATE: 06-Oct-2003
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/09/568,528
;            FILING DATE: 09-May-2000
;            APPLICATION NUMBER: 09/267,517
;            FILING DATE: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Knight, Matthew W.
;            REGISTRATION NUMBER: 36,846
;            REFERENCE/DOCKET NUMBER: A-416
;  INFORMATION FOR SEQ ID NO: 8:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 1150 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: double
;            TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-679-999-8

  Query Match           97.4%;  Score 1105;  DB 16;  Length 1150;
  Best Local Similarity  98.7%;  Pred. No. 0;
  Matches 1114;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy         7 CTGTTTTGAGTGTGTACGGGTGGCACGGGTCGAGGCCTTGAGCTTCCACCAGGCAGTCAG 66
Db        22 CTGTTTTGAGTGTGTACGGGTGGCACGGGTCGTGGACTTGAGGACCCCCCTGGCAGTCAG 81

Qy        67 AAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGT 126
Db        82 AAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGT 141

Qy       127 ACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTG 186
Db       142 ACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTG 201

Qy       187 CCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATG 246
Db       202 CCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATG 261

Qy       247 GCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTTCGAATGCGT 306
Db       262 GCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATGTTC 321

Qy       307 ACGCGCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTT 366
Db       322 ACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTT 381

Qy       367 CCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTC 426
Db       382 CCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTC 441
```

```
Qy        427 TTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTC 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        442 TTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTC 501

Qy        487 ACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGG 546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        502 ACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGG 561

Qy        547 CTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCC 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        562 CTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCC 621

Qy        607 TTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCG 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        622 TTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCG 681

Qy        667 GAGAGGGACAGAGGCCCATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAAT 726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        682 GAGAGGGACAGAGGCCCATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAAT 741

Qy        727 TAATTTTGCTAGCAATGCGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTT 786
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        742 TAATTTTGCTAGCAATGCGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTT 801

Qy        787 GTCTTTCAATGTCCGGACCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTT 846
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        802 GTCTTTCAATGTCCGGACCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTT 861

Qy        847 TACCTGGTCTGGGACCGACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAA 906
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        862 TACCTGGTCTGGGACCGACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAA 921

Qy        907 TAGGTCTAGAGATTGCTGGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGG 966
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        922 TAGGTCTAGAGATTGCTGGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGG 981

Qy        967 TTTAGGACGGTGGACGGTACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAG 1026
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        982 TTTAGGACGGTGGACGGTACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAG 1041

Qy       1027 GACCTTCGTAGGCCAATGTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAA 1086
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1042 GACCTTCGTAGGCCAATGTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAA 1101

Qy       1087 GTCCTGTACGAAACCGTCGACCTGGACAGAGGCCCAACAATTACCTAGG 1135
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db       1102 GTCCTGTACGAAACCGTCGACCTGGACAGAGGCCCAACAATTACCTAGG 1150
```

```
RESULT 4
US-10-679-999-11
; Sequence 11, Application US/10679999
; Publication No. US20040067520A1
;   GENERAL INFORMATION:
;        APPLICANT: Mann, Michael B.
;                   Hecht, Randy I.
;        TITLE OF INVENTION: OB FUSION PROTEIN COMPOSITIONS AND
;                            METHODS
;        NUMBER OF SEQUENCES: 18
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Amgen Inc.
;             STREET: 1840 DeHavilland Drive
;             CITY: Thousand Oaks
;             STATE: CA
;             COUNTRY: USA
;             ZIP: 91320-1789
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/679,999
;             FILING DATE: 06-Oct-2003
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/568,528
;             FILING DATE: 09-May-2000
;             APPLICATION NUMBER: 09/267,517
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Knight, Matthew W.
;             REGISTRATION NUMBER: 36,846
;             REFERENCE/DOCKET NUMBER: A-416
;   INFORMATION FOR SEQ ID NO: 11:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1150 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-679-999-11

  Query Match             97.2%;  Score 1103.4;  DB 16;  Length 1150;
  Best Local Similarity   98.6%;  Pred. No. 0;
  Matches 1113;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;
```

```
Qy          7 CTGTTTTGAGTGTGTACGGGTGGCACGGGTCGAGGCCTTGAGCTTCCACCAGGCAGTCAG 66
              |||||||||||||||| ||||| || ||||||||||||||   || ||||| |||||||
Db         22 CTGTTTTGAGTGTGTACAGGTGGAACAGGTCGAGGCCTTGAGGACCCCCCAGGAAGTCAG 81

Qy         67 AAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGT 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         82 AAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGT 141

Qy        127 ACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTG 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        142 ACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTG 201

Qy        187 CCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATG 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        202 CCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATG 261

Qy        247 GCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTTCGAATGCGT 306
              |||||||||||||||||||||||||||||||||||||||||||||||| |  |||
Db        262 GCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATGTTC 321

Qy        307 ACGCGCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTT 366
              |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        322 ACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTT 381

Qy        367 CCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTC 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        382 CCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTC 441

Qy        427 TTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTC 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        442 TTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTC 501

Qy        487 ACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGG 546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        502 ACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGG 561

Qy        547 CTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCC 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        562 CTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCC 621

Qy        607 TTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCG 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        622 TTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCG 681

Qy        667 GAGAGGGACAGAGGCCCATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAAT 726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        682 GAGAGGGACAGAGGCCCATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAAT 741
```

```
Qy        727 TAATTTTGCTAGCAATGCGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTT 786
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        742 TAATTTTGCTAGCAATGCGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTT 801

Qy        787 GTCTTTCAATGTCCGGACCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTT 846
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        802 GTCTTTCAATGTCCGGACCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTT 861

Qy        847 TACCTGGTCTGGGACCGACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAA 906
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        862 TACCTGGTCTGGGACCGACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAA 921

Qy        907 TAGGTCTAGAGATTGCTGGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGG 966
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        922 TAGGTCTAGAGATTGCTGGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGG 981

Qy        967 TTTAGGACGGTGGACGGTACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAG 1026
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        982 TTTAGGACGGTGGACGGTACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAG 1041

Qy       1027 GACCTTCGTAGGCCAATGTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAA 1086
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1042 GACCTTCGTAGGCCAATGTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAA 1101

Qy       1087 GTCCTGTACGAAACCGTCGACCTGGACAGAGGCCCAACAATTACCTAGG 1135
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db       1102 GTCCTGTACGAAACCGTCGACCTGGACAGAGGCCCAACAATTACCTAGG 1150
```

RESULT 5
US-10-666-480-122
; Sequence 122, Application US/10666480
; Publication No. US20040121959A1
; GENERAL INFORMATION:
; APPLICANT: Boone, Thomas C
; APPLICANT: Wild, Kenneth D
; APPLICANT: Sitney, Karen C
; APPLICANT: Min, Hosung
; APPLICANT: Kimmel, Bruce
; TITLE OF INVENTION: Peptides and Related Molecules That Modulate Nerve Growth Factor
; FILE REFERENCE: A-827US
; CURRENT APPLICATION NUMBER: US/10/666,480
; CURRENT FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: 60/412,524
; PRIOR FILING DATE: 2002-09-19
; NUMBER OF SEQ ID NOS: 286
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 122
; LENGTH: 777
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Expression vector
US-10-666-480-122

Query Match 58.4%; Score 662.4; DB 17; Length 777;
Best Local Similarity 97.7%; Pred. No. 8.4e-200;
Matches 672; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

```
Qy          1 GTATACCTGTTTTGAGTGTGTACGGGTGGCACGGGTCGAGGCCTTGAGCTTCCACCAGGC 60
              |||||||||||||||||||||| ||||| || ||||||||||||||   || || |||
Db         36 GTATACCTGTTTTGAGTGTGTACAGGTGGAACAGGTCGAGGCCTTGAGGACCCCCCTGGC 95

Qy         61 AGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         96 AGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTC 155

Qy        121 CAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        156 CAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATG 215

Qy        181 CACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        216 CACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCG 275

Qy        241 TGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTTCGA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        276 TGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTC 335

Qy        301 ATGCGTACGCGCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTT 360
              ||| ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        336 ATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTT 395

Qy        361 CGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGAC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        396 CGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGAC 455

Qy        421 TGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        456 TGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGG 515

Qy        481 CACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGAC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        516 CACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGAC 575

Qy        541 CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        576 CTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTC 635

Qy        601 GTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        636 GTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTC 695

Qy        661 TTCTCGGAGAGGGACAGAGGCCCATTTC 688
              ||||||||||||||||||||||||||||
Db        696 TTCTCGGAGAGGGACAGAGGCCCATTTC 723
```

RESULT 6
US-10-666-480-62
; Sequence 62, Application US/10666480
; Publication No. US20040121959A1
; GENERAL INFORMATION:
; APPLICANT: Boone, Thomas C
; APPLICANT: Wild, Kenneth D
; APPLICANT: Sitney, Karen C
; APPLICANT: Min, Hosung
; APPLICANT: Kimmel, Bruce
; TITLE OF INVENTION: Peptides and Related Molecules That Modulate Nerve Growth Factor
; FILE REFERENCE: A-827US
; CURRENT APPLICATION NUMBER: US/10/666,480
; CURRENT FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: 60/412,524
; PRIOR FILING DATE: 2002-09-19
; NUMBER OF SEQ ID NOS: 286
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 62
; LENGTH: 780
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Expression vector component
US-10-666-480-62

Query Match 57.9%; Score 656.8; DB 17; Length 780;
Best Local Similarity 96.8%; Pred. No. 5.1e-198;
Matches 670; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

```
Qy          6 CCTGTTTTGAGTGTGTACGGGTGGCACGGGTCGAGGCCTTGAGCTTCCACCAGGCAGTCA 65
              |||||||||||||||| ||||| |||||||| || ||||||   || || ||||||||
Db         89 CCTGTTTTGAGTGTGTACAGGTGGAACGGGTCGTGGACTTGAGGACCCCCCTGGCAGTCA 148

Qy         66 GAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTG 125
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        149 AAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTG 208
```

```
Qy        126 TACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCT 185
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        209 TACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCT 268

Qy        186 GCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCAT 245
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        269 GCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCAT 328

Qy        246 GGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTTCGAATGCG 305
              ||||||||||||||||||||||||||||||||||||||||||||||||||||  |  |||
Db        329 GGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATGTT 388

Qy        306 TACGCGCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTT 365
              |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        389 CACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTT 448

Qy        366 TCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTT 425
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        449 TCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTT 508

Qy        426 CTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCT 485
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        509 CTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCT 568

Qy        486 CACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAG 545
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        569 CACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAG 628

Qy        546 GCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCC 605
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        629 GCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCC 688

Qy        606 CTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTCTC 665
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        689 CTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTCTC 748

Qy        666 GGAGAGGGACAGAGGCCCATTTCATGGCTAGG 697
              |||||||||||||||||||||||  |  |||||
Db        749 GGAGAGGGACAGAGGCCCATTTATTACCTAGG 780
```

```
RESULT 7
US-10-157-408-9
; Sequence 9, Application US/10157408
; Publication No. US20030104535A1
;   GENERAL INFORMATION:
;        APPLICANT: Capon, Daniel J.
;                   Gregory, Timothy J.
;        TITLE OF INVENTION: Adheson Variants
;        NUMBER OF SEQUENCES: 25
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Genentech, Inc.
;             STREET: 460 Point San Bruno Blvd
;             CITY: South San Francisco
;             STATE: California
;             COUNTRY: USA
;             ZIP: 94080
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: patin (Genentech)
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/157,408
;             FILING DATE: 28-May-2002
;             CLASSIFICATION: 435
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/457,918
;             FILING DATE: 1-JUN-1995
;             APPLICATION NUMBER: 08/236311
;             FILING DATE: 02-MAY-1994
;             APPLICATION NUMBER: 07/936190
;             FILING DATE: 26-AUG-1992
;             APPLICATION NUMBER: 07/842777
;             FILING DATE: 18-FEB-1992
;             APPLICATION NUMBER: 07/250785
;             FILING DATE: 28-SEP-1988
;             APPLICATION NUMBER: 07/104329
;             FILING DATE: 02-OCT-1987
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Kubinec, Jeffrey S.
;             REGISTRATION NUMBER: 36,575
;             REFERENCE/DOCKET NUMBER: P0444P1C3
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 415/225-8228
;             TELEFAX: 415/952-9881
;             TELEX: 910/371-7168
;   INFORMATION FOR SEQ ID NO: 9:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1142 bases
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-157-408-9

  Query Match           56.2%;  Score 638.4;  DB 15;  Length 1142;
  Best Local Similarity  96.7%;  Pred. No. 4.1e-192;
  Matches  665;  Conservative    0;  Mismatches   16;  Indels    7;  Gaps    1;

Qy          7 CTGTTTTGAGTGTGTACGGGTGGCACGGGTCGAGGCCTTGAGCTTCCACCAGGCAGTCAG 66
              |||||||||||||||||||||||||||||||||| || ||||||   || || |||||||||
Db        440 CTGTTTTGAGTGTGTACGGGTGGCACGGGTCGTGGACTTGAGGACCCCCCTGGCAGTCAG 499

Qy         67 AAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGT 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        500 AAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGT 559

Qy        127 ACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTG 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        560 ACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTG 619

Qy        187 CCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATG 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        620 CCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATG 679

Qy        247 GCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTTCGAATGCGT 306
              || |||||||||||||||||||||||||||||||||||||||||||||  |  |||||||
Db        680 GCCCACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATGTTC 739

Qy        307 ACGCGCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTT 366
              |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        740 ACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTT 799

Qy        367 CCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTC 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        800 CCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTC 859

Qy        427 TTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTC 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        860 TTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTC 919

Qy        487 ACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGG 546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        920 ACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGG 979

Qy        547 CTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCC 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        980 CTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCC 1039

Qy        607 TTGCAGAAGAGTACGAGGC--------ACTACGTACTCCGAGACGTGTTGGTGATGTGCGT 659
              |||||||||||||||||||        ||||||||||||||||||||||||||||||||||
Db       1040 TTGCAGAAGAGTACGAGGCACTACGTACTACGTACTCCGAGACGTGTTGGTGATGTGCGT 1099

Qy        660 CTTCTCGGAGAGGGACAGAGGCCCATTT 687
```

```
                    ||||||||||||||||||||||||||||
Db       1100 CTTCTCGGAGAGGGACAGAGGCCCATTT 1127


RESULT 8
US-10-097-044A-9
; Sequence 9, Application US/10097044A
; Publication No. US20030143220A1
;   GENERAL INFORMATION:
;        APPLICANT: Capon, Daniel J.
;                   Gregory, Timothy J.
;        TITLE OF INVENTION: Adheson Variants
;        NUMBER OF SEQUENCES: 25
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Genentech, Inc.
;             STREET: 460 Point San Bruno Blvd
;             CITY: South San Francisco
;             STATE: California
;             COUNTRY: USA
;             ZIP: 94080
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: patin (Genentech)
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/097,044A
;             FILING DATE: 28-May-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/457,918
;             FILING DATE: 1-JUN-1995
;             APPLICATION NUMBER: 08/236311
;             FILING DATE: 02-MAY-1994
;             APPLICATION NUMBER: 07/936190
;             FILING DATE: 26-AUG-1992
;             APPLICATION NUMBER: 07/842777
;             FILING DATE: 18-FEB-1992
;             APPLICATION NUMBER: 07/250785
;             FILING DATE: 28-SEP-1988
;             APPLICATION NUMBER: 07/104329
;             FILING DATE: 02-OCT-1987
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Kubinec, Jeffrey S.
;             REGISTRATION NUMBER: 36,575
;             REFERENCE/DOCKET NUMBER: P0444P1C3
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 415/225-8228
;             TELEFAX: 415/952-9881
;             TELEX: 910/371-7168
;   INFORMATION FOR SEQ ID NO: 9:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1142 bases
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-097-044A-9

  Query Match           56.2%;  Score 638.4;  DB 15;  Length 1142;
  Best Local Similarity  96.7%;  Pred. No. 4.1e-192;
  Matches  665;  Conservative    0;  Mismatches   16;  Indels    7;  Gaps    1;

Qy          7 CTGTTTTGAGTGTGTACGGGTGGCACGGGTCGAGGCCTTGAGCTTCCACCAGGCAGTCAG 66
              |||||||||||||||||||||||||||||| || ||||||   || || |||||||||
Db        440 CTGTTTTGAGTGTGTACGGGTGGCACGGGTCGTGGACTTGAGGACCCCCCTGGCAGTCAG 499

Qy         67 AAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGT 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        500 AAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGT 559

Qy        127 ACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTG 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        560 ACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTG 619

Qy        187 CCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATG 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        620 CCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATG 679

Qy        247 GCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTTCGAATGCGT 306
              || |||||||||||||||||||||||||||||||||||||||||||||||| |  |||
Db        680 GCCCACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATGTTC 739

Qy        307 ACGCGCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTT 366
              |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        740 ACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTT 799

Qy        367 CCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTC 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        800 CCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTC 859

Qy        427 TTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTC 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        860 TTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTC 919

Qy        487 ACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGG 546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        920 ACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGG 979

Qy        547 CTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCC 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        980 CTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCC 1039

Qy        607 TTGCAGAAGAGTACGAGGC-------ACTACGTACTCCGAGACGTGTTGGTGATGTGCGT 659
              ||||||||||||||||||       ||||||||||||||||||||||||||||||||
Db       1040 TTGCAGAAGAGTACGAGGCACTACGTACTACGTACTCCGAGACGTGTTGGTGATGTGCGT 1099

Qy        660 CTTCTCGGAGAGGGACAGAGGCCCATTT 687
              ||||||||||||||||||||||||||||
Db       1100 CTTCTCGGAGAGGGACAGAGGCCCATTT 1127


RESULT 9
US-10-769-247-9
; Sequence 9, Application US/10769247
; Publication No. US20040197809A1
;   GENERAL INFORMATION:
;        APPLICANT: Capon, Daniel J.
;                   Gregory, Timothy J.
;        TITLE OF INVENTION: Adheson Variants
;        NUMBER OF SEQUENCES: 25
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Genentech, Inc.
;             STREET: 460 Point San Bruno Blvd
;             CITY: South San Francisco
;             STATE: California
;             COUNTRY: USA
;             ZIP: 94080
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: patin (Genentech)
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/769,247
;             FILING DATE: 30-Jan-2004
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/457,918
;             FILING DATE: 1-JUN-1995
;             APPLICATION NUMBER: 08/236311
;             FILING DATE: 02-MAY-1994
;             APPLICATION NUMBER: 07/936190
;             FILING DATE: 26-AUG-1992
;             APPLICATION NUMBER: 07/842777
;             FILING DATE: 18-FEB-1992
```

```
;             APPLICATION NUMBER: 07/250785
;             FILING DATE: 28-SEP-1988
;             APPLICATION NUMBER: 07/104329
;             FILING DATE: 02-OCT-1987
;       ATTORNEY/AGENT INFORMATION:
;             NAME: Kubinec, Jeffrey S.
;             REGISTRATION NUMBER: 36,575
;             REFERENCE/DOCKET NUMBER: P0444P1C3
;       TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 415/225-8228
;             TELEFAX: 415/952-9881
;             TELEX: 910/371-7168
;   INFORMATION FOR SEQ ID NO: 9:
;       SEQUENCE CHARACTERISTICS:
;             LENGTH: 1142 bases
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-769-247-9

  Query Match           56.2%;  Score 638.4;  DB 18;  Length 1142;
  Best Local Similarity  96.7%;  Pred. No. 4.1e-192;
  Matches  665;  Conservative    0;  Mismatches   16;  Indels    7;  Gaps    1;

Qy          7 CTGTTTTGAGTGTGTACGGGTGGCACGGGTCGAGGCCTTGAGCTTCCACCAGGCAGTCAG 66
              ||||||||||||||||||||||||||||||||| || ||||||   || || |||||||||
Db        440 CTGTTTTGAGTGTGTACGGGTGGCACGGGTCGTGGACTTGAGGACCCCCCTGGCAGTCAG 499

Qy         67 AAGGAGAAGGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGT 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        500 AAGGAGAAGGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGT 559

Qy        127 ACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTG 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        560 ACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTG 619

Qy        187 CCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATG 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        620 CCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATG 679

Qy        247 GCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTTCGAATGCGT 306
              || |||||||||||||||||||||||||||||||||||||||||||||||| | |||
Db        680 GCCCACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATGTTC 739

Qy        307 ACGCGCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTT 366
              ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        740 ACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTT 799

Qy        367 CCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTC 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        800 CCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTC 859

Qy        427 TTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTC 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        860 TTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTC 919

Qy        487 ACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGG 546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        920 ACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGG 979

Qy        547 CTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCC 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        980 CTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCC 1039

Qy        607 TTGCAGAAGAGTACGAGGC-------ACTACGTACTCCGAGACGTGTTGGTGATGTGCGT 659
              ||||||||||||||||||       ||||||||||||||||||||||||||||||||||
Db       1040 TTGCAGAAGAGTACGAGGCACTACGTACTACGTACTCCGAGACGTGTTGGTGATGTGCGT 1099

Qy        660 CTTCTCGGAGAGGGACAGAGGCCCATTT 687
              ||||||||||||||||||||||||||||
Db       1100 CTTCTCGGAGAGGGACAGAGGCCCATTT 1127
```

```
RESULT 10
US-10-630-406-4
; Sequence 4, Application US/10630406
; Publication No. US20040105855A1
; GENERAL INFORMATION:
;  APPLICANT: Jure-Kunkel, Maria
;  APPLICANT:  Ganguly, Subinay
;  APPLICANT:  Abraham, Ralph
;  APPLICANT:  Hollenbaugh, Diane L.
;  APPLICANT:  Rillema, Jill
;  APPLICANT:  Thorne, Barbara
;  APPLICANT:  Shuford, Walter W.
;  APPLICANT:  Mittler, Robert S.
;  TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST HUMAN 4-1BB
;  FILE REFERENCE: D0288 NP
;  CURRENT APPLICATION NUMBER: US/10/630,406
;  CURRENT FILING DATE:  2003-07-30
;  PRIOR APPLICATION NUMBER: US 60/399,646
;  PRIOR FILING DATE: 2002-07-30
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
;   LENGTH: 7033
;   TYPE: DNA
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Synthetic
US-10-630-406-4

  Query Match           52.7%;  Score 598.4;  DB 17;  Length 7033;
  Best Local Similarity  92.5%;  Pred. No. 4.2e-179;
  Matches  629;  Conservative    0;  Mismatches   51;  Indels    0;  Gaps    0;

Qy         15 AGTGTGTACGGGTGGCACGGGTCGAGGCCTTGAGCTTCCACCAGGCAGTCAGAAGGAGAA 74
              ||    | |||||||| |||||||| || ||   ||   || || || |||||||||| ||
Db       1400 AGGTGGAACGGGTGGAACGGGTCGTGGACTCAAGGACCCCCCTGGTAGTCAGAAGGACAA 1459

Qy         75 GGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGCACCA 134
              |||||||||||||||||||| ||||||||||||||||||||||||||||| |||||||||
Db       1460 GGGGGGTTTTGGGTTCCTGTGAGAGTACTAGAGGGCCTGGGGACTCCAGTGCACGCACCA 1519

Qy        135 CCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGCACCT 194
              |||||||||||||| |||||||| |||||| |||||||||||||||||| |||||||||
Db       1520 CCACCTGCACTCGGTCCTTCTGGGGCTCCAGGTCAAGTTGACCATGCACCTACCGCACCT 1579

Qy        195 CCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATGGCACACCA 254
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db       1580 CCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCAAGTTGTCGTGCATGGCACACCA 1639

Qy        255 GTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTTCGAATGCGTACGCGCCA 314
              |||||||||||||||||||||||||||||||||||| | ||| ||| |||||||||||||
Db       1640 GTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTGCCGTTCCTCATGTTCACGTTCCA 1699

Qy        315 GAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTTCCCGTCGG 374
              |||||||||| |||||| || ||||||||||||||||||||||||||||||||||||||
Db       1700 GAGGTTGTTTCCGGAGGGCAGGAGGTAGCTCTTTTGGTAGAGGTTTCGGTTTCCCGTCGG 1759

Qy        375 GGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTCTTGGTCCA 434
              |||||| |||||||||||||||||||||||||| ||| ||| ||||||||||||||||||
Db       1760 GGCTCTCGGTGTCCACATGTGGGACGGGGGTAGGGTCCTCCTCTACTGGTTCTTGGTCCA 1819

Qy        435 GTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCACCCTCTC 494
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1820 GTCGGACTGGACGGACCAGTTTCCGAAGATGGGGTCGCTGTAGCGGCACCTCACCCTCTC 1879

Qy        495 GTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGGCTGCCGAG 554
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1880 GTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGGCTGCCGAG 1939

Qy        555 GAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCCTTGCAGAA 614
              |||||||||||||||| ||| |||||||||||||||||||||||| ||||||| |||||
Db       1940 GAAGAAGGAGATGTCGTCCGATTGGCACCTGTTCTCGTCCACCGTCCTCCCCTTACAGAA 1999
```

```
Qy        615 GAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCGGAGAGGGA 674
              ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db       2000 GAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGTGTCTTCTCGGAGAGGGA 2059

Qy        675 CAGAGGCCCATTTCATGGCT 694
              ||||| |||||||  | | |
Db       2060 CAGAGACCCATTTACTAGAT 2079


RESULT 11
US-09-229-200A-12
; Sequence 12, Application US/09229200A
; Patent No. US20020099179A1
;   GENERAL INFORMATION:
;        APPLICANT: Jolliffe et al.
;        TITLE OF INVENTION: CD4 Specific Recombinant Antibody
;        NUMBER OF SEQUENCES: 28
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Johnson & Johnson
;             STREET: One Johnson & Johnson Plaza
;             CITY: New Brunswick
;             STATE: NJ
;             COUNTRY: USA
;             ZIP: 08933-7003
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
;             COMPUTER: IBM
;             OPERATING SYSTEM: PC-DOS
;             SOFTWARE: <Unknown>
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/229,200A
;             FILING DATE: 13-Jan-1999
;             CLASSIFICATION: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: John W. Wallen, III
;             REGISTRATION NUMBER: 35,403
;             REFERENCE/DOCKET NUMBER: ORT-948
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (858) 784-3239
;             TELEFAX: (908) 524-2808
;   INFORMATION FOR SEQ ID NO: 12:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 2366
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: linear
;        ANTI-SENSE: no
;        SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-229-200A-12

  Query Match             42.0%;  Score 476.6;  DB 9;  Length 2366;
  Best Local Similarity   80.3%;  Pred. No. 1.5e-140;
  Matches  616;  Conservative    0;  Mismatches   54;  Indels   97;  Gaps    1;

Qy         18 GTGTACGGGTGGCACGGGTCGAGGCCTTGAGCTTCCACCAGGCAGTCAGAAGGAGAAGGG 77
              ||| | |    | | | |||| || ||  ||    || || || ||||||||||| |||||
Db       1253 GTGGAGGTAGAGAAGGAGTCGTGGACTCAAGGACCCCCCTGGTAGTCAGAAGGACAAGGG 1312

Qy         78 GGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGCACCACCA 137
              |||||||||||||||||| |||||||||||||||||||||||||||| ||||||||||
Db       1313 GGGTTTTGGGTTCCTGTGAGAGTACTAGAGGGCCTGGGGACTCCAGTGCACGCACCACCA 1372

Qy        138 CCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGCACCTCCA 197
              |||||||||||| |||||||| |||||| |||||||||||||||||| ||||||||||
Db       1373 CCTGCACTCGGTCCTTCTGGGGCTCCAGGTCAAGTTGACCATGCACCTACCGCACCTCCA 1432

Qy        198 CGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATGGCACACCAGTC 257
              |||||||||||||||||||||||||  ||||||| |||||||||||||||||||||||||
Db       1433 CGTATTACGGTTCTGTTTCGGCGCCCGTCTCGTCAAGTTGTCGTGCATGGCACACCAGTC 1492

Qy        258 GCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTTCGAATGCGTACGCGCCAGAG 317
              |||||||||||||||||||||||||||||||||| ||||| |  |||   |||  ||||||
```

```
Db       1493 GCAGGAGTGGCAGGACGTGGTCCTGACCGACTTGCCGTTCCTCATGTTCACGTTCCAGAG 1552

Qy        318 GTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTT---------- 365
              |||||||| ||||||  || |||||||||||||||||||||||||||||
Db       1553 GTTGTTTCCGGAGGGCAGGAGGTAGCTCTTTTGGTAGAGGTTTCGGTTTCCACCCTGGGT 1612

Qy        366 ---------------------------------------------------------- 365

Db       1613 GCCCCACGCTCCCGGTGTGCCTGTCTCCGGTCGAGCCGGGTGGGAGACGGGACCCTCACT 1672

Qy        366 -------------------------TCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACG 400
                                        |||||||||||||||| ||||||||||||||||||
Db       1673 GGCGACACGGTTGGAGACAGGGATGTCCCGTCGGGGCTCTCGGTGTCCACATGTGGGACG 1732

Qy        401 GGGGTAGGGCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGA 460
              ||||||||| ||| ||| ||||||||||||||||||||||||||||||||||||||||||
Db       1733 GGGGTAGGGTCCTCCTCTACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGA 1792

Qy        461 AGATAGGGTCGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGT 520
              |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1793 AGATGGGGTCGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGT 1852

Qy        521 TCTGGTGCGGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGC 580
              |||||||||||||||||||||||||||||||||||||||||||||||||| ||| ||||
Db       1853 TCTGGTGCGGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTCCGATTGGC 1912

Qy        581 ACCTGTTCTCGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAG 640
              |||||||||||||||||| ||||| | ||||||||||||||||||||||||||||||||
Db       1913 ACCTGTTCTCGTCCACCGTCCTCCCCCTACAGAAGAGTACGAGGCACTACGTACTCCGAG 1972

Qy        641 ACGTGTTGGTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCATTT 687
              |||||||||||||||| ||||||||||||||||||||| |||||||
Db       1973 ACGTGTTGGTGATGTGTGTCTTCTCGGAGAGGGACAGAGACCCATTT 2019


RESULT 12
US-09-366-133-5
; Sequence 5, Application US/09366133
; Patent No. US20020009798A1
;  GENERAL INFORMATION:
;    APPLICANT:  Pelleymounter, Mary Ann
;    APPLICANT:  Hecht, Randy I
;    APPLICANT:  Mann, Michael B
;    TITLE OF INVENTION:  OB PROTEIN COMPOSITIONS AND METHODS
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Amgen Inc.
;      STREET:  1840 Dehavilland Drive
;      CITY:  Thousand Oaks
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  91230-1789
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/366,133
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/920,608
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Pessin, Karol M.
;      REFERENCE/DOCKET NUMBER:  A-345
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  454 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
```

```
;    MOLECULE TYPE:  cDNA
US-09-366-133-5

  Query Match             38.8%;  Score 440.8;  DB 9;  Length 454;
  Best Local Similarity   98.5%;  Pred. No. 2e-129;
  Matches  445;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy        684 ATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATG 743
              ||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 ATACCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATG 62

Qy        744 CGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTTGTCTTTCAATGTCCGGA 803
              ||||||||||||||||||||||||||||||||||||||||||||||    ||||||||||
Db         63 CGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTTGTCGCACAATGTCCGGA 122

Qy        804 CCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCG 863
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 CCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCG 182

Qy        864 ACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAATAGGTCTAGAGATTGCT 923
              |||||||||||||||||||||||||||||||||||||||| | ||||||||||||||
Db        183 ACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAAGAAGTCTAGAGATTGCT 242

Qy        924 GGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGG 983
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        243 GGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGG 302

Qy        984 TACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCAAT 1043
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        303 TACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCAAT 362

Qy       1044 GTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAAGTCCTGTACGAAACCGT 1103
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        363 GTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAAGTCCTGTACGAAACCGT 422

Qy       1104 CGACCTGGACAGAGGCCCAACAATTACCTAGG 1135
              |||||||||||||||||||||||||||||||
Db        423 CGACCTGGACAGAGGCCCAACAATTACCTAGG 454


RESULT 13
US-10-214-037-5
; Sequence 5, Application US/10214037
; Publication No. US20030054997A1
;   GENERAL INFORMATION:
;        APPLICANT: Pelleymounter, Mary Ann
;                   Hecht, Randy I
;                   Mann, Michael B
;        TITLE OF INVENTION: OB PROTEIN COMPOSITIONS AND METHODS
;        NUMBER OF SEQUENCES: 6
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Amgen Inc.
;             STREET: 1840 Dehavilland Drive
;             CITY: Thousand Oaks
;             STATE: California
;             COUNTRY: U.S.A.
;             ZIP: 91230-1789
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/214,037
;             FILING DATE: 05-Aug-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/920,608
;             FILING DATE: 07-JUN-1995
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Pessin, Karol M.
;             REFERENCE/DOCKET NUMBER: A-345
;    INFORMATION FOR SEQ ID NO: 5:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 454 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-214-037-5

  Query Match             38.8%;  Score 440.8;  DB 14;  Length 454;
  Best Local Similarity   98.5%;  Pred. No. 2e-129;
  Matches  445;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy        684 ATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATG 743
              ||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 ATACCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATG 62

Qy        744 CGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTTGTCTTTCAATGTCCGGA 803
              ||||||||||||||||||||||||||||||||||||||||||||||    ||||||||||
Db         63 CGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTTGTCGCACAATGTCCGGA 122

Qy        804 CCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCG 863
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 CCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCG 182

Qy        864 ACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAATAGGTCTAGAGATTGCT 923
              |||||||||||||||||||||||||||||||||||||||| | ||||||||||||||
Db        183 ACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAAGAAGTCTAGAGATTGCT 242

Qy        924 GGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGG 983
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        243 GGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGG 302

Qy        984 TACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCAAT 1043
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        303 TACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCAAT 362

Qy       1044 GTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAAGTCCTGTACGAAACCGT 1103
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        363 GTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAAGTCCTGTACGAAACCGT 422

Qy       1104 CGACCTGGACAGAGGCCCAACAATTACCTAGG 1135
              |||||||||||||||||||||||||||||||
Db        423 CGACCTGGACAGAGGCCCAACAATTACCTAGG 454


RESULT 14
US-10-679-999-5
; Sequence 5, Application US/10679999
; Publication No. US20040067520A1
;   GENERAL INFORMATION:
;        APPLICANT: Mann, Michael B.
;                   Hecht, Randy I.
;        TITLE OF INVENTION: OB FUSION PROTEIN COMPOSITIONS AND
;                            METHODS
;        NUMBER OF SEQUENCES: 18
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Amgen Inc.
;             STREET: 1840 DeHavilland Drive
;             CITY: Thousand Oaks
;             STATE: CA
;             COUNTRY: USA
;             ZIP: 91320-1789
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/679,999
;             FILING DATE: 06-Oct-2003
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
```

```
;            APPLICATION NUMBER: US/09/568,528
;            FILING DATE: 09-May-2000
;            APPLICATION NUMBER: 09/267,517
;            FILING DATE: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Knight, Matthew W.
;            REGISTRATION NUMBER: 36,846
;            REFERENCE/DOCKET NUMBER: A-416
;   INFORMATION FOR SEQ ID NO: 5:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 454 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: double
;            TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-679-999-5

  Query Match             38.8%;  Score 440.8;  DB 16;  Length 454;
  Best Local Similarity   98.5%;  Pred. No. 2e-129;
  Matches  445;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy        684 ATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATG 743
              ||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 ATACCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATG 62

Qy        744 CGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTTGTCTTTCAATGTCCGGA 803
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         63 CGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTTGTCGCACAATGTCCGGA 122

Qy        804 CCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCG 863
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 CCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCG 182

Qy        864 ACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAATAGGTCTAGAGATTGCT 923
              |||||||||||||||||||||||||||||||||||||||||||| | ||||||||||||||
Db        183 ACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAAGAAGTCTAGAGATTGCT 242

Qy        924 GGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGG 983
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        243 GGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGG 302

Qy        984 TACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCAAT 1043
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        303 TACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCAAT 362

Qy       1044 GTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAAGTCCTGTACGAAACCGT 1103
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        363 GTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAAGTCCTGTACGAAACCGT 422

Qy       1104 CGACCTGGACAGAGGCCCAACAATTACCTAGG 1135
              |||||||||||||||||||||||||||||||
Db        423 CGACCTGGACAGAGGCCCAACAATTACCTAGG 454


RESULT 15
US-09-366-133-2
; Sequence 2, Application US/09366133
; Patent No. US20020009798A1
;  GENERAL INFORMATION:
;    APPLICANT:  Pelleymounter, Mary Ann
;    APPLICANT:  Hecht, Randy I
;    APPLICANT:  Mann, Michael B
;    TITLE OF INVENTION:  OB PROTEIN COMPOSITIONS AND METHODS
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Amgen Inc.
;      STREET:  1840 Dehavilland Drive
;      CITY:  Thousand Oaks
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  91230-1789
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/366,133
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/920,608
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Pessin, Karol M.
;      REFERENCE/DOCKET NUMBER:  A-345
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  491 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-366-133-2

  Query Match             33.3%;  Score 378.4;  DB 9;  Length 491;
  Best Local Similarity   89.8%;  Pred. No. 1.4e-109;
  Matches  406;  Conservative    0;  Mismatches   46;  Indels    0;  Gaps    0;

Qy        684 ATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATG 743
              ||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         40 ATACCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATG 99

Qy        744 CGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTTGTCTTTCAATGTCCGGA 803
              ||||||||||||||||||||||||||||||||||||  | ||||||||  ||||| || ||
Db        100 CGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCAGAGGCGATTTGTCGCACAATGGCCAGA 159

Qy        804 CCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCG 863
              |||||||||||||||||||||||||||||| | ||||||||||||||||||||||||||
Db        160 CCTGAAGTAGGGCCCAGACGTGGGCTAGGATTCGAACAGGTTTTACCTGGTCTGGGACCG 219

Qy        864 ACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAATAGGTCTAGAGATTGCT 923
              |||||||||||||| | |||||||| |||||||  |||||| | |||||| |||||||
Db        220 ACATATGGTCGTCCACAATTGGAGGGACGGCAGGGTCTTGCAAGAAGTCTAGCGATTGCT 279

Qy        924 GGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGG 983
              |||||||||||||||||||||||||||||| |||||||||||||||||||  ||||||
Db        280 GGAGCTCTTGGAAGCGCTGGACGACGTGGACGACCGTAAGAGGTTTAGGACGAGGGACGG 339

Qy        984 TACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCAAT 1043
              | | |||||||||  |||  | |||  || |||| ||||||||||||||||||    ||
Db        340 CGTCTGGAGTCCAGAAGTCTTTGGCCTTAGGGACCTGCCCCAGGACCTTCGTAGGGACAT 399

Qy       1044 GTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAAGTCCTGTACGAAACCGT 1103
              |||||||||||||||||||||||||||||||||||||||||||||||||||  |||  |||
Db        400 GTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAAGTCCTGTAGGAAGTCGT 459

Qy       1104 CGACCTGGACAGAGGCCCAACAATTACCTAGG 1135
              |||||||  | |||||||  ||||||||||||
Db        460 CGACCTGCAAAGAGGCCTTACAATTACCTAGG 491


Search completed: October 17, 2004, 18:19:01
Job time : 585.552 secs
```

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 17, 2004, 15:27:13 ; Search time 102.696 Seconds
(without alignments)
7855.635 Million cell updates/sec

Title: US-10-679-999-17
Perfect score: 1135
Sequence: 1 GTATACCTGTTTTGAGTGTG.....AGGCCCAACAATTACCTAGG 1135

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	638.4	56.2	1142	1	US-08-236-311-9	Sequence 9, Appli
	2	638.4	56.2	1142	3	US-08-457-918-9	Sequence 9, Appli
	3	638.4	56.2	1142	4	US-10-157-408-9	Sequence 9, Appli
	4	60	5.3	2287	1	US-08-480-036-1	Sequence 1, Appli
	5	60	5.3	2287	1	US-08-461-968A-1	Sequence 1, Appli
	6	60	5.3	2287	2	US-08-462-571-1	Sequence 1, Appli
	7	60	5.3	2287	4	US-08-472-888A-1	Sequence 1, Appli
	8	43	3.8	468	1	US-08-236-311-12	Sequence 12, Appl
	9	43	3.8	468	3	US-08-457-918-12	Sequence 12, Appl
	10	43	3.8	468	4	US-10-157-408-12	Sequence 12, Appl
	11	42	3.7	1161	4	US-09-252-991A-7703	Sequence 7703, Ap
c	12	42	3.7	1287	4	US-09-252-991A-7860	Sequence 7860, Ap
	13	42	3.7	1359	4	US-09-252-991A-7624	Sequence 7624, Ap
c	14	39.6	3.5	1425	4	US-09-489-039A-1509	Sequence 1509, Ap
	15	39.6	3.5	2016	4	US-09-489-039A-1492	Sequence 1492, Ap
c	16	39.4	3.5	5331	4	US-09-453-956-1	Sequence 1, Appli
c	17	39.2	3.5	1482	4	US-09-977-897-1	Sequence 1, Appli
c	18	39	3.4	688	3	US-08-998-416-915	Sequence 915, App
c	19	38.6	3.4	1440	4	US-09-672-749-13	Sequence 13, Appl
c	20	38.6	3.4	3489	2	US-08-728-323A-1	Sequence 1, Appli
c	21	38.6	3.4	3489	3	US-09-298-568-1	Sequence 1, Appli
c	22	38.6	3.4	3489	4	US-09-410-399-1	Sequence 1, Appli
c	23	38.6	3.4	3489	4	US-09-894-273-1	Sequence 1, Appli
	24	38.6	3.4	32207	2	US-08-770-379-20	Sequence 20, Appl
	25	38.6	3.4	32207	3	US-08-757-669A-20	Sequence 20, Appl
	26	38.6	3.4	32207	3	US-09-230-371A-20	Sequence 20, Appl
c	27	38.4	3.4	533	6	5482709-5	Patent No. 5482709
c	28	38.4	3.4	543	6	5273901-6	Patent No. 5273901
	29	37.4	3.3	7559	2	US-08-250-848-2	Sequence 2, Appli
c	30	37.4	3.3	4403765	3	US-09-103-840A-2	Sequence 2, Appli
c	31	37.4	3.3	4411529	3	US-09-103-840A-1	Sequence 1, Appli
	32	36.6	3.2	23673	3	US-09-773-816-1	Sequence 1, Appli
	33	36.4	3.2	1125	4	US-09-252-991A-16469	Sequence 16469, A
	34	36.4	3.2	1173	4	US-09-252-991A-16248	Sequence 16248, A
c	35	36.4	3.2	1296	4	US-09-252-991A-16018	Sequence 16018, A
	36	36.4	3.2	2582	2	US-08-816-105A-2	Sequence 2, Appli
c	37	36.2	3.2	615	4	US-09-252-991A-242	Sequence 242, App
	38	36.2	3.2	1041	4	US-09-252-991A-296	Sequence 296, App
	39	36.2	3.2	1140	4	US-09-252-991A-269	Sequence 269, App
	40	36.2	3.2	1233	4	US-09-252-991A-3735	Sequence 3735, Ap
c	41	36.2	3.2	1491	4	US-09-252-991A-3636	Sequence 3636, Ap
	42	36.2	3.2	4884	4	US-09-252-991A-3824	Sequence 3824, Ap
c	43	36	3.2	909	4	US-09-252-991A-7481	Sequence 7481, Ap
	44	36	3.2	1149	4	US-09-252-991A-7156	Sequence 7156, Ap
c	45	36	3.2	1335	4	US-09-252-991A-7421	Sequence 7421, Ap

ALIGNMENTS

```
RESULT 1
US-08-236-311-9
; Sequence 9, Application US/08236311
; Patent No. 5565335
;  GENERAL INFORMATION:
;    APPLICANT:  Capon, Daniel J.
;    APPLICANT:  Gregory, Timothy J.
;    TITLE OF INVENTION:  Adheson Variants
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  5.25 inch, 360 Kb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  patin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/236,311
;      FILING DATE:  02-MAY-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/936190
;      FILING DATE:  26-AUG-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/842777
;      FILING DATE:  18-FEB-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/250785
;      FILING DATE:  28-SEP-1988
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/104329
;      FILING DATE:  02-OCT-1987
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hasak, Janet E.
;      REGISTRATION NUMBER:  28,616
;      REFERENCE/DOCKET NUMBER:  444P1C2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/225-1896
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1142 bases
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
```

```
;      TOPOLOGY:  linear
US-08-236-311-9

  Query Match             56.2%;  Score 638.4;  DB 1;  Length 1142;
  Best Local Similarity   96.7%;  Pred. No. 2.5e-168;
  Matches  665;  Conservative    0;  Mismatches   16;  Indels    7;  Gaps    1;

Qy          7 CTGTTTTGAGTGTGTACGGGTGGCACGGGTCGAGGCCTTGAGCTTCCACCAGGCAGTCAG 66
              |||||||||||||||||||||||||||||||| || ||||||   || || |||||||||
Db        440 CTGTTTTGAGTGTGTACGGGTGGCACGGGTCGTGGACTTGAGGACCCCCCTGGCAGTCAG 499

Qy         67 AAGGAGAAGGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGT 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        500 AAGGAGAAGGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGT 559

Qy        127 ACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTG 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        560 ACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTG 619

Qy        187 CCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATG 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        620 CCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATG 679

Qy        247 GCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTTCGAATGCGT 306
              || |||||||||||||||||||||||||||||||||||||||||||| |   |||
Db        680 GCCCACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATGTTC 739

Qy        307 ACGCGCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTT 366
              |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        740 ACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTT 799

Qy        367 CCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTC 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        800 CCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTC 859

Qy        427 TTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTC 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        860 TTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTC 919

Qy        487 ACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGG 546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        920 ACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGG 979

Qy        547 CTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCC 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        980 CTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCC 1039

Qy        607 TTGCAGAAGAGTACGAGGC-------ACTACGTACTCCGAGACGTGTTGGTGATGTGCGT 659
              |||||||||||||||||||       ||||||||||||||||||||||||||||||||
Db       1040 TTGCAGAAGAGTACGAGGCACTACGTACTACGTACTCCGAGACGTGTTGGTGATGTGCGT 1099

Qy        660 CTTCTCGGAGAGGGACAGAGGCCCATTT 687
              |||||||||||||||||||||||||||||
Db       1100 CTTCTCGGAGAGGGACAGAGGCCCATTT 1127


RESULT 2
US-08-457-918-9
; Sequence 9, Application US/08457918
; Patent No. 6117655
;  GENERAL INFORMATION:
;    APPLICANT:  Capon, Daniel J.
;    APPLICANT:  Gregory, Timothy J.
;    TITLE OF INVENTION:  Adheson Variants
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  5.25 inch, 360 Kb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  patin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/457,918
;      FILING DATE:  1-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/236311
;      FILING DATE:  02-MAY-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/936190
;      FILING DATE:  26-AUG-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/842777
;      FILING DATE:  18-FEB-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/250785
;      FILING DATE:  28-SEP-1988
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/104329
;      FILING DATE:  02-OCT-1987
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kubinec, Jeffrey S.
;      REGISTRATION NUMBER:  36,575
;      REFERENCE/DOCKET NUMBER:  P0444P1C3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/225-8228
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1142 bases
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-457-918-9

  Query Match             56.2%;  Score 638.4;  DB 3;  Length 1142;
  Best Local Similarity   96.7%;  Pred. No. 2.5e-168;
  Matches  665;  Conservative    0;  Mismatches   16;  Indels    7;  Gaps    1;

Qy          7 CTGTTTTGAGTGTGTACGGGTGGCACGGGTCGAGGCCTTGAGCTTCCACCAGGCAGTCAG 66
              |||||||||||||||||||||||||||||||| || ||||||   || || |||||||||
Db        440 CTGTTTTGAGTGTGTACGGGTGGCACGGGTCGTGGACTTGAGGACCCCCCTGGCAGTCAG 499

Qy         67 AAGGAGAAGGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGT 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        500 AAGGAGAAGGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGT 559

Qy        127 ACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTG 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        560 ACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTG 619

Qy        187 CCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATG 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        620 CCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATG 679

Qy        247 GCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTTCGAATGCGT 306
              || |||||||||||||||||||||||||||||||||||||||||||| |   |||
Db        680 GCCCACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATGTTC 739

Qy        307 ACGCGCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTT 366
              |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        740 ACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTT 799

Qy        367 CCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTC 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        800 CCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTC 859

Qy        427 TTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTC 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        860 TTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTC 919

Qy        487 ACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGG 546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        920 ACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGG 979

Qy        547 CTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCC 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        980 CTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCC 1039

Qy        607 TTGCAGAAGAGTACGAGGC-------ACTACGTACTCCGAGACGTGTTGGTGATGTGCGT 659
              |||||||||||||||||||       ||||||||||||||||||||||||||||||||
Db       1040 TTGCAGAAGAGTACGAGGCACTACGTACTACGTACTCCGAGACGTGTTGGTGATGTGCGT 1099

Qy        660 CTTCTCGGAGAGGGACAGAGGCCCATTT 687
              ||||||||||||||||||||||||||||
Db       1100 CTTCTCGGAGAGGGACAGAGGCCCATTT 1127
```

```
RESULT 3
US-10-157-408-9
; Sequence 9, Application US/10157408
; Patent No. 6710169
;  GENERAL INFORMATION:
;       APPLICANT: Capon, Daniel J.
;                  Gregory, Timothy J.
;       TITLE OF INVENTION: Adheson Variants
;       NUMBER OF SEQUENCES: 25
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Genentech, Inc.
;            STREET: 460 Point San Bruno Blvd
;            CITY: South San Francisco
;            STATE: California
;            COUNTRY: USA
;            ZIP: 94080
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: patin (Genentech)
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/157,408
;            FILING DATE: 28-May-2002
;            CLASSIFICATION: 435
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/08/457,918
;            FILING DATE: 1-JUN-1995
;            APPLICATION NUMBER: 08/236311
;            FILING DATE: 02-MAY-1994
;            APPLICATION NUMBER: 07/936190
;            FILING DATE: 26-AUG-1992
;            APPLICATION NUMBER: 07/842777
;            FILING DATE: 18-FEB-1992
;            APPLICATION NUMBER: 07/250785
;            FILING DATE: 28-SEP-1988
;            APPLICATION NUMBER: 07/104329
;            FILING DATE: 02-OCT-1987
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Kubinec, Jeffrey S.
;            REGISTRATION NUMBER: 36,575
;            REFERENCE/DOCKET NUMBER: P0444P1C3
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 415/225-8228
;            TELEFAX: 415/952-9881
;            TELEX: 910/371-7168
;  INFORMATION FOR SEQ ID NO: 9:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 1142 bases
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-157-408-9
```

```
  Query Match           56.2%;  Score 638.4;  DB 4;  Length 1142;
  Best Local Similarity  96.7%;  Pred. No. 2.5e-168;
  Matches  665;  Conservative    0;  Mismatches   16;  Indels    7;  Gaps    1;

Qy          7 CTGTTTTGAGTGTGTACGGGTGGCACGGGTCGAGGCCTTGAGCTTCCACCAGGCAGTCAG 66
              |||||||||||||||||||||||||||||| || ||||||  || || |||||||||
Db        440 CTGTTTTGAGTGTGTACGGGTGGCACGGGTCGTGGACTTGAGGACCCCCCTGGCAGTCAG 499

Qy         67 AAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGT 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        500 AAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGT 559

Qy        127 ACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTG 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        560 ACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTG 619

Qy        187 CCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATG 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        620 CCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATG 679

Qy        247 GCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTTCGAATGCGT 306
              || |||||||||||||||||||||||||||||||||||||||||||||| | |||
Db        680 GCCCACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATGTTC 739

Qy        307 ACGCGCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTT 366
              ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        740 ACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTT 799

Qy        367 CCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTC 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        800 CCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTC 859

Qy        427 TTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTC 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        860 TTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTC 919

Qy        487 ACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGG 546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        920 ACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGG 979

Qy        547 CTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCC 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        980 CTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCC 1039

Qy        607 TTGCAGAAGAGTACGAGGC-------ACTACGTACTCCGAGACGTGTTGGTGATGTGCGT 659
              |||||||||||||||||||       ||||||||||||||||||||||||||||||||
Db       1040 TTGCAGAAGAGTACGAGGCACTACGTACTACGTACTCCGAGACGTGTTGGTGATGTGCGT 1099

Qy        660 CTTCTCGGAGAGGGACAGAGGCCCATTT 687
              ||||||||||||||||||||||||||||
Db       1100 CTTCTCGGAGAGGGACAGAGGCCCATTT 1127
```

```
RESULT 4
US-08-480-036-1
; Sequence 1, Application US/08480036
; Patent No. 5723583
;  GENERAL INFORMATION:
;    APPLICANT:  Seed, Brian et al.
;    TITLE OF INVENTION:  INHIBITION OF CELL ADHESION
;    TITLE OF INVENTION:  PROTEIN-CARBOHYDRATE
;    TITLE OF INVENTION:  INTERACTIONS
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson
;      STREET:  225 Franklin Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  U.S.A.
;      ZIP:  02110-2804
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
```

```
;       COMPUTER:  IBM PS/2 Model 50Z or 55SX
;       OPERATING SYSTEM:  IBM P.C. DOS (Version 5.00)
;       SOFTWARE:  WordPerfect (Version 5.1)
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/480,036
;       FILING DATE:
;       CLASSIFICATION:  424
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US/07/618,314C
;       FILING DATE:  No. 5723583ember 23, 1990
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Clark, Paul T.
;       REGISTRATION NUMBER:  30,162
;       REFERENCE/DOCKET NUMBER:  00786/067001
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (617) 542-5070
;       TELEFAX:  (617) 542-8906
;       TELEX:  200154
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  2287
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
US-08-480-036-1

  Query Match             5.3%;  Score 60;  DB 1;  Length 2287;
  Best Local Similarity   100.0%;  Pred. No. 6.8e-07;
  Matches   60;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         74 AGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGCACC 133
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 AGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGCACC 1620


RESULT 5
US-08-461-968A-1
; Sequence 1, Application US/08461968A
; Patent No. 5801044
;  GENERAL INFORMATION:
;    APPLICANT:  Seed et al., Brian
;    TITLE OF INVENTION:  INHIBITION OF CELL ADHESION
;    TITLE OF INVENTION:  PROTEIN-CARBOHYDRATE INTERACTIONS
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson P.C.
;      STREET:  225 Franklin Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  0210-2804
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/461,968A
;      FILING DATE:  05-JUN-1995
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/618,314
;      FILING DATE:  23-NOV-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Lech, Karen F.
;      REGISTRATION NUMBER:  35,238
;      REFERENCE/DOCKET NUMBER:  00786/067003
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617/542-5070
;      TELEFAX:  617/542-8906
;      TELEX:  200154
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2287
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-461-968A-1

  Query Match             5.3%;  Score 60;  DB 1;  Length 2287;
  Best Local Similarity   100.0%;  Pred. No. 6.8e-07;
  Matches   60;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         74 AGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGCACC 133
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 AGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGCACC 1620


RESULT 6
US-08-462-571-1
; Sequence 1, Application US/08462571
; Patent No. 5858983
;  GENERAL INFORMATION:
;    APPLICANT:  Seed, Brian et al.
;    TITLE OF INVENTION:  INHIBITION OF CELL ADHESION
;    TITLE OF INVENTION:  PROTEIN-CARBOHYDRATE INTERACTIONS
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson P.C.
;      STREET:  225 Franklin Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  U.S.A.
;      ZIP:  02110-2804
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      COMPUTER:  IBM PS/2 Model 50Z or 55SX
;      OPERATING SYSTEM:  IBM P.C. DOS (Version 3.30)
;      SOFTWARE:  WordPerfect (Version 5.0)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/462,571
;      FILING DATE:  05 June 1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/618,314
;      FILING DATE:  23 No. 5858983ember 1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Lech, Karen F.
;      REGISTRATION NUMBER:  35,238
;      REFERENCE/DOCKET NUMBER:  00786/067002
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 542-5070
;      TELEFAX:  (617) 542-8906
;      TELEX:  200154
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2287
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-462-571-1

  Query Match             5.3%;  Score 60;  DB 2;  Length 2287;
  Best Local Similarity   100.0%;  Pred. No. 6.8e-07;
  Matches   60;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         74 AGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGCACC 133
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 AGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGCACC 1620


RESULT 7
US-08-472-888A-1
; Sequence 1, Application US/08472888A
; Patent No. 6613746
;  GENERAL INFORMATION:
```

```
;    APPLICANT:  Seed, Brian
;    APPLICANT:  Walz, Gerd
;    TITLE OF INVENTION:  AGP-ANTIBODY FUSION PROTEINS
;    TITLE OF INVENTION:  AND RELATED MOLECULES AND METHODS
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Clark & Elbing LLP
;      STREET:  176 Federal Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02110
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/472,888A
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/618,314
;      FILING DATE:  23-NOV-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Elbing, Karen L
;      REGISTRATION NUMBER:  35,238
;      REFERENCE/DOCKET NUMBER:  00786/258001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-428-0200
;      TELEFAX:  617-428-7045
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2287 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Genomic DNA
;    FEATURE:
;      NAME/KEY:  Coding Sequence
;      LOCATION:  1...300, 361...453, 679...903, 961...972,
;      LOCATION:  1360...1404, 1524...1853, 1950...2270
;      OTHER INFORMATION:
US-08-472-888A-1

  Query Match             5.3%;  Score 60;  DB 4;  Length 2287;
  Best Local Similarity   100.0%;  Pred. No. 6.8e-07;
  Matches   60;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         74 AGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGCACC 133
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 AGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGCACC 1620


RESULT 8
US-08-236-311-12
; Sequence 12, Application US/08236311
; Patent No. 5565335
;  GENERAL INFORMATION:
;    APPLICANT:  Capon, Daniel J.
;    APPLICANT:  Gregory, Timothy J.
;    TITLE OF INVENTION:  Adheson Variants
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  5.25 inch, 360 Kb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  patin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/236,311
;      FILING DATE:  02-MAY-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/936190
;      FILING DATE:  26-AUG-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/842777
;      FILING DATE:  18-FEB-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/250785
;      FILING DATE:  28-SEP-1988
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/104329
;      FILING DATE:  02-OCT-1987
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hasak, Janet E.
;      REGISTRATION NUMBER:  28,616
;      REFERENCE/DOCKET NUMBER:  444P1C2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/225-1896
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  468 bases
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-236-311-12

  Query Match             3.8%;  Score 43;  DB 1;  Length 468;
  Best Local Similarity   49.5%;  Pred. No. 0.02;
  Matches  143;  Conservative    0;  Mismatches  140;  Indels    6;  Gaps    1;

Qy        379 CTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTCTTGGTCCAGTCG 438
              | ||||   || | || | | || |||||    ||  || |||          | |
Db        127 CGTGGTAGACAGAAGTAGAAGGGCGGTAGACTACTCGTCAACTTTAGACCTTGACGGAGA 186

Qy        439 GACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCAC------CCTC 492
              |    |||||| | ||   |||||||||||| ||   |   ||  ||||       |||
Db        187 CAACACACGGACGACTTATTGAAGATAGGGTCTCTCCGGTTTCATGTCACCTTCCACCTA 246

Qy        493 TCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGGCTGCCG 552
              | |       ||  |||  |||  | |  |||       |       |       | ||| ||
Db        247 TTGCGGGAGGTTAGCCCATTGAGGGTCCTCTCACAGTGTCTCGTCCTGTCGTTCCTGTCG 306

Qy        553 AGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCCTTGCAG 612
              |||  |  ||||  |||||  || ||  ||  |||       |  || |   || |||
Db        307 TGGATGTCGGAGTCGTCGTGGGACTGCGACTCGTTTCGTCTGATGCTCTTTGTGTTTCAG 366

Qy        613 AAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCT 661
              | | | |||   || |  ||| |||  |||  |   | |  |||  |||
Db        367 ATGCGGACGCTTCAGTGGGTAGTCCCGGACTCGAGCGGGCAGTGTTTCT 415


RESULT 9
US-08-457-918-12
; Sequence 12, Application US/08457918
; Patent No. 6117655
;  GENERAL INFORMATION:
;    APPLICANT:  Capon, Daniel J.
;    APPLICANT:  Gregory, Timothy J.
;    TITLE OF INVENTION:  Adheson Variants
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
```

```
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  5.25 inch, 360 Kb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  patin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/457,918
;      FILING DATE:  1-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/236311
;      FILING DATE:  02-MAY-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/936190
;      FILING DATE:  26-AUG-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/842777
;      FILING DATE:  18-FEB-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/250785
;      FILING DATE:  28-SEP-1988
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/104329
;      FILING DATE:  02-OCT-1987
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kubinec, Jeffrey S.
;      REGISTRATION NUMBER:  36,575
;      REFERENCE/DOCKET NUMBER:  P0444P1C3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/225-8228
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  468 bases
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-457-918-12

  Query Match             3.8%;  Score 43;  DB 3;  Length 468;
  Best Local Similarity   49.5%;  Pred. No. 0.02;
  Matches  143;  Conservative    0;  Mismatches  140;  Indels    6;  Gaps    1;

Qy        379 CTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTCTTGGTCCAGTCG 438
              | ||||   || | || | | | || |||||    ||  || |||          | |
Db        127 CGTGGTAGACAGAAGTAGAAGGGCGGTAGACTACTCGTCAACTTTAGACCTTGACGGAGA 186

Qy        439 GACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCAC------CCTC 492
              |    |||||| | ||   |||||||||||| ||    |   ||  ||||      |||
Db        187 CAACACACGGACGACTTATTGAAGATAGGGTCTCTCCGGTTTCATGTCACCTTCCACCTA 246

Qy        493 TCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGGCTGCCG 552
              | |      ||  |||  |||  | | |||     |     |     |   ||| ||
Db        247 TTGCGGGAGGTTAGCCCATTGAGGGTCCTCTCACAGTGTCTCGTCCTGTCGTTCCTGTCG 306

Qy        553 AGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCCTTGCAG 612
              |||  |  ||||  |||||  || ||  ||  |||       |   || |    || |||
Db        307 TGGATGTCGGAGTCGTCGTGGGACTGCGACTCGTTTCGTCTGATGCTCTTTGTGTTTCAG 366

Qy        613 AAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCT 661
              | | | |||   || |  ||| |||  |||  |  | | |||  |||
Db        367 ATGCGGACGCTTCAGTGGGTAGTCCCGGACTCGAGCGGGCAGTGTTTCT 415


RESULT 10
US-10-157-408-12
; Sequence 12, Application US/10157408
; Patent No. 6710169
;   GENERAL INFORMATION:
;       APPLICANT: Capon, Daniel J.
;                  Gregory, Timothy J.
;       TITLE OF INVENTION: Adheson Variants
;       NUMBER OF SEQUENCES: 25
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Genentech, Inc.
;            STREET: 460 Point San Bruno Blvd
;            CITY: South San Francisco
;            STATE: California
;            COUNTRY: USA
;            ZIP: 94080
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: patin (Genentech)
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/157,408
;            FILING DATE: 28-May-2002
;            CLASSIFICATION: 435
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/08/457,918
;            FILING DATE: 1-JUN-1995
;            APPLICATION NUMBER: 08/236311
;            FILING DATE: 02-MAY-1994
;            APPLICATION NUMBER: 07/936190
;            FILING DATE: 26-AUG-1992
;            APPLICATION NUMBER: 07/842777
;            FILING DATE: 18-FEB-1992
;            APPLICATION NUMBER: 07/250785
;            FILING DATE: 28-SEP-1988
;            APPLICATION NUMBER: 07/104329
;            FILING DATE: 02-OCT-1987
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Kubinec, Jeffrey S.
;            REGISTRATION NUMBER: 36,575
;            REFERENCE/DOCKET NUMBER: P0444P1C3
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 415/225-8228
;            TELEFAX: 415/952-9881
;            TELEX: 910/371-7168
;   INFORMATION FOR SEQ ID NO: 12:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 468 bases
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-10-157-408-12

  Query Match             3.8%;  Score 43;  DB 4;  Length 468;
  Best Local Similarity   49.5%;  Pred. No. 0.02;
  Matches  143;  Conservative    0;  Mismatches  140;  Indels    6;  Gaps    1;

Qy        379 CTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTCTTGGTCCAGTCG 438
              | ||||   || | || | | | || |||||    ||  || |||          | |
Db        127 CGTGGTAGACAGAAGTAGAAGGGCGGTAGACTACTCGTCAACTTTAGACCTTGACGGAGA 186

Qy        439 GACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCAC------CCTC 492
              |    |||||| | ||   |||||||||||| ||    |   ||  ||||      |||
Db        187 CAACACACGGACGACTTATTGAAGATAGGGTCTCTCCGGTTTCATGTCACCTTCCACCTA 246

Qy        493 TCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGGCTGCCG 552
              | |      ||  |||  |||  | | |||     |     |     |   ||| ||
Db        247 TTGCGGGAGGTTAGCCCATTGAGGGTCCTCTCACAGTGTCTCGTCCTGTCGTTCCTGTCG 306

Qy        553 AGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCCTTGCAG 612
              |||  |  ||||  |||||  || ||  ||  |||       |   || |    || |||
Db        307 TGGATGTCGGAGTCGTCGTGGGACTGCGACTCGTTTCGTCTGATGCTCTTTGTGTTTCAG 366

Qy        613 AAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCT 661
              | | | |||   || |  ||| |||  |||  |  | | |||  |||
Db        367 ATGCGGACGCTTCAGTGGGTAGTCCCGGACTCGAGCGGGCAGTGTTTCT 415
```

RESULT 11
US-09-252-991A-7703
; Sequence 7703, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 7703
; LENGTH: 1161
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-7703

Query Match 3.7%; Score 42; DB 4; Length 1161;
Best Local Similarity 47.1%; Pred. No. 0.054;
Matches 129; Conservative 0; Mismatches 145; Indels 0; Gaps 0;

```
Qy        119 TCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCA 178
              |||||  | || |   |  |  |  ||  ||| |  |      |       | |  ||| |
Db        332 TCCAGCCTTCGGAGATCGCCAAGGTCTGCGTGGTGATCTTCATGGCCGGCTACCTGATCC 391

Qy        179 TGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGT 238
                | || || | |  |||  | |    || |  | |||  |   | | ||||  |||||
Db        392 GCCGCCAGCAGGAGGTCCGGGAAAGCTGGATGGGCTTCTTCAAGCCCTTCGTGGTGTTGC 451

Qy        239 CGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTTC 298
              |   |||||   || |  || |     || |||| | | |   ||||   ||  | |
Db        452 TGCCGATGGCCGGCCTGCTGCTGCGCGAGCCGGACTTCGGCGCCACCGTGGTAATGATGG 511

Qy        299 GAATGCGTACGCGCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGT 358
              |         ||  |  |  |||  |  | | ||   ||  ||  | |||  |   ||| |
Db        512 GCGCTGCCGCGGCCATGCTGTTCCTCGGCGGGGTGGGGCTGTTCCGCTTCGGCCTGATGG 571

Qy        359 TTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACAT 392
              | | | |  | ||||| ||  | |   | |  ||
Db        572 TGCTGCTGGCGGTCGGCGCGGTGGTCCTGCTGAT 605
```

RESULT 12
US-09-252-991A-7860/c
; Sequence 7860, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 7860
; LENGTH: 1287
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-7860

Query Match 3.7%; Score 42; DB 4; Length 1287;
Best Local Similarity 47.1%; Pred. No. 0.056;
Matches 129; Conservative 0; Mismatches 145; Indels 0; Gaps 0;

```
Qy        119 TCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCA 178
              |||||  | || |   |  |  |  ||  ||| |  |      |       | |  ||| |
Db        908 TCCAGCCTTCGGAGATCGCCAAGGTCTGCGTGGTGATCTTCATGGCCGGCTACCTGATCC 849

Qy        179 TGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGT 238
                | || || | |  |||  | |    || |  | |||  |   | | ||||  |||||
Db        848 GCCGCCAGCAGGAGGTCCGGGAAAGCTGGATGGGCTTCTTCAAGCCCTTCGTGGTGTTGC 789

Qy        239 CGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTTC 298
              |   |||||   || |  || |     || |||| | | |   ||||   ||  | |
Db        788 TGCCGATGGCCGGCCTGCTGCTGCGCGAGCCGGACTTCGGCGCCACCGTGGTAATGATGG 729

Qy        299 GAATGCGTACGCGCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGT 358
              |         ||  |  |  |||  |  | | ||   ||  ||  | |||  |   ||| |
Db        728 GCGCTGCCGCGGCCATGCTGTTCCTCGGCGGGGTGGGGCTGTTCCGCTTCGGCCTGATGG 669

Qy        359 TTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACAT 392
              | | | |  | ||||| ||  | |   | |  ||
Db        668 TGCTGCTGGCGGTCGGCGCGGTGGTCCTGCTGAT 635
```

RESULT 13
US-09-252-991A-7624
; Sequence 7624, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 7624
; LENGTH: 1359
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-7624

Query Match 3.7%; Score 42; DB 4; Length 1359;
Best Local Similarity 47.1%; Pred. No. 0.058;
Matches 129; Conservative 0; Mismatches 145; Indels 0; Gaps 0;

```
Qy        119 TCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCA 178
              |||||  | || |   |  |  |  ||  ||| |  |      |       | |  ||| |
Db        576 TCCAGCCTTCGGAGATCGCCAAGGTCTGCGTGGTGATCTTCATGGCCGGCTACCTGATCC 635

Qy        179 TGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGT 238
                | || || | |  |||  | |    || |  | |||  |   | | ||||  |||||
Db        636 GCCGCCAGCAGGAGGTCCGGGAAAGCTGGATGGGCTTCTTCAAGCCCTTCGTGGTGTTGC 695

Qy        239 CGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTTC 298
              |   |||||   || |  || |     || |||| | | |   ||||   ||  | |
Db        696 TGCCGATGGCCGGCCTGCTGCTGCGCGAGCCGGACTTCGGCGCCACCGTGGTAATGATGG 755

Qy        299 GAATGCGTACGCGCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGT 358
              |         ||  |  |  |||  |  | | ||   ||  ||  | |||  |   ||| |
Db        756 GCGCTGCCGCGGCCATGCTGTTCCTCGGCGGGGTGGGGCTGTTCCGCTTCGGCCTGATGG 815

Qy        359 TTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACAT 392
              | | | |  | ||||| ||  | |   | |  ||
Db        816 TGCTGCTGGCGGTCGGCGCGGTGGTCCTGCTGAT 849
```

RESULT 14
US-09-489-039A-1509/c
; Sequence 1509, Application US/09489039A

; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 1509
; LENGTH: 1425
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-1509

Query Match 3.5%; Score 39.6; DB 4; Length 1425;
Best Local Similarity 47.9%; Pred. No. 0.27;
Matches 114; Conservative 0; Mismatches 124; Indels 0; Gaps 0;

```
Qy        417 CGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTA 476
              |||||||  |    | | | ||    |  ||||  ||    | |  |  | | ||| ||
Db       1387 CGACTGGCGCGGCTTGCTGGCGTTTAGCCCGGATAAGCCGACCAGCACCGAGGCGCAGTG 1328

Qy        477 GCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCA 536
                |   |  |  | | |   ||| || |  | |  |  |  |||| |||| | | |
Db       1327 CAACTATTACTACGCCAAGCTGAGCGTGGGGCAGTCGCAGGAGGCCTGGAGCGGGGCGAA 1268

Qy        537 CGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCAC 596
               || ||| || || || | |||||  ||         |      |  ||||||    ||
Db       1267 AGAGCTGTGGTTGACGGGCAAGAATCAGCCCGGCGCCTGTGAACCGCTGTTCAGCGCCTG 1208

Qy        597 CGTCGTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATG 654
              || | ||   ||| ||  | ||  |  |||  |    ||   |    ||| ||||
Db       1207 GCGCGACTCCGGTCAGCAGGATCCGCTGGCCTATCTCGAACGGATCCGCCTGGCGATG 1150
```

RESULT 15
US-09-489-039A-1492
; Sequence 1492, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 1492
; LENGTH: 2016
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-1492

Query Match 3.5%; Score 39.6; DB 4; Length 2016;
Best Local Similarity 47.9%; Pred. No. 0.32;
Matches 114; Conservative 0; Mismatches 124; Indels 0; Gaps 0;

```
Qy        417 CGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTA 476
              |||||||  |    | | | ||    |  ||||  ||    | |  |  | | ||| ||
Db        417 CGACTGGCGCGGCTTGCTGGCGTTTAGCCCGGATAAGCCGACCAGCACCGAGGCGCAGTG 476

Qy        477 GCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCA 536
                |   |  |  | | |   ||| || |  | |  |  |  |||| |||| | | |
Db        477 CAACTATTACTACGCCAAGCTGAGCGTGGGGCAGTCGCAGGAGGCCTGGAGCGGGGCGAA 536

Qy        537 CGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCAC 596
               || ||| || || || | |||||  ||         |      |  ||||||    ||
Db        537 AGAGCTGTGGTTGACGGGCAAGAATCAGCCCGGCGCCTGTGAACCGCTGTTCAGCGCCTG 596

Qy        597 CGTCGTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATG 654
              || | ||   ||| ||  | ||  |  |||  |    ||   |    ||| ||||
Db        597 GCGCGACTCCGGTCAGCAGGATCCGCTGGCCTATCTCGAACGGATCCGCCTGGCGATG 654
```

Search completed: October 17, 2004, 17:00:49
Job time : 108.696 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 17, 2004, 15:34:57 ; Search time 4411.65 Seconds
(without alignments)
11298.387 Million cell updates/sec

Title: US-10-679-999-7
Perfect score: 1150
Sequence: 1 CATATGGAACCCAAATCTTG.....TCCGGGTTGTTAATGGATCC 1150

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1150	100.0	1150	6	BD056517	BD056517 OB fusion
2	1134	98.6	1150	6	BD056519	BD056519 OB fusion
3	1117.8	97.2	1135	6	BD056521	BD056521 OB fusion
4	1105	96.1	1135	6	BD056523	BD056523 OB fusion
5	697	60.6	2190	6	AX268713	AX268713 Sequence
6	697	60.6	2220	6	AX268719	AX268719 Sequence
7	696.8	60.6	1288	6	AX039180	AX039180 Sequence
8	695.8	60.5	1304	6	AX039184	AX039184 Sequence
9	695.8	60.5	2196	6	AX268709	AX268709 Sequence
10	695.8	60.5	2226	6	AX268715	AX268715 Sequence
11	695.6	60.5	1720	6	AR381777	AR381777 Sequence
12	695.6	60.5	1720	6	AX180193	AX180193 Sequence
13	695.6	60.5	1720	6	AX180693	AX180693 Sequence
14	695.6	60.5	1720	6	AX406502	AX406502 Sequence
15	695.4	60.5	1443	6	AX357958	AX357958 Sequence
16	695.4	60.5	1494	6	AR435731	AR435731 Sequence
17	695.4	60.5	1578	6	AR435730	AR435730 Sequence
18	695.4	60.5	1869	6	AR435729	AR435729 Sequence
19	695.2	60.5	1080	6	AR173437	AR173437 Sequence
20	695.2	60.5	1182	6	AR173440	AR173440 Sequence
21	694.8	60.4	990	6	BD270544	BD270544 Cytokine
22	694.8	60.4	990	6	AX047023	AX047023 Sequence
23	694.8	60.4	990	6	AX365185	AX365185 Sequence
24	694.8	60.4	990	6	AX478510	AX478510 Sequence
25	694.8	60.4	990	9	HSA294730	AJ294730 Homo sapi
26	694.8	60.4	1159	9	HSA17957	Y17957 Homo sapien
27	694.8	60.4	1229	6	AX398961	AX398961 Sequence
28	694.8	60.4	1345	6	AX039178	AX039178 Sequence
29	694.8	60.4	1356	6	AX357970	AX357970 Sequence
30	694.8	60.4	1367	6	AX039182	AX039182 Sequence
31	694.8	60.4	1392	6	AX594307	AX594307 Sequence
32	694.8	60.4	1392	6	AX616608	AX616608 Sequence
33	694.8	60.4	1392	6	AX616908	AX616908 Sequence
34	694.8	60.4	1404	6	AX268679	AX268679 Sequence
35	694.8	60.4	1407	6	AX556959	AX556959 Sequence
36	694.8	60.4	1407	6	AX709558	AX709558 Sequence
37	694.8	60.4	1418	6	AX076856	AX076856 Sequence
38	694.8	60.4	1422	6	BD013334	BD013334 Novel pep
39	694.8	60.4	1422	6	BD013336	BD013336 Novel pep
40	694.8	60.4	1422	6	BD013337	BD013337 Novel pep
41	694.8	60.4	1422	6	BD013338	BD013338 Novel pep
42	694.8	60.4	1422	6	BD013340	BD013340 Novel pep
43	694.8	60.4	1431	6	E10697	E10697 cDNA encodi
44	694.8	60.4	1442	6	BD266675	BD266675 Human mon
45	694.8	60.4	1465	10	S79307	S79307 Ig gamma =i

ALIGNMENTS

RESULT 1
BD056517
LOCUS BD056517 1150 bp DNA linear PAT 27-AUG-2002
DEFINITION OB fusion protein compositions and methods.
ACCESSION BD056517
VERSION BD056517.1 GI:22602123
KEYWORDS JP 2001512417-A/5.
SOURCE Aequorea victoria
ORGANISM Aequorea victoria
Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae; Aequoreidae; Aequorea.
REFERENCE 1 (bases 1 to 1150)
AUTHORS Mann,M.B. and Hecht,R.I.
TITLE OB fusion protein compositions and methods
JOURNAL Patent: JP 2001512417-A 5 21-AUG-2001;

```
            AMGEN INC
COMMENT     PN   JP 2001512417-A/5
            PD   21-AUG-2001
            PF   11-DEC-1997 JP 1998528896
            PR   20-DEC-1996 US    08/770973
            PI   MICHAEL BENJAMIN MANN,RANDY IRA HECHT
            PC   C07K14/575,A61K38/00,A61P3/04,A61P3/06,A61P3/10,A61P9/10, PC
            A61P43/00,
            PC   C12N15/09,C12N15/00,A61K37/02
            CC   Strandedness: Double;
            CC   Topology: Linear;
            CC   /note= 'Met = ATG'
            FH   Key             Location/Qualifiers.
FEATURES                 Location/Qualifiers
     source              1. .1150
                         /organism="Aequorea victoria"
                         /mol_type="genomic DNA"
                         /db_xref="taxon:6100"
ORIGIN

  Query Match             100.0%;  Score 1150;  DB 6;  Length 1150;
  Best Local Similarity   100.0%;  Pred. No. 4e-232;
  Matches 1150;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CATATGGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CATATGGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAA 60

Qy         61 CTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATC 120

Qy        121 TCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTC 180

Qy        181 AAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAG 240

Qy        241 GAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGG 300

Qy        301 CTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAG 360

Qy        361 AAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCA 420

Qy        421 TCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTAT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTAT 480

Qy        481 CCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACC 540

Qy        541 ACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGAC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 ACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGAC 600

Qy        601 AAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCAC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCAC 660

Qy        661 AACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTT 720

Qy        721 CAGGACGACACCAAAACCTTAATTAAAACGATCGTTACGCGTATCAACGACATCAGTCAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CAGGACGACACCAAAACCTTAATTAAAACGATCGTTACGCGTATCAACGACATCAGTCAC 780

Qy        781 ACCCAGTCGGTGAGCTCTAAACAGAAAGTTACAGGCCTGGACTTCATCCCGGGTCTGCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 ACCCAGTCGGTGAGCTCTAAACAGAAAGTTACAGGCCTGGACTTCATCCCGGGTCTGCAC 840

Qy        841 CCGATCCTGACCTTGTCCAAAATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CCGATCCTGACCTTGTCCAAAATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACC 900

Qy        901 TCCATGCCGTCCCGTAACGTTATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TCCATGCCGTCCCGTAACGTTATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTG 960

Qy        961 CTGCACGTGCTGGCATTCTCCAAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CTGCACGTGCTGGCATTCTCCAAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACT 1020

Qy       1021 CTGGACTCTCTGGGCGGGGTCCTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTG 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 CTGGACTCTCTGGGCGGGGTCCTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTG 1080

Qy       1081 TCCCGTCTGCAGGGTTCCCTTCAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TCCCGTCTGCAGGGTTCCCTTCAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGT 1140

Qy       1141 TAATGGATCC 1150
              ||||||||||
Db       1141 TAATGGATCC 1150
```

```
RESULT 2
BD056519
LOCUS       BD056519                1150 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  OB fusion protein compositions and methods.
ACCESSION   BD056519
VERSION     BD056519.1  GI:22602125
KEYWORDS    JP 2001512417-A/7.
SOURCE      Aequorea victoria
  ORGANISM  Aequorea victoria
            Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
            Aequoreidae; Aequorea.
REFERENCE   1  (bases 1 to 1150)
  AUTHORS   Mann,M.B. and Hecht,R.I.
  TITLE     OB fusion protein compositions and methods
  JOURNAL   Patent: JP 2001512417-A 7 21-AUG-2001;
            AMGEN INC
COMMENT     PN   JP 2001512417-A/7
            PD   21-AUG-2001
            PF   11-DEC-1997 JP 1998528896
            PR   20-DEC-1996 US    08/770973
            PI   MICHAEL BENJAMIN MANN,RANDY IRA HECHT
            PC   C07K14/575,A61K38/00,A61P3/04,A61P3/06,A61P3/10,A61P9/10, PC
            A61P43/00,
            PC   C12N15/09,C12N15/00,A61K37/02
            CC   Strandedness: Double;
            CC   Topology: Linear;
            CC   /note= 'Met = ATG'
            FH   Key             Location/Qualifiers.
FEATURES                 Location/Qualifiers
     source              1. .1150
                         /organism="Aequorea victoria"
                         /mol_type="genomic DNA"
                         /db_xref="taxon:6100"
ORIGIN

  Query Match             98.6%;  Score 1134;  DB 6;  Length 1150;
  Best Local Similarity   99.1%;  Pred. No. 9.3e-229;
  Matches 1140;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          1 CATATGGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAA 60
              |||||||||||| ||||||  |||||||||||||||||||| ||||| || ||||| || |||
```

```
Db          1 CATATGGAACCAAAATCTGCTGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAA 60
Qy         61 CTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATC 120
Db         61 CTCCTGGGGGGTCCTTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATC 120
Qy        121 TCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTC 180
Db        121 TCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTC 180
Qy        181 AAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAG 240
Db        181 AAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAG 240
Qy        241 GAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGG 300
Db        241 GAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGG 300
Qy        301 CTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAG 360
Db        301 CTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAG 360
Qy        361 AAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCA 420
Db        361 AAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCA 420
Qy        421 TCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTAT 480
Db        421 TCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTAT 480
Qy        481 CCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACC 540
Db        481 CCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACC 540
Qy        541 ACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGAC 600
Db        541 ACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGAC 600
Qy        601 AAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCAC 660
Db        601 AAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCAC 660
Qy        661 AACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTT 720
Db        661 AACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTT 720
Qy        721 CAGGACGACACCAAAACCTTAATTAAAACGATCGTTACGCGTATCAACGACATCAGTCAC 780
Db        721 CAGGACGACACCAAAACCTTAATTAAAACGATCGTTACGCGTATCAACGACATCAGTCAC 780
Qy        781 ACCCAGTCGGTGAGCTCTAAACAGAAAGTTACAGGCCTGGACTTCATCCCGGGTCTGCAC 840
Db        781 ACCCAGTCGGTGAGCTCTAAACAGAAAGTTACAGGCCTGGACTTCATCCCGGGTCTGCAC 840
Qy        841 CCGATCCTGACCTTGTCCAAAATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACC 900
Db        841 CCGATCCTGACCTTGTCCAAAATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACC 900
Qy        901 TCCATGCCGTCCCGTAACGTTATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTG 960
Db        901 TCCATGCCGTCCCGTAACGTTATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTG 960
Qy        961 CTGCACGTGCTGGCATTCTCCAAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACT 1020
Db        961 CTGCACGTGCTGGCATTCTCCAAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACT 1020
Qy       1021 CTGGACTCTCTGGGCGGGGTCCTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTG 1080
Db       1021 CTGGACTCTCTGGGCGGGGTCCTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTG 1080
Qy       1081 TCCCGTCTGCAGGGTTCCCTTCAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGT 1140
Db       1081 TCCCGTCTGCAGGGTTCCCTTCAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGT 1140
Qy       1141 TAATGGATCC 1150
Db       1141 TAATGGATCC 1150
```

RESULT 3
BD056521

```
LOCUS       BD056521                1135 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  OB fusion protein compositions and methods.
ACCESSION   BD056521
VERSION     BD056521.1  GI:22602127
KEYWORDS    JP 2001512417-A/9.
SOURCE      Aequorea victoria
  ORGANISM  Aequorea victoria
            Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
            Aequoreidae; Aequorea.
REFERENCE   1  (bases 1 to 1135)
  AUTHORS   Mann,M.B. and Hecht,R.I.
  TITLE     OB fusion protein compositions and methods
  JOURNAL   Patent: JP 2001512417-A 9 21-AUG-2001;
            AMGEN INC
COMMENT     PN   JP 2001512417-A/9
            PD   21-AUG-2001
            PF   11-DEC-1997 JP 1998528896
            PR   20-DEC-1996 US    08/770973
            PI   MICHAEL BENJAMIN MANN,RANDY IRA HECHT
            PC   C07K14/575,A61K38/00,A61P3/04,A61P3/06,A61P3/10,A61P9/10, PC
            A61P43/00,
            PC   C12N15/09,C12N15/00,A61K37/02
            CC   Strandedness: Double;
            CC   Topology: Linear;
            CC   /note= 'Met = ATG'
            FH   Key             Location/Qualifiers.
FEATURES                Location/Qualifiers
     source             1. .1135
                        /organism="Aequorea victoria"
                        /mol_type="genomic DNA"
                        /db_xref="taxon:6100"
ORIGIN
```

Query Match 97.2%; Score 1117.8; DB 6; Length 1135;
Best Local Similarity 99.4%; Pred. No. 2.4e-225;
Matches 1122; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

```
Qy         22 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC 81
Db          7 GACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGTCCTTCAGTC 66
Qy         82 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 141
Db         67 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 126
Qy        142 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 201
Db        127 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 186
Qy        202 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 261
Db        187 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 246
Qy        262 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 321
Db        247 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 306
Qy        322 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 381
Db        307 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 366
Qy        382 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 441
Db        367 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 426
```

```
Qy        442 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 501
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 486

Qy        502 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 561
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 546

Qy        562 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 621
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 606

Qy        622 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 681
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 666

Qy        682 CTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTTCAGGACGACACCAAAACCTTA 741
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 CTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTTCAGGACGACACCAAAACCTTA 726

Qy        742 ATTAAAACGATCGTTACGCGTATCAACGACATCAGTCACACCCAGTCGGTGAGCTCTAAA 801
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        727 ATTAAAACGATCGTTACGCGTATCAACGACATCAGTCACACCCAGTCGGTGAGCTCTAAA 786

Qy        802 CAGAAAGTTACAGGCCTGGACTTCATCCCGGGTCTGCACCCGATCCTGACCTTGTCCAAA 861
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 CAGAAAGTTACAGGCCTGGACTTCATCCCGGGTCTGCACCCGATCCTGACCTTGTCCAAA 846

Qy        862 ATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACCTCCATGCCGTCCCGTAACGTT 921
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 ATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACCTCCATGCCGTCCCGTAACGTT 906

Qy        922 ATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTGCTGCACGTGCTGGCATTCTCC 981
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        907 ATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTGCTGCACGTGCTGGCATTCTCC 966

Qy        982 AAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACTCTGGACTCTCTGGGCGGGGTC 1041
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        967 AAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACTCTGGACTCTCTGGGCGGGGTC 1026

Qy       1042 CTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTGTCCCGTCTGCAGGGTTCCCTT 1101
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1027 CTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTGTCCCGTCTGCAGGGTTCCCTT 1086

Qy       1102 CAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGTTAATGGATCC 1150
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db       1087 CAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGTTAATGGATCC 1135
```

RESULT 4
BD056523

```
LOCUS       BD056523               1135 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  OB fusion protein compositions and methods.
ACCESSION   BD056523
VERSION     BD056523.1  GI:22602129
KEYWORDS    JP 2001512417-A/11.
SOURCE      Aequorea victoria
  ORGANISM  Aequorea victoria
            Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
            Aequoreidae; Aequorea.
REFERENCE   1  (bases 1 to 1135)
  AUTHORS   Mann,M.B. and Hecht,R.I.
  TITLE     OB fusion protein compositions and methods
  JOURNAL   Patent: JP 2001512417-A 11 21-AUG-2001;
            AMGEN INC
COMMENT     PN   JP 2001512417-A/11
            PD   21-AUG-2001
            PF   11-DEC-1997 JP 1998528896
            PR   20-DEC-1996 US    08/770973
            PI   MICHAEL BENJAMIN MANN,RANDY IRA HECHT
            PC   C07K14/575,A61K38/00,A61P3/04,A61P3/06,A61P3/10,A61P9/10, PC
            A61P43/00,
            PC   C12N15/09,C12N15/00,A61K37/02
            CC   Strandedness: Double;
            CC   Topology: Linear;
            CC   /note= 'Met = ATG'
            FH   Key             Location/Qualifiers.
FEATURES                Location/Qualifiers
     source             1. .1135
                        /organism="Aequorea victoria"
                        /mol_type="genomic DNA"
                        /db_xref="taxon:6100"
ORIGIN

  Query Match             96.1%;  Score 1105;  DB 6;  Length 1135;
  Best Local Similarity   98.7%;  Pred. No. 1.2e-222;
  Matches 1114;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy         22 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC 81
              ||||||||||||||||||||||||||||||||| || ||||||  || || |||||||||
Db          7 GACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCGTCAGTC 66

Qy         82 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 141
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 126

Qy        142 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 201
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 186

Qy        202 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 261
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 246

Qy        262 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 321
              |||||||||||||||||||||||||||||||||||||||||||||||||||| | |||
Db        247 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCTTACGCA 306

Qy        322 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 381
              ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 TGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 366

Qy        382 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 441
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 426

Qy        442 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 501
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 486

Qy        502 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 561
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 546

Qy        562 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 621
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 606

Qy        622 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 681
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 666

Qy        682 CTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTTCAGGACGACACCAAAACCTTA 741
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 CTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTTCAGGACGACACCAAAACCTTA 726

Qy        742 ATTAAAACGATCGTTACGCGTATCAACGACATCAGTCACACCCAGTCGGTGAGCTCTAAA 801
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        727 ATTAAAACGATCGTTACGCGTATCAACGACATCAGTCACACCCAGTCGGTGAGCTCTAAA 786

Qy        802 CAGAAAGTTACAGGCCTGGACTTCATCCCGGGTCTGCACCCGATCCTGACCTTGTCCAAA 861
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 CAGAAAGTTACAGGCCTGGACTTCATCCCGGGTCTGCACCCGATCCTGACCTTGTCCAAA 846

Qy        862 ATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACCTCCATGCCGTCCCGTAACGTT 921
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        847 ATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACCTCCATGCCGTCCCGTAACGTT 906

Qy        922 ATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTGCTGCACGTGCTGGCATTCTCC 981
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        907 ATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTGCTGCACGTGCTGGCATTCTCC 966

Qy        982 AAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACTCTGGACTCTCTGGGCGGGGTC 1041
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        967 AAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACTCTGGACTCTCTGGGCGGGGTC 1026

Qy       1042 CTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTGTCCCGTCTGCAGGGTTCCCTT 1101
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1027 CTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTGTCCCGTCTGCAGGGTTCCCTT 1086

Qy       1102 CAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGTTAATGGATCC 1150
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db       1087 CAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGTTAATGGATCC 1135
```

RESULT 5
AX268713
LOCUS AX268713 2190 bp DNA linear PAT 29-OCT-2001
DEFINITION Sequence 44 from Patent WO0174905.
ACCESSION AX268713
VERSION AX268713.1 GI:16541800
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Young,R.J.
TITLE Compounds for targeting
JOURNAL Patent: WO 0174905-A 44 11-OCT-2001;
ANTISOMA RESEARCH LIMITED (GB)
FEATURES Location/Qualifiers
source 1. .2190
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Humanised HMFG1 heavy chain - DNase I fusion"
ORIGIN

Query Match 60.6%; Score 697; DB 6; Length 2190;
Best Local Similarity 93.6%; Pred. No. 1.2e-136;
Matches 727; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

```
Qy          5 TGGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 64
              | || ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        704 TTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 763

Qy         65 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        764 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 823

Qy        125 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        824 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 883

Qy        185 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        884 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 943

Qy        245 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 304
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        944 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 1003

Qy        305 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1004 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 1063

Qy        365 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1064 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 1123

Qy        425 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 484
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1124 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 1183

Qy        485 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 544
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1184 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 1243

Qy        545 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 604
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1244 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 1303

Qy        605 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 664
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1304 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 1363

Qy        665 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTTCAGG 724
              |||||||||||||||||||||||||||||| ||||| |  |    | |  ||| |
Db       1364 ACTACACGCAGAAGAGCCTCTCCCTGTCCCCGGGGAGCGGCGGGCTGAAGATCGCAGCCT 1423

Qy        725 ACGACACCAAAACCTTAATTAAAACGATCGTTACGCGTATCAACGACATCAGTCACA 781
              | |||| | | || ||     | || |   | |   |  || |  |||| |||
Db       1424 TCAACATCCAGACATTTGGGGAGACCAAGATGTCCAATGCCACCCTCGTCAGCTACA 1480
```

RESULT 6
AX268719
LOCUS AX268719 2220 bp DNA linear PAT 29-OCT-2001
DEFINITION Sequence 50 from Patent WO0174905.
ACCESSION AX268719
VERSION AX268719.1 GI:16541803
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Young,R.J.
TITLE Compounds for targeting
JOURNAL Patent: WO 0174905-A 50 11-OCT-2001;
ANTISOMA RESEARCH LIMITED (GB)
FEATURES Location/Qualifiers
source 1. .2220
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Humanised HMFG1 heavy chain - DNase I fusion"
ORIGIN

Query Match 60.6%; Score 697; DB 6; Length 2220;
Best Local Similarity 93.6%; Pred. No. 1.2e-136;
Matches 727; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

```
Qy          5 TGGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 64
              | || ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        704 TTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 763

Qy         65 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        764 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 823

Qy        125 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        824 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 883

Qy        185 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        884 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 943

Qy        245 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 304
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        944 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 1003
```

```
Qy        305 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 364
Db       1004 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 1063

Qy        365 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 424
Db       1064 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 1123

Qy        425 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 484
Db       1124 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 1183

Qy        485 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 544
Db       1184 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 1243

Qy        545 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 604
Db       1244 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 1303

Qy        605 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 664
Db       1304 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 1363

Qy        665 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTTCAGG 724
Db       1364 ACTACACGCAGAAGAGCCTCTCCCTGTCCCCGGGGAGCGGCGGGCTGAAGATCGCAGCCT 1423

Qy        725 ACGACACCAAAACCTTAATTAAAACGATCGTTACGCGTATCAACGACATCAGTCACA 781
Db       1424 TCAACATCCAGACATTTGGGGAGACCAAGATGTCCAATGCCACCCTCGTCAGCTACA 1480
```

RESULT 7
AX039180
LOCUS AX039180 1288 bp DNA linear PAT 18-NOV-2000
DEFINITION Sequence 37 from Patent WO0063253.
ACCESSION AX039180
VERSION AX039180.1 GI:11229320
KEYWORDS .
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Hsu,H. and Meng,S.Y.
TITLE Agp-1 fusion protein compositions and methods
JOURNAL Patent: WO 0063253-A 37 26-OCT-2000;
Amgen Inc. (US)
FEATURES Location/Qualifiers
source 1. .1288
/organism="Mus musculus"
/mol_type="unassigned DNA"
/db_xref="taxon:10090"
ORIGIN

Query Match 60.6%; Score 696.8; DB 6; Length 1288;
Best Local Similarity 99.7%; Pred. No. 1.4e-136;
Matches 698; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy          5 TGGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 64
Db         78 TTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 137

Qy         65 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 124
Db        138 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 197

Qy        125 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 184
Db        198 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 257

Qy        185 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 244
Db        258 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 317

Qy        245 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 304
Db        318 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 377

Qy        305 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 364
Db        378 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 437

Qy        365 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 424
Db        438 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 497

Qy        425 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 484
Db        498 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 557

Qy        485 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 544
Db        558 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 617

Qy        545 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 604
Db        618 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 677

Qy        605 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 664
Db        678 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 737

Qy        665 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAGT 704
Db        738 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAGT 777
```

RESULT 8
AX039184
LOCUS AX039184 1304 bp DNA linear PAT 18-NOV-2000
DEFINITION Sequence 41 from Patent WO0063253.
ACCESSION AX039184
VERSION AX039184.1 GI:11229322
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Hsu,H. and Meng,S.Y.
TITLE Agp-1 fusion protein compositions and methods
JOURNAL Patent: WO 0063253-A 41 26-OCT-2000;
Amgen Inc. (US)
FEATURES Location/Qualifiers
source 1. .1304
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
ORIGIN

Query Match 60.5%; Score 695.8; DB 6; Length 1304;
Best Local Similarity 99.7%; Pred. No. 2.3e-136;
Matches 697; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy          5 TGGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 64
Db         78 TTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 137

Qy         65 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 124
Db        138 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 197

Qy        125 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 184
Db        198 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 257
```

```
Qy        185 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        258 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 317

Qy        245 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 304
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        318 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 377

Qy        305 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        378 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 437

Qy        365 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        438 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 497

Qy        425 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 484
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        498 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 557

Qy        485 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 544
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        558 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 617

Qy        545 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 604
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        618 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 677

Qy        605 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 664
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        678 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 737

Qy        665 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAG 703
              |||||||||||||||||||||||||||||||||||||||
Db        738 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAG 776
```

RESULT 9
AX268709
LOCUS AX268709 2196 bp DNA linear PAT 29-OCT-2001
DEFINITION Sequence 40 from Patent WO0174905.
ACCESSION AX268709
VERSION AX268709.1 GI:16541798
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Young,R.J.
TITLE Compounds for targeting
JOURNAL Patent: WO 0174905-A 40 11-OCT-2001;
ANTISOMA RESEARCH LIMITED (GB)
FEATURES Location/Qualifiers
source 1. .2196
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Humanised HMFG1 heavy chain - DNase I fusion"
ORIGIN

Query Match 60.5%; Score 695.8; DB 6; Length 2196;
Best Local Similarity 99.7%; Pred. No. 2.2e-136;
Matches 697; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy          5 TGGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 64
              | || ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        704 TTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 763

Qy         65 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        764 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 823

Qy        125 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        824 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 883

Qy        185 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        884 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 943

Qy        245 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 304
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        944 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 1003

Qy        305 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1004 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 1063

Qy        365 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1064 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 1123

Qy        425 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 484
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1124 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 1183

Qy        485 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 544
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1184 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 1243

Qy        545 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 604
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1244 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 1303

Qy        605 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 664
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1304 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 1363

Qy        665 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAG 703
              |||||||||||||||||||||||||||||||||||||||
Db       1364 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAG 1402
```

RESULT 10
AX268715
LOCUS AX268715 2226 bp DNA linear PAT 29-OCT-2001
DEFINITION Sequence 46 from Patent WO0174905.
ACCESSION AX268715
VERSION AX268715.1 GI:16541801
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Young,R.J.
TITLE Compounds for targeting
JOURNAL Patent: WO 0174905-A 46 11-OCT-2001;
ANTISOMA RESEARCH LIMITED (GB)
FEATURES Location/Qualifiers
source 1. .2226
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Humanised HMFG1 heavy chain - DNase I fusion"
ORIGIN

Query Match 60.5%; Score 695.8; DB 6; Length 2226;
Best Local Similarity 99.7%; Pred. No. 2.2e-136;
Matches 697; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy          5 TGGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 64
              | || ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        704 TTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 763

Qy         65 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 124
```

```
Db        764 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 823

Qy        125 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 184

Db        824 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 883

Qy        185 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 244

Db        884 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 943

Qy        245 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 304

Db        944 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 1003

Qy        305 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 364

Db       1004 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 1063

Qy        365 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 424

Db       1064 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 1123

Qy        425 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 484

Db       1124 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 1183

Qy        485 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 544

Db       1184 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 1243

Qy        545 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 604

Db       1244 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 1303

Qy        605 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 664

Db       1304 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 1363

Qy        665 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAG 703

Db       1364 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAG 1402
```

```
RESULT 11
AR381777
LOCUS       AR381777               1720 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 52 from patent US 6610286.
ACCESSION   AR381777
VERSION     AR381777.1  GI:40089999
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1720)
  AUTHORS   Thompson,P., Foster,D.C., Xu,W., Kelly,J.D., Blumberg,H. and
            Chandrasekher,Y.A.
  TITLE     Method for treating inflammation using soluble receptors to
            interleukin-20
  JOURNAL   Patent: US 6610286-A 52 26-AUG-2003;
FEATURES             Location/Qualifiers
     source          1. .1720
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             60.5%;  Score 695.6;  DB 6;  Length 1720;
  Best Local Similarity   99.4%;  Pred. No. 2.5e-136;
  Matches  698;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          5 TGGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 64

Db       1016 TTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 1075
```

```
Qy         65 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 124

Db       1076 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 1135

Qy        125 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 184

Db       1136 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 1195

Qy        185 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 244

Db       1196 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 1255

Qy        245 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 304

Db       1256 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 1315

Qy        305 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 364

Db       1316 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 1375

Qy        365 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 424

Db       1376 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 1435

Qy        425 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 484

Db       1436 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 1495

Qy        485 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 544

Db       1496 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 1555

Qy        545 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 604

Db       1556 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 1615

Qy        605 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 664

Db       1616 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 1675

Qy        665 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAGTAC 706

Db       1676 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGAC 1717
```

```
RESULT 12
AX180193
LOCUS       AX180193               1720 bp    DNA     linear   PAT 06-AUG-2001
DEFINITION  Sequence 52 from Patent WO0146261.
ACCESSION   AX180193
VERSION     AX180193.1  GI:15132221
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Thompson,P., Foster,D.C., Wenfeng,X., Madden,K.L., Kelly,J.D.,
            Sprecher,C.A., Blumberg,H., Eagan,M.A., Jaspers,S.R.,
            Chandrasekher,J.A. and Novak,J.E.
  TITLE     Method for treating inflammation
  JOURNAL   Patent: WO 0146261-A 52 28-JUN-2001;
            ZymoGenetics, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .1720
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
     CDS             1. .1716
                     /note="unnamed protein product"
                     /codon_start=1
                     /protein_id="CAC49992.1"
```

/db_xref="GI:15132222"
/db_xref="REMTREMBL:CAC49992"
/translation="MRAPGRPALRPLLLLLLAAPWGRAVPCVSGGLPKPANITFLSIN
MKNVLQWTPPEGLQGVKVTYTVQYFIYGQKKWLNKSECRNINRTYCDLSAETSDYEHQ
YYAKVKAIWGTKCSKWAESGRFYPFLETQIGPPEVALTTDEKSISVVLTAPEKWKRNP
EDLPVSMQQIYSNLKYNVSVLNTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVESFVP
GPPRRAQPSEKQCARTLKDQSSEASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPE
PVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTK
VDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH
EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK
ALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESN
GQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS
LSPGK"

ORIGIN

Query Match 60.5%; Score 695.6; DB 6; Length 1720;
Best Local Similarity 99.4%; Pred. No. 2.5e-136;
Matches 698; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
Qy          5 TGGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 64
              | || ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1016 TTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 1075

Qy         65 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1076 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 1135

Qy         125 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1136 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 1195

Qy         185 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1196 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 1255

Qy         245 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 304
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1256 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 1315

Qy         305 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1316 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 1375

Qy         365 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1376 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 1435

Qy         425 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 484
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1436 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 1495

Qy         485 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 544
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1496 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 1555

Qy         545 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 604
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1556 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 1615

Qy         605 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 664
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1616 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 1675

Qy         665 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAGTAC 706
              ||||||||||||||||||||||||||||||||||||||   ||
Db       1676 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGAC 1717
```

RESULT 13
AX180693
LOCUS AX180693 1720 bp DNA linear PAT 06-AUG-2001
DEFINITION Sequence 52 from Patent WO0146232.
ACCESSION AX180693

VERSION AX180693.1 GI:15132566
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Foster,D.C., Xu,W., Madden,K.L., Kelly,J.D., Sprecher,C.A.,
Brandt,C.S., Rixon,M.W., Presnell,S.R. and Fox,B.A.
TITLE Soluble interleukin-20 receptor
JOURNAL Patent: WO 0146232-A 52 28-JUN-2001;
ZymoGenetics, Inc. (US)
FEATURES Location/Qualifiers
source 1. .1720
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
CDS 1. .1716
/note="unnamed protein product"
/codon_start=1
/protein_id="CAC50002.1"
/db_xref="GI:15132567"
/db_xref="REMTREMBL:CAC50002"
/translation="MRAPGRPALRPLLLLLLAAPWGRAVPCVSGGLPKPANITFLSIN
MKNVLQWTPPEGLQGVKVTYTVQYFIYGQKKWLNKSECRNINRTYCDLSAETSDYEHQ
YYAKVKAIWGTKCSKWAESGRFYPFLETQIGPPEVALTTDEKSISVVLTAPEKWKRNP
EDLPVSMQQIYSNLKYNVSVLNTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVESFVP
GPPRRAQPSEKQCARTLKDQSSEASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPE
PVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTK
VDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH
EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK
ALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESN
GQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS
LSPGK"

ORIGIN

Query Match 60.5%; Score 695.6; DB 6; Length 1720;
Best Local Similarity 99.4%; Pred. No. 2.5e-136;
Matches 698; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
Qy          5 TGGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 64
              | || ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1016 TTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 1075

Qy         65 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1076 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 1135

Qy         125 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1136 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 1195

Qy         185 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1196 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 1255

Qy         245 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 304
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1256 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 1315

Qy         305 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1316 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 1375

Qy         365 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1376 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 1435

Qy         425 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 484
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1436 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 1495

Qy         485 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 544
```

```
Db       1496 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 1555

Qy        545 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 604
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1556 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 1615

Qy        605 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 664
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1616 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 1675

Qy        665 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAGTAC 706
              |||||||||||||||||||||||||||||||||||||||  ||
Db       1676 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGAC 1717
```

```
RESULT 14
AX406502
LOCUS       AX406502               1720 bp    DNA     linear   PAT 14-JUN-2002
DEFINITION  Sequence 29 from Patent WO0222153.
ACCESSION   AX406502
VERSION     AX406502.1  GI:21439525
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Chandrasekher,Y.A. and Jaspers,S.R.
  TITLE     Use of a polypeptide comprising the extracellular domains of
            il-20ra and il-20rb for the treatment of inflammation
  JOURNAL   Patent: WO 0222153-A 29 21-MAR-2002;
            ZymoGenetics, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .1720
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
     CDS             1. .1716
                     /note="unnamed protein product"
                     /codon_start=1
                     /protein_id="CAD35141.1"
                     /db_xref="GI:21439526"
                     /db_xref="REMTREMBL:CAD35141"
                     /translation="MRAPGRPALRPLLLLLLAAPWGRAVPCVSGGLPKPANITFLSIN
                     MKNVLQWTPPEGLQGVKVTYTVQYFIYGQKKWLNKSECRNINRTYCDLSAETSDYEHQ
                     YYAKVKAIWGTKCSKWAESGRFYPFLETQIGPPEVALTTDEKSISVVLTAPEKWKRNP
                     EDLPVSMQQIYSNLKYNVSVLNTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVESFVP
                     GPPRRAQPSEKQCARTLKDQSSEASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPE
                     PVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTK
                     VDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH
                     EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK
                     ALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESN
                     GQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS
                     LSPGK"
ORIGIN

  Query Match           60.5%;  Score 695.6;  DB 6;  Length 1720;
  Best Local Similarity   99.4%;  Pred. No. 2.5e-136;
  Matches  698;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          5 TGGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 64
              | || ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1016 TTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 1075

Qy         65 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1076 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 1135

Qy        125 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1136 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 1195
```

```
Qy        185 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1196 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 1255

Qy        245 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 304
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1256 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 1315

Qy        305 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1316 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 1375

Qy        365 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1376 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 1435

Qy        425 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 484
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1436 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 1495

Qy        485 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 544
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1496 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 1555

Qy        545 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 604
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1556 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 1615

Qy        605 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 664
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1616 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 1675

Qy        665 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAGTAC 706
              |||||||||||||||||||||||||||||||||||||||  ||
Db       1676 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGAC 1717
```

```
RESULT 15
AX357958
LOCUS       AX357958               1443 bp    DNA     linear   PAT 13-FEB-2002
DEFINITION  Sequence 4 from Patent WO0194413.
ACCESSION   AX357958
VERSION     AX357958.1  GI:18674736
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Mikesell,G.E., Chang,H., Finger,J.N., Yang,G., Lu,P., Zhou,X.D. and
            Peach,R.
  TITLE     B7-related nucleic acids and polypeptides and their uses for
            immunomodulation
  JOURNAL   Patent: WO 0194413-A 4 13-DEC-2001;
            Bristol-Myers Squibb Company (US)
FEATURES             Location/Qualifiers
     source          1. .1443
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic fusion construct"
ORIGIN

  Query Match           60.5%;  Score 695.4;  DB 6;  Length 1443;
  Best Local Similarity   99.9%;  Pred. No. 2.7e-136;
  Matches  696;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 GGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCT 65
              ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        744 GGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCT 803

Qy         66 GGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCG 125
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        804 GGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCG 863
```

```
Qy        126 GACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTT 185
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        864 GACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTT 923

Qy        186 CAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCA 245
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        924 CAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCA 983

Qy        246 GTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAA 305
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        984 GTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAA 1043

Qy        306 TGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAAC 365
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1044 TGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAAC 1103

Qy        366 CATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCG 425
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1104 CATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCG 1163

Qy        426 GGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAG 485
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1164 GGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAG 1223

Qy        486 CGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCC 545
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1224 CGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCC 1283

Qy        546 TCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAG 605
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1284 TCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAG 1343

Qy        606 CAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCA 665
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1344 CAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCA 1403

Qy        666 CTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 702
              |||||||||||||||||||||||||||||||||||||
Db       1404 CTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 1440
```

Search completed: October 18, 2004, 01:19:39
Job time : 4416.65 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 17, 2004, 15:27:13 ; Search time 4046.52 Seconds
(without alignments)
10355.995 Million cell updates/sec

Title: US-10-679-999-7
Perfect score: 1150
Sequence: 1 CATATGGAACCCAAATCTTG.....TCCGGGTTGTTAATGGATCC 1150

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	694.8	60.4	871	4	BG753979	BG753979 602709506
2	694.8	60.4	983	5	BQ708975	BQ708975 AGENCOURT
3	694	60.3	843	4	BM007897	BM007897 603617582
4	693.8	60.3	941	5	BQ712021	BQ712021 AGENCOURT
5	693.2	60.3	925	5	BQ709152	BQ709152 AGENCOURT
6	693.2	60.3	1022	3	CR611254	CR611254 full-leng
7	693.2	60.3	1048	3	CR595172	CR595172 full-leng
8	693.2	60.3	1090	3	CR612308	CR612308 full-leng
9	693.2	60.3	1091	3	CR604961	CR604961 full-leng
10	693.2	60.3	1093	3	CR616804	CR616804 full-leng
11	693.2	60.3	1098	3	CR626477	CR626477 full-leng
12	693.2	60.3	1100	3	CR612813	CR612813 full-leng
13	693.2	60.3	1102	3	CR601777	CR601777 full-leng
14	693.2	60.3	1102	3	CR625051	CR625051 full-leng
15	693.2	60.3	1103	3	CR595194	CR595194 full-leng
16	693.2	60.3	1104	3	CR591904	CR591904 full-leng
17	693.2	60.3	1106	3	CR613460	CR613460 full-leng
18	693.2	60.3	1106	3	CR620071	CR620071 full-leng
19	693.2	60.3	1107	3	CR598548	CR598548 full-leng
20	693.2	60.3	1109	3	CR614200	CR614200 full-leng
21	693.2	60.3	1109	3	CR619687	CR619687 full-leng
22	693.2	60.3	1111	3	CR606782	CR606782 full-leng
23	693.2	60.3	1114	3	CR593349	CR593349 full-leng
24	693.2	60.3	1114	3	CR618075	CR618075 full-leng
25	693.2	60.3	1118	3	CR613511	CR613511 full-leng
26	693.2	60.3	1120	3	CR619868	CR619868 full-leng
27	693.2	60.3	1124	3	CR611468	CR611468 full-leng
28	693.2	60.3	1136	3	CR598462	CR598462 full-leng
29	693.2	60.3	1142	3	CR598316	CR598316 full-leng
30	693.2	60.3	1179	3	CR607277	CR607277 full-leng
31	693.2	60.3	1287	3	CR611016	CR611016 full-leng
32	693.2	60.3	1289	3	CR594000	CR594000 full-leng
33	692.4	60.2	973	5	BQ706204	BQ706204 AGENCOURT
34	692.2	60.2	851	5	BX346946	BX346946 BX346946
35	691.6	60.1	919	5	BQ709339	BQ709339 AGENCOURT
36	691	60.1	897	5	BQ709144	BQ709144 AGENCOURT
37	690	60.0	947	5	BQ709771	BQ709771 AGENCOURT
38	689.8	60.0	881	5	BQ711291	BQ711291 AGENCOURT
c 39	687.8	59.8	1013	5	BX360518	BX360518 BX360518
40	687.4	59.8	757	4	BG674795	BG674795 602620925
41	687.4	59.8	914	5	BQ712363	BQ712363 AGENCOURT
42	685.6	59.6	856	5	BQ709859	BQ709859 AGENCOURT
43	682.8	59.4	892	4	BG397723	BG397723 602438784
44	682.8	59.4	897	4	BM008412	BM008412 603617406
45	682.8	59.4	902	5	BU146962	BU146962 AGENCOURT

ALIGNMENTS

RESULT 1
BG753979
LOCUS BG753979 871 bp mRNA linear EST 15-MAY-2001
DEFINITION 602709506F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4846201 5', mRNA sequence.
ACCESSION BG753979
VERSION BG753979.1 GI:14064632
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 871)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1686 row: k column: 02
High quality sequence stop: 848.
FEATURES Location/Qualifiers
source 1. .871
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4846201"
/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_48"
/note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
ORIGIN

```
  Query Match             60.4%;  Score 694.8;  DB 4;  Length 871;
  Best Local Similarity   99.7%;  Pred. No. 3.9e-169;
  Matches  696;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 TGGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 64
              | || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         20 TTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 79

Qy         65 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         80 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 139

Qy        125 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 199

Qy        185 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        200 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 259

Qy        245 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 304
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        260 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 319

Qy        305 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        320 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 379

Qy        365 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        380 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 439

Qy        425 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 484
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        440 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 499

Qy        485 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 544
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        500 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 559

Qy        545 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 604
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        560 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 619

Qy        605 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 664
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        620 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 679

Qy        665 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 702
              |||||||||||||||||||||||||||||||||||||||
Db        680 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 717


RESULT 2
BQ708975
LOCUS       BQ708975                983 bp    mRNA    linear   EST 16-JUL-2002
DEFINITION  AGENCOURT_8353514 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6279683
            5', mRNA sequence.
ACCESSION   BQ708975
VERSION     BQ708975.1  GI:21847874
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 983)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2469  row: k  column: 12
            High quality sequence stop: 604.
FEATURES             Location/Qualifiers
     source          1. .983
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6279683"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_113"
                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed  by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of  California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
ORIGIN

  Query Match             60.4%;  Score 694.8;  DB 5;  Length 983;
  Best Local Similarity   99.7%;  Pred. No. 4e-169;
  Matches  696;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 TGGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 64
              | || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          7 TTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 66

Qy         65 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 126

Qy        125 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 186

Qy        185 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 246

Qy        245 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 304
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 306

Qy        305 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 366

Qy        365 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 426

Qy        425 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 484
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 486

Qy        485 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 544
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 546

Qy        545 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 604
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 606

Qy        605 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 664
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 666
```

```
Qy        665 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 702
              |||||||||||||||||||||||||||||||||||||||
Db        667 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 704


RESULT 3
BM007897
LOCUS       BM007897                843 bp    mRNA    linear   EST 30-OCT-2001
DEFINITION  603617582F1 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:5450469 5',
            mRNA sequence.
ACCESSION   BM007897
VERSION     BM007897.1  GI:16522238
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 843)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1939  row: d  column: 22
            High quality sequence stop: 833.
FEATURES             Location/Qualifiers
     source          1. .843
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5450469"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_113"
                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed  by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of  California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
ORIGIN

  Query Match             60.3%;  Score 694;  DB 4;  Length 843;
  Best Local Similarity   99.3%;  Pred. No. 6.3e-169;
  Matches  697;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          5 TGGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 64
              | || ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         91 TTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 150

Qy         65 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        151 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 210

Qy        125 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        211 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 270

Qy        185 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        271 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 330

Qy        245 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 304
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        331 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 390

Qy        305 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        391 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 450

Qy        365 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        451 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 510

Qy        425 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 484
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        511 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 570

Qy        485 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 544
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        571 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 630

Qy        545 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 604
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        631 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 690

Qy        605 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 664
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        691 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 750

Qy        665 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAGTAC 706
              | ||||||||||||||||||||||||||||||||||  ||
Db        751 ATTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGAC 792


RESULT 4
BQ712021
LOCUS       BQ712021                941 bp    mRNA    linear   EST 16-JUL-2002
DEFINITION  AGENCOURT_8418162 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6281403
            5', mRNA sequence.
ACCESSION   BQ712021
VERSION     BQ712021.1  GI:21850920
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 941)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2474  row: c  column: 04
            High quality sequence stop: 638.
FEATURES             Location/Qualifiers
     source          1. .941
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6281403"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_113"
                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed  by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of  California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
```

ORIGIN

Query Match 60.3%; Score 693.8; DB 5; Length 941;
Best Local Similarity 99.6%; Pred. No. 7.3e-169;
Matches 695; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy          5 TGGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 64
              | || ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         33 TTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 92

Qy         65 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         93 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 152

Qy        125 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        153 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 212

Qy        185 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        213 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 272

Qy        245 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 304
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        273 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 332

Qy        305 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        333 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 392

Qy        365 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        393 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 452

Qy        425 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 484
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        453 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 512

Qy        485 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 544
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        513 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 572

Qy        545 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 604
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        573 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 632

Qy        605 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 664
              |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db        633 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGANGCTCTGCACAACC 692

Qy        665 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 702
              |||||||||||||||||||||||||||||||||||||
Db        693 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 730
```

RESULT 5
BQ709152
LOCUS BQ709152 925 bp mRNA linear EST 16-JUL-2002
DEFINITION AGENCOURT_8485151 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6301245 5', mRNA sequence.
ACCESSION BQ709152
VERSION BQ709152.1 GI:21848051
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 925)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2516 row: m column: 22
High quality sequence stop: 739.

FEATURES Location/Qualifiers
source 1. .925
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6301245"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_113"
/note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 60.3%; Score 693.2; DB 5; Length 925;
Best Local Similarity 99.6%; Pred. No. 1e-168;
Matches 695; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy          5 TGGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 64
              | || ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         31 TTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 90

Qy         65 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         91 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 150

Qy        125 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        151 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 210

Qy        185 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        211 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 270

Qy        245 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 304
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        271 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 330

Qy        305 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        331 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 390

Qy        365 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        391 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 450

Qy        425 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 484
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        451 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 510

Qy        485 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 544
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        511 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 570

Qy        545 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 604
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        571 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 630

Qy        605 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 664
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        631 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 690

Qy        665 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 702
              ||||||| |||||||||||||||||||||||||||||||
Db        691 ACTACACACAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 728


RESULT 6
CR611254
LOCUS       CR611254               1022 bp    mRNA    linear   HTC 21-JUL-2004
DEFINITION  full-length cDNA clone CS0DE007YJ17 of Placenta of Homo sapiens
            (human).
ACCESSION   CR611254
VERSION     CR611254.1  GI:50492061
KEYWORDS    HTC; CNSLT_cDNA.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1022)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished
  REMARK    Contact : Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue
REFERENCE   2  (bases 1 to 1022)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen.
FEATURES             Location/Qualifiers
     source          1. .1022
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DE007YJ17"
                     /tissue_type="Placenta"
                     /plasmid="pCMVSPORT_6"
ORIGIN

  Query Match             60.3%;  Score 693.2;  DB 3;  Length 1022;
  Best Local Similarity   99.6%;  Pred. No. 1.1e-168;
  Matches  695;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          5 TGGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 64
              | || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 TTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 365

Qy         65 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 425

Qy        125 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 485

Qy        185 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 545

Qy        245 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 304
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        546 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 605

Qy        305 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        606 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 665

Qy        365 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        666 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 725

Qy        425 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 484
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        726 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 785

Qy        485 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 544
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        786 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 845

Qy        545 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 604
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        846 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 905

Qy        605 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 664
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        906 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 965

Qy        665 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 702
              ||||||| |||||||||||||||||||||||||||||||
Db        966 ACTACACACAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 1003


RESULT 7
CR595172
LOCUS       CR595172               1048 bp    mRNA    linear   HTC 21-JUL-2004
DEFINITION  full-length cDNA clone CS0DI040YA16 of Placenta Cot 25-normalized
            of Homo sapiens (human).
ACCESSION   CR595172
VERSION     CR595172.1  GI:50475979
KEYWORDS    HTC; CNSLT_cDNA.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1048)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished
  REMARK    Contact : Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue
REFERENCE   2  (bases 1 to 1048)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen.
FEATURES             Location/Qualifiers
     source          1. .1048
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DI040YA16"
                     /tissue_type="Placenta Cot 25-normalized"
                     /plasmid="pCMVSPORT_6"
ORIGIN

  Query Match             60.3%;  Score 693.2;  DB 3;  Length 1048;
  Best Local Similarity   99.6%;  Pred. No. 1.1e-168;
  Matches  695;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          5 TGGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 64
              | || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        319 TTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 378

Qy         65 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        379 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 438

Qy        125 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        439 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 498

Qy        185 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        499 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 558

Qy        245 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 304
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        559 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 618

Qy        305 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        619 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 678

Qy        365 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        679 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 738

Qy        425 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 484
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        739 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 798

Qy        485 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 544
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        799 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 858

Qy        545 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 604
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        859 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 918

Qy        605 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 664
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        919 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 978

Qy        665 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 702
              ||||||| |||||||||||||||||||||||||||||
Db        979 ACTACACACAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 1016


RESULT 8
CR612308
LOCUS       CR612308               1090 bp    mRNA    linear   HTC 21-JUL-2004
DEFINITION  full-length cDNA clone CS0DI071YG21 of Placenta Cot 25-normalized
            of Homo sapiens (human).
ACCESSION   CR612308
VERSION     CR612308.1  GI:50493115
KEYWORDS    HTC; CNSLT_cDNA.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1090)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished
  REMARK    Contact : Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue
REFERENCE   2  (bases 1 to 1090)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen.
FEATURES             Location/Qualifiers
     source          1. .1090
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DI071YG21"
                     /tissue_type="Placenta Cot 25-normalized"
                     /plasmid="pCMVSPORT_6"
ORIGIN

  Query Match             60.3%;  Score 693.2;  DB 3;  Length 1090;
  Best Local Similarity   99.6%;  Pred. No. 1.1e-168;
  Matches  695;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          5 TGGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 64
              | || ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 TTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 365

Qy         65 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 425

Qy        125 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 485

Qy        185 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 545

Qy        245 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 304
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        546 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 605

Qy        305 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 665

Qy        365 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        666 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 725

Qy        425 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 484
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        726 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 785

Qy        485 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 544
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        786 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 845

Qy        545 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 604
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        846 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 905

Qy        605 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 664
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        906 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 965

Qy        665 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 702
              ||||||| |||||||||||||||||||||||||||||
Db        966 ACTACACACAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 1003


RESULT 9
CR604961
LOCUS       CR604961               1091 bp    mRNA    linear   HTC 21-JUL-2004
DEFINITION  full-length cDNA clone CS0DI009YJ10 of Placenta Cot 25-normalized
            of Homo sapiens (human).
ACCESSION   CR604961
```

```
VERSION     CR604961.1  GI:50485768
KEYWORDS    HTC; CNSLT_cDNA.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1091)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished
  REMARK    Contact : Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue
REFERENCE   2  (bases 1 to 1091)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen.
FEATURES             Location/Qualifiers
     source          1. .1091
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DI009YJ10"
                     /tissue_type="Placenta Cot 25-normalized"
                     /plasmid="pCMVSPORT_6"
ORIGIN

  Query Match             60.3%;  Score 693.2;  DB 3;  Length 1091;
  Best Local Similarity   99.6%;  Pred. No. 1.1e-168;
  Matches  695;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          5 TGGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 64
              | || ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 TTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 365

Qy         65 TGGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 TGGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 425

Qy        125 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 485

Qy        185 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 545

Qy        245 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 304
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        546 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 605

Qy        305 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 665

Qy        365 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        666 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 725

Qy        425 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 484
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        726 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 785

Qy        485 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 544
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        786 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 845

Qy        545 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 604
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        846 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 905

Qy        605 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 664
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        906 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 965

Qy        665 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 702
              ||||||| |||||||||||||||||||||||||||||||
Db        966 ACTACACACAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 1003


RESULT 10
CR616804
LOCUS       CR616804               1093 bp    mRNA    linear   HTC 21-JUL-2004
DEFINITION  full-length cDNA clone CS0DI048YC07 of Placenta Cot 25-normalized
            of Homo sapiens (human).
ACCESSION   CR616804
VERSION     CR616804.1  GI:50497611
KEYWORDS    HTC; CNSLT_cDNA.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1093)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished
  REMARK    Contact : Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue
REFERENCE   2  (bases 1 to 1093)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen.
FEATURES             Location/Qualifiers
     source          1. .1093
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DI048YC07"
                     /tissue_type="Placenta Cot 25-normalized"
                     /plasmid="pCMVSPORT_6"
ORIGIN

  Query Match             60.3%;  Score 693.2;  DB 3;  Length 1093;
  Best Local Similarity   99.6%;  Pred. No. 1.1e-168;
  Matches  695;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          5 TGGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 64
              | || ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 TTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 365

Qy         65 TGGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 TGGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 425

Qy        125 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 485

Qy        185 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 545
```

```
Qy        245 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 304
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        546 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 605

Qy        305 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 665

Qy        365 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        666 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 725

Qy        425 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 484
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        726 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 785

Qy        485 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 544
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        786 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 845

Qy        545 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 604
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        846 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 905

Qy        605 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 664
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        906 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 965

Qy        665 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 702
              ||||||| |||||||||||||||||||||||||||||||
Db        966 ACTACACACAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 1003
```

RESULT 11
CR626477
LOCUS CR626477 1098 bp mRNA linear HTC 21-JUL-2004
DEFINITION full-length cDNA clone CS0CAP001YI13 of Thymus of Homo sapiens (human).
ACCESSION CR626477
VERSION CR626477.1 GI:50507284
KEYWORDS HTC; CNSLT_cDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1098)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InVitroGen Corporation 1600 Faraday Avenue
REFERENCE 2 (bases 1 to 1098)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
FEATURES Location/Qualifiers
source 1. .1098
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0CAP001YI13"
/tissue_type="Thymus"
/plasmid="pCMVSPORT_6"
ORIGIN

```
  Query Match            60.3%;  Score 693.2;  DB 3;  Length 1098;
  Best Local Similarity  99.6%;  Pred. No. 1.1e-168;
  Matches  695;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          5 TGGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 64
              | || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 TTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 365

Qy         65 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 425

Qy        125 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 485

Qy        185 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 545

Qy        245 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 304
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        546 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 605

Qy        305 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 665

Qy        365 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        666 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 725

Qy        425 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 484
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        726 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 785

Qy        485 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 544
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        786 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 845

Qy        545 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 604
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        846 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 905

Qy        605 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 664
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        906 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 965

Qy        665 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 702
              ||||||| |||||||||||||||||||||||||||||||
Db        966 ACTACACACAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 1003
```

RESULT 12
CR612813
LOCUS CR612813 1100 bp mRNA linear HTC 21-JUL-2004
DEFINITION full-length cDNA clone CS0DI081YF02 of Placenta Cot 25-normalized of Homo sapiens (human).
ACCESSION CR612813
VERSION CR612813.1 GI:50493620
KEYWORDS HTC; CNSLT_cDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1100)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InVitroGen Corporation 1600 Faraday Avenue

```
REFERENCE   2  (bases 1 to 1100)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen.
FEATURES             Location/Qualifiers
     source          1. .1100
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DI081YF02"
                     /tissue_type="Placenta Cot 25-normalized"
                     /plasmid="pCMVSPORT_6"
ORIGIN

  Query Match             60.3%;  Score 693.2;  DB 3;  Length 1100;
  Best Local Similarity   99.6%;  Pred. No. 1.1e-168;
  Matches  695;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          5 TGGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 64
              | || ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 TTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 361

Qy         65 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 421

Qy        125 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        422 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 481

Qy        185 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        482 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 541

Qy        245 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 304
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        542 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 601

Qy        305 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        602 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 661

Qy        365 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        662 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 721

Qy        425 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 484
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        722 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 781

Qy        485 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 544
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        782 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 841

Qy        545 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 604
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        842 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 901

Qy        605 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 664
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        902 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 961

Qy        665 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 702
              ||||||| |||||||||||||||||||||||||||||
Db        962 ACTACACACAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 999
```

```
RESULT 13
CR601777
LOCUS       CR601777               1102 bp    mRNA    linear   HTC 21-JUL-2004
DEFINITION  full-length cDNA clone CS0CAP008YF07 of Thymus of Homo sapiens
            (human).
ACCESSION   CR601777
VERSION     CR601777.1  GI:50482584
KEYWORDS    HTC; CNSLT_cDNA.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1102)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished
  REMARK    Contact : Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue
REFERENCE   2  (bases 1 to 1102)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen.
FEATURES             Location/Qualifiers
     source          1. .1102
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0CAP008YF07"
                     /tissue_type="Thymus"
                     /plasmid="pCMVSPORT_6"
ORIGIN

  Query Match             60.3%;  Score 693.2;  DB 3;  Length 1102;
  Best Local Similarity   99.6%;  Pred. No. 1.1e-168;
  Matches  695;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          5 TGGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 64
              | || ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 TTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 361

Qy         65 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 421

Qy        125 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        422 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 481

Qy        185 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        482 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 541

Qy        245 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 304
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        542 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 601

Qy        305 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        602 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 661

Qy        365 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        662 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 721
```

```
Qy        425 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 484
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        722 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 781

Qy        485 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 544
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        782 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 841

Qy        545 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 604
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        842 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 901

Qy        605 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 664
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        902 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 961

Qy        665 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 702
              ||||||| ||||||||||||||||||||||||||||||
Db        962 ACTACACACAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 999
```

RESULT 14
CR625051
LOCUS CR625051 1102 bp mRNA linear HTC 21-JUL-2004
DEFINITION full-length cDNA clone CS0DI059YL06 of Placenta Cot 25-normalized of Homo sapiens (human).
ACCESSION CR625051
VERSION CR625051.1 GI:50505858
KEYWORDS HTC; CNSLT_cDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1102)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL *Unpublished*
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InVitroGen Corporation 1600 Faraday Avenue
REFERENCE 2 (bases 1 to 1102)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
FEATURES Location/Qualifiers
source 1. .1102
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI059YL06"
/tissue_type="Placenta Cot 25-normalized"
/plasmid="pCMVSPORT_6"
ORIGIN

Query Match 60.3%; Score 693.2; DB 3; Length 1102;
Best Local Similarity 99.6%; Pred. No. 1.1e-168;
Matches 695; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy          5 TGGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 64
              | || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 TTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 365

Qy         65 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 425

Qy        125 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 485

Qy        185 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 545

Qy        245 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 304
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        546 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 605

Qy        305 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 665

Qy        365 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        666 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 725

Qy        425 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 484
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        726 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 785

Qy        485 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 544
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        786 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 845

Qy        545 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 604
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        846 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 905

Qy        605 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 664
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        906 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 965

Qy        665 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 702
              ||||||| ||||||||||||||||||||||||||||||
Db        966 ACTACACACAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 1003
```

RESULT 15
CR595194
LOCUS CR595194 1103 bp mRNA linear HTC 21-JUL-2004
DEFINITION full-length cDNA clone CS0DE010YH13 of Placenta of Homo sapiens (human).
ACCESSION CR595194
VERSION CR595194.1 GI:50476001
KEYWORDS HTC; CNSLT_cDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1103)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InVitroGen Corporation 1600 Faraday Avenue
REFERENCE 2 (bases 1 to 1103)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
FEATURES Location/Qualifiers
source 1. .1103

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DE010YH13"
/tissue_type="Placenta"
/plasmid="pCMVSPORT_6"

ORIGIN

Query Match 60.3%; Score 693.2; DB 3; Length 1103;
Best Local Similarity 99.6%; Pred. No. 1.1e-168;
Matches 695; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy          5 TGGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 64
              | || ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 TTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 361

Qy         65 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 421

Qy        125 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        422 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 481

Qy        185 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        482 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 541

Qy        245 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 304
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        542 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 601

Qy        305 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        602 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 661

Qy        365 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        662 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 721

Qy        425 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 484
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        722 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 781

Qy        485 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 544
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        782 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 841

Qy        545 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 604
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        842 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 901

Qy        605 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 664
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        902 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 961

Qy        665 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 702
              ||||||| ||||||||||||||||||||||||||||||
Db        962 ACTACACACAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 999
```

Search completed: October 18, 2004, 03:14:25
Job time : 4050.64 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 17, 2004, 15:27:12 ; Search time 596.39 Seconds
(without alignments)
10122.301 Million cell updates/sec

Title: US-10-679-999-7
Perfect score: 1150
Sequence: 1 CATATGGAACCCAAATCTTG.....TCCGGGTTGTTAATGGATCC 1150

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_23Sep04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1150	100.0	1150	2	AAV32900	Aav32900 Recombina
2	1150	100.0	1150	2	AAV69685	Aav69685 Recombina
3	1134	98.6	1150	2	AAV32901	Aav32901 Recombina
4	1117.8	97.2	1135	2	AAV32902	Aav32902 Recombina
5	1117.8	97.2	1135	2	AAV69686	Aav69686 Recombina
6	1105	96.1	1135	2	AAV32903	Aav32903 Recombina
7	698.8	60.8	1645	10	ADD25779	Add25779 Binding d
8	697	60.6	1002	12	ADN97484	Adn97484 Artificia
9	697	60.6	2154	12	ADN97490	Adn97490 Artificia
10	697	60.6	2160	12	ADN97488	Adn97488 Artificia
11	697	60.6	2190	4	ABA02694	Aba02694 Humanised
12	697	60.6	2220	4	ABA02700	Aba02700 Humanised
13	696.8	60.6	1288	3	AAC67833	Aac67833 Fc-huAGP-
14	696.2	60.5	1435	12	ADM97512	Adm97512 CD1d-IgG-
15	696.2	60.5	1522	12	ADM97492	Adm97492 CD1d-IgG-
16	696.2	60.5	1580	12	ADF71883	Adf71883 Humanised
17	696.2	60.5	1580	12	ADF71906	Adf71906 Hu3G8VH-1
18	696.2	60.5	1580	12	ADF71871	Adf71871 Chimeric
19	696.2	60.5	1963	12	ADM97530	Adm97530 CD1d-IgG
20	695.8	60.5	1304	3	AAC67835	Aac67835 Fc-muAGP-
21	695.8	60.5	2196	4	ABA02690	Aba02690 Humanised
22	695.8	60.5	2226	4	ABA02696	Aba02696 Humanised
23	695.6	60.5	1714	6	AAD46568	Aad46568 Human IL-
24	695.6	60.5	1720	4	AAH22845	Aah22845 Human IL-
25	695.6	60.5	1720	5	AAS07675	Aas07675 Human IL-
26	695.6	60.5	1720	6	ABK96208	Abk96208 DNA encod
27	695.6	60.5	1720	6	AAD37573	Aad37573 Human IL-
28	695.6	60.5	1720	12	ADJ83332	Adj83332 Human IL-
29	695.4	60.5	1012	12	ADJ95911	Adj95911 Human IgG
30	695.4	60.5	1094	12	ADJ95975	Adj95975 Immunoglo
31	695.4	60.5	1443	6	ABK24012	Abk24012 DNA encod
32	695.4	60.5	1494	3	AAA52129	Aaa52129 Human FGF
33	695.4	60.5	1509	8	ABZ81714	Abz81714 Human LP2
34	695.4	60.5	1578	3	AAA52128	Aaa52128 Human FGF
35	695.4	60.5	1869	3	AAA52127	Aaa52127 Human FGF
36	695.4	60.5	2067	3	AAA51343	Aaa51343 Ang-1-FD-
37	695.4	60.5	2070	3	AAA51344	Aaa51344 Ang-2-FD-
38	695.4	60.5	2151	8	ABZ81712	Abz81712 Human LP2
39	695.4	60.5	2454	12	ADQ80622	Adq80622 Binding d
40	695.4	60.5	5576	12	ADQ80628	Adq80628 Binding d
41	695.2	60.5	714	10	ADD25646	Add25646 Binding d
42	695.2	60.5	1182	2	AAV34430	Aav34430 Antigenic
43	695.2	60.5	1491	10	ADD25777	Add25777 Binding d
44	695.2	60.5	1518	6	ABK89848	Abk89848 Synthetic
45	695.2	60.5	1518	10	ADD25441	Add25441 Binding d

ALIGNMENTS

RESULT 1
AAV32900
ID AAV32900 standard; cDNA; 1150 BP.
XX
AC AAV32900;
XX
DT 18-NOV-1998 (first entry)
XX
DE Recombinant human MetFc-OB cDNA.
XX
KW Recombinant human MetFc-OB cDNA; chimeric; immunoglobulin; diabetes;
KW high blood lipid level; arterial sclerosis; stroke; Fc-OB fusion protein;
KW ds.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT CDS 4. .1143
FT /*tag= a
FT /product= "Recombinant human Fc-OB"
FT mat_peptide 7. .1140
FT /*tag= b
FT misc_feature 700. .1140
FT /*tag= c
FT /note= "Encodes for the OB part of the fusion protein"
XX
PN WO9828427-A1.
XX
PD 02-JUL-1998.
XX
PF 11-DEC-1997; 97WO-US023183.
XX
PR 20-DEC-1996; 96US-00770973.
XX
PA (AMGE-) AMGEN INC.
XX
PI Mann MB, Hecht RI;
XX
DR WPI; 1998-377658/32.
DR P-PSDB; AAW49073.
XX
PT New fusion proteins of OB and Fc - used for treating e.g. excess weight,
PT diabetes, arterial sclerosis, arterial plaque, high blood lipid level,

PT gall stones or stroke.
XX
PS Disclosure; Fig 3A-3C; 107pp; English.
XX
CC The present sequence represents a recombinant human MetFc-OB cDNA which
CC encodes a recombinant human Fc-OB fusion protein. The invention provides
CC Fc-OB fusion proteins whereby the Fc region of an immunoglobulin or its
CC analogue is linked, either directly or indirectly using a linker, to the
CC N-terminus of an OB protein or its analogue. The Fc-OB fusion proteins
CC are claimed to demonstrate increased stability and clearance rate and
CC decreased degradation as compared to OB protein or a fusion of Fc to the
CC C-terminus of the OB protein. These Fc-OB fusion proteins are also
CC claimed to be useful for treating excess weight in an individual or
CC animal or for treating co-morbidities associated with excess fat such as
CC diabetes, high blood lipid level, arterial sclerosis and stroke
XX
SQ Sequence 1150 BP; 278 A; 367 C; 286 G; 219 T; 0 U; 0 Other;

Query Match 100.0%; Score 1150; DB 2; Length 1150;
Best Local Similarity 100.0%; Pred. No. 5.5e-251;
Matches 1150; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 CATATGGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CATATGGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAA 60

Qy         61 CTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATC 120

Qy        121 TCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTC 180

Qy        181 AAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAG 240

Qy        241 GAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGG 300

Qy        301 CTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAG 360

Qy        361 AAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCA 420

Qy        421 TCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTAT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTAT 480

Qy        481 CCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACC 540

Qy        541 ACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGAC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 ACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGAC 600

Qy        601 AAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCAC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCAC 660

Qy        661 AACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTT 720

Qy        721 CAGGACGACACCAAAACCTTAATTAAAACGATCGTTACGCGTATCAACGACATCAGTCAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CAGGACGACACCAAAACCTTAATTAAAACGATCGTTACGCGTATCAACGACATCAGTCAC 780

Qy        781 ACCCAGTCGGTGAGCTCTAAACAGAAAGTTACAGGCCTGGACTTCATCCCGGGTCTGCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 ACCCAGTCGGTGAGCTCTAAACAGAAAGTTACAGGCCTGGACTTCATCCCGGGTCTGCAC 840

Qy        841 CCGATCCTGACCTTGTCCAAAATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CCGATCCTGACCTTGTCCAAAATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACC 900

Qy        901 TCCATGCCGTCCCGTAACGTTATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TCCATGCCGTCCCGTAACGTTATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTG 960

Qy        961 CTGCACGTGCTGGCATTCTCCAAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CTGCACGTGCTGGCATTCTCCAAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACT 1020

Qy       1021 CTGGACTCTCTGGGCGGGGTCCTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTG 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 CTGGACTCTCTGGGCGGGGTCCTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTG 1080

Qy       1081 TCCCGTCTGCAGGGTTCCCTTCAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TCCCGTCTGCAGGGTTCCCTTCAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGT 1140

Qy       1141 TAATGGATCC 1150
              ||||||||||
Db       1141 TAATGGATCC 1150
```

RESULT 2
AAV69685
ID AAV69685 standard; DNA; 1150 BP.
XX
AC AAV69685;
XX
DT 05-FEB-1999 (first entry)
XX
DE Recombinant human metFc-OB protein encoding DNA.
XX
KW Recombinant; metFc-OB protein; Fc region; immunoglobulin; Ig; OB;
KW obesity; human; adiposity; blood lipid; diabetes type II; insulin;
KW hypoglycaemic; antihypertensive; diuretic; appetite suppressant;
KW suspension; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 4. .1143
FT /*tag= a
FT /product= "metFc-OB protein"
XX
PN WO9846257-A1.
XX
PD 22-OCT-1998.
XX
PF 16-APR-1998; 98WO-US007828.
XX
PR 17-APR-1997; 97US-00843971.
PR 14-APR-1998; 98US-00059467.
XX
PA (AMGE-) AMGEN INC.
XX
PI Brems DN, French DL, Speed MA;
XX
DR WPI; 1998-594525/50.
DR P-PSDB; AAW83962.
XX
PT Concentrated suspension of fusion of obesity protein with Fc
PT immunoglobulin fragment - stable at physiological pH, used for e.g.
PT reduction of weight and blood lipid levels, and for treatment of type II
PT diabetes.
XX

```
PS   Disclosure; Fig 5A-C; 47pp; English.
XX
CC   This DNA encodes a recombinant metFc-OB protein which consists of an Fc
CC   region of human immunoglobulin (Ig) fused to a human OB (obesity)
CC   protein. The invention provides a human OB protein suspension that
CC   contains at least 0.5 mg/ml of the human OB protein derivatised by
CC   attachment of the Fc region of an Ig to the N-terminus of OB, and has a
CC   pH 6-8. The suspensions are used to reduce weight, adiposity and blood
CC   lipid levels, to treat or prevent diabetes type II, and to increase lean
CC   mass and insulin sensitivity. They may be used in conjunction with
CC   insulin, hypoglycaemics, antihypertensives, diuretics, appetite
CC   suppressants etc. These suspensions are stable and active at
CC   physiological pH and are ready-for-use formulations that do not require
CC   freezing or freeze drying. As they are very concentrated, only small
CC   volumes are required and they provide a sustained-release effect, with
CC   increased potency and reduced frequency of injection
XX
SQ   Sequence 1150 BP; 278 A; 367 C; 286 G; 219 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 1150;  DB 2;  Length 1150;
  Best Local Similarity   100.0%;  Pred. No. 5.5e-251;
  Matches 1150;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CATATGGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CATATGGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAA 60

Qy         61 CTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATC 120

Qy        121 TCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTC 180

Qy        181 AAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAG 240

Qy        241 GAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGG 300

Qy        301 CTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAG 360

Qy        361 AAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCA 420

Qy        421 TCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTAT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTAT 480

Qy        481 CCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACC 540

Qy        541 ACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGAC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 ACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGAC 600

Qy        601 AAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCAC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCAC 660

Qy        661 AACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTT 720

Qy        721 CAGGACGACACCAAAACCTTAATTAAAACGATCGTTACGCGTATCAACGACATCAGTCAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CAGGACGACACCAAAACCTTAATTAAAACGATCGTTACGCGTATCAACGACATCAGTCAC 780

Qy        781 ACCCAGTCGGTGAGCTCTAAACAGAAAGTTACAGGCCTGGACTTCATCCCGGGTCTGCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 ACCCAGTCGGTGAGCTCTAAACAGAAAGTTACAGGCCTGGACTTCATCCCGGGTCTGCAC 840

Qy        841 CCGATCCTGACCTTGTCCAAAATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CCGATCCTGACCTTGTCCAAAATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACC 900

Qy        901 TCCATGCCGTCCCGTAACGTTATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TCCATGCCGTCCCGTAACGTTATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTG 960

Qy        961 CTGCACGTGCTGGCATTCTCCAAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CTGCACGTGCTGGCATTCTCCAAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACT 1020

Qy       1021 CTGGACTCTCTGGGCGGGGTCCTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTG 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 CTGGACTCTCTGGGCGGGGTCCTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTG 1080

Qy       1081 TCCCGTCTGCAGGGTTCCCTTCAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TCCCGTCTGCAGGGTTCCCTTCAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGT 1140

Qy       1141 TAATGGATCC 1150
              ||||||||||
Db       1141 TAATGGATCC 1150


RESULT 3
AAV32901
ID   AAV32901 standard; cDNA; 1150 BP.
XX
AC   AAV32901;
XX
DT   18-NOV-1998  (first entry)
XX
DE   Recombinant human MetFc-OB variant 1 cDNA.
XX
KW   Recombinant human MetFc-OB variant 1 cDNA; chimeric; immunoglobulin;
KW   high blood lipid level; arterial sclerosis; stroke; Fc-OB fusion protein;
KW   diabetes; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             4. .1143
FT                   /*tag=  a
FT                   /product= "Recombinant human Fc-OB variant 1"
FT   mat_peptide     7. .1140
FT                   /*tag=  b
FT   mutation        19. .21
FT                   /*tag=  c
FT                   /note= "Changed from TGT in wild-type (AAV32900) to GCT
FT                   in mutant"
FT   misc_feature    700. .1140
FT                   /*tag=  d
FT                   /note= "Encodes for the OB part of the fusion protein"
XX
PN   WO9828427-A1.
XX
PD   02-JUL-1998.
XX
PF   11-DEC-1997;   97WO-US023183.
XX
PR   20-DEC-1996;   96US-00770973.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Mann MB,  Hecht RI;
```

```
XX
DR   WPI; 1998-377658/32.
DR   P-PSDB; AAW49074.
XX
PT   New fusion proteins of OB and Fc - used for treating e.g. excess weight,
PT   diabetes, arterial sclerosis, arterial plaque, high blood lipid level,
PT   gall stones or stroke.
XX
PS   Disclosure; Fig 4A-4C; 107pp; English.
XX
CC   The present sequence represents a recombinant human MetFc-OB variant 1
CC   cDNA which encodes a recombinant human Fc-OB fusion variant 1 protein
CC   having a C6A substitution when compared with the wild-type Fc-OB protein
CC   sequence shown in AAW49073. The invention provides Fc-OB fusion proteins
CC   whereby the Fc region of an immunoglobulin or its analogue is linked,
CC   either directly or indirectly using a linker, to the N-terminus of an OB
CC   protein or its analogue. The Fc-OB fusion proteins are claimed to
CC   demonstrate increased stability and clearance rate and decreased
CC   degradation as compared to OB protein or a fusion of Fc to the C-terminus
CC   of the OB protein. These Fc-OB fusion proteins are also claimed to be
CC   useful for treating excess weight in an individual or animal or for
CC   treating co-morbidities associated with excess fat such as diabetes, high
CC   blood lipid level, arterial sclerosis and stroke
XX
SQ   Sequence 1150 BP; 277 A; 365 C; 285 G; 223 T; 0 U; 0 Other;

  Query Match             98.6%;  Score 1134;  DB 2;  Length 1150;
  Best Local Similarity   99.1%;  Pred. No. 2.3e-247;
  Matches 1140;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          1 CATATGGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAA 60
              |||||||||||| |||||||  |||||||||||||||||| ||||| || ||||| || |||
Db          1 CATATGGAACCAAAATCTGCTGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAA 60

Qy         61 CTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATC 120
              |||||||||||| || ||||||||||||||||||||||||||||||||||||||||||||
Db         61 CTCCTGGGGGGTCCTTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATC 120

Qy        121 TCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTC 180

Qy        181 AAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAG 240

Qy        241 GAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGG 300

Qy        301 CTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAG 360

Qy        361 AAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCA 420

Qy        421 TCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTAT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTAT 480

Qy        481 CCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACC 540

Qy        541 ACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGAC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 ACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGAC 600

Qy        601 AAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCAC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCAC 660

Qy        661 AACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTT 720

Qy        721 CAGGACGACACCAAAACCTTAATTAAAACGATCGTTACGCGTATCAACGACATCAGTCAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CAGGACGACACCAAAACCTTAATTAAAACGATCGTTACGCGTATCAACGACATCAGTCAC 780

Qy        781 ACCCAGTCGGTGAGCTCTAAACAGAAAGTTACAGGCCTGGACTTCATCCCGGGTCTGCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 ACCCAGTCGGTGAGCTCTAAACAGAAAGTTACAGGCCTGGACTTCATCCCGGGTCTGCAC 840

Qy        841 CCGATCCTGACCTTGTCCAAAATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CCGATCCTGACCTTGTCCAAAATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACC 900

Qy        901 TCCATGCCGTCCCGTAACGTTATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TCCATGCCGTCCCGTAACGTTATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTG 960

Qy        961 CTGCACGTGCTGGCATTCTCCAAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CTGCACGTGCTGGCATTCTCCAAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACT 1020

Qy       1021 CTGGACTCTCTGGGCGGGGTCCTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTG 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 CTGGACTCTCTGGGCGGGGTCCTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTG 1080

Qy       1081 TCCCGTCTGCAGGGTTCCCTTCAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TCCCGTCTGCAGGGTTCCCTTCAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGT 1140

Qy       1141 TAATGGATCC 1150
              ||||||||||
Db       1141 TAATGGATCC 1150


RESULT 4
AAV32902
ID   AAV32902 standard; cDNA; 1135 BP.
XX
AC   AAV32902;
XX
DT   18-NOV-1998  (first entry)
XX
DE   Recombinant human MetFc-OB variant 2 cDNA.
XX
KW   Recombinant human MetFc-OB variant 2 cDNA; chimeric; immunoglobulin;
KW   high blood lipid level; arterial sclerosis; stroke; Fc-OB fusion protein;
KW   diabetes; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             4. .1128
FT                   /*tag=  a
FT                   /product= "Recombinant human Fc-OB variant 2"
FT   mat_peptide     7. .1125
FT                   /*tag=  b
FT   misc_feature    685. .1125
FT                   /*tag=  c
FT                   /note= "Encodes for the OB part of the fusion protein"
XX
PN   WO9828427-A1.
XX
PD   02-JUL-1998.
XX
PF   11-DEC-1997;   97WO-US023183.
XX
PR   20-DEC-1996;   96US-00770973.
XX
```

PA (AMGE-) AMGEN INC.
XX
PI Mann MB, Hecht RI;
XX
DR WPI; 1998-377658/32.
DR P-PSDB; AAW49075.
XX
PT New fusion proteins of OB and Fc - used for treating e.g. excess weight,
PT diabetes, arterial sclerosis, arterial plaque, high blood lipid level,
PT gall stones or stroke.
XX
PS Disclosure; Fig 5A-5C; 107pp; English.
XX
CC The present sequence represents a recombinant human MetFc-OB variant 2
CC cDNA which encodes a recombinant human Fc-OB fusion variant 2 protein
CC having a 5 residue deletion of residues 2-6 of the wild-type Fc-OB
CC protein sequence shown in AAW49073. The invention provides Fc-OB fusion
CC proteins whereby the Fc region of an immunoglobulin or its analogue is
CC linked, either directly or indirectly using a linker, to the N-terminus
CC of an OB protein or its analogue. The Fc-OB fusion proteins are claimed
CC to demonstrate increased stability and clearance rate and decreased
CC degradation as compared to OB protein or a fusion of Fc to the C-terminus
CC of the OB protein. These Fc-OB fusion proteins are also claimed to be
CC useful for treating excess weight in an individual or animal or for
CC treating co-morbidities associated with excess fat such as diabetes, high
CC blood lipid level, arterial sclerosis and stroke
XX
SQ Sequence 1135 BP; 271 A; 361 C; 283 G; 220 T; 0 U; 0 Other;

Query Match 97.2%; Score 1117.8; DB 2; Length 1135;
Best Local Similarity 99.4%; Pred. No. 1.1e-243;
Matches 1122; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

```
Qy        22 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC 81
             ||||||||||||||||| ||||| || ||||| || ||||||||||||| || ||||||
Db         7 GACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGTCCTTCAGTC 66

Qy        82 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 141
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        67 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 126

Qy       142 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 201
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       127 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 186

Qy       202 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 261
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       187 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 246

Qy       262 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 321
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       247 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 306

Qy       322 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 381
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       307 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 366

Qy       382 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 441
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       367 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 426

Qy       442 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 501
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       427 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 486

Qy       502 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 561
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       487 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 546

Qy       562 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 621
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       547 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 606

Qy       622 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 681
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       607 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 666

Qy       682 CTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTTCAGGACGACACCAAAACCTTA 741
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       667 CTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTTCAGGACGACACCAAAACCTTA 726

Qy       742 ATTAAAACGATCGTTACGCGTATCAACGACATCAGTCACACCCAGTCGGTGAGCTCTAAA 801
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       727 ATTAAAACGATCGTTACGCGTATCAACGACATCAGTCACACCCAGTCGGTGAGCTCTAAA 786

Qy       802 CAGAAAGTTACAGGCCTGGACTTCATCCCGGGTCTGCACCCGATCCTGACCTTGTCCAAA 861
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       787 CAGAAAGTTACAGGCCTGGACTTCATCCCGGGTCTGCACCCGATCCTGACCTTGTCCAAA 846

Qy       862 ATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACCTCCATGCCGTCCCGTAACGTT 921
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       847 ATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACCTCCATGCCGTCCCGTAACGTT 906

Qy       922 ATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTGCTGCACGTGCTGGCATTCTCC 981
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       907 ATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTGCTGCACGTGCTGGCATTCTCC 966

Qy       982 AAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACTCTGGACTCTCTGGGCGGGGTC 1041
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       967 AAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACTCTGGACTCTCTGGGCGGGGTC 1026

Qy      1042 CTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTGTCCCGTCTGCAGGGTTCCCTT 1101
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1027 CTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTGTCCCGTCTGCAGGGTTCCCTT 1086

Qy      1102 CAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGTTAATGGATCC 1150
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1087 CAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGTTAATGGATCC 1135
```

RESULT 5
AAV69686
ID AAV69686 standard; DNA; 1135 BP.
XX
AC AAV69686;
XX
DT 05-FEB-1999 (first entry)
XX
DE Recombinant human metFc-OB protein variant encoding DNA.
XX
KW Recombinant; metFc-OB protein; Fc region; immunoglobulin; Ig; OB;
KW obesity; human; adiposity; blood lipid; diabetes type II; insulin;
KW hypoglycaemic; antihypertensive; diuretic; appetite suppressant;
KW suspension; variant; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 4. .1128
FT /*tag= a
FT /product= "metFc-OB protein variant"
XX
PN WO9846257-A1.
XX
PD 22-OCT-1998.
XX
PF 16-APR-1998; 98WO-US007828.
XX
PR 17-APR-1997; 97US-00843971.
PR 14-APR-1998; 98US-00059467.
XX
PA (AMGE-) AMGEN INC.
XX
PI Brems DN, French DL, Speed MA;
XX
DR WPI; 1998-594525/50.

```
DR   P-PSDB; AAW83963.
XX
PT   Concentrated suspension of fusion of obesity protein with Fc
PT   immunoglobulin fragment - stable at physiological pH, used for e.g.
PT   reduction of weight and blood lipid levels, and for treatment of type II
PT   diabetes.
XX
PS   Disclosure; Fig 6A-C; 47pp; English.
XX
CC   This DNA encodes a recombinant metFc-OB protein variant which consists of
CC   an Fc region of human immunoglobulin (Ig) fused to a human OB (obesity)
CC   protein. The invention provides a human OB protein suspension that
CC   contains at least 0.5 mg/ml of the human OB protein derivatised by
CC   attachment of the Fc region of an Ig to the N-terminus of OB, and has a
CC   pH 6-8. The suspensions are used to reduce weight, adiposity and blood
CC   lipid levels, to treat or prevent diabetes type II, and to increase lean
CC   mass and insulin sensitivity. They may be used in conjunction with
CC   insulin, hypoglycaemics, antihypertensives, diuretics, appetite
CC   suppressants etc. These suspensions are stable and active at
CC   physiological pH and are ready-for-use formulations that do not require
CC   freezing or freeze drying. As they are very concentrated, only small
CC   volumes are required and they provide a sustained-release effect, with
CC   increased potency and reduced frequency of injection
XX
SQ   Sequence 1135 BP; 271 A; 361 C; 283 G; 220 T; 0 U; 0 Other;

  Query Match             97.2%;  Score 1117.8;  DB 2;  Length 1135;
  Best Local Similarity   99.4%;  Pred. No. 1.1e-243;
  Matches 1122;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy         22 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC 81
               ||||||||||||||||| ||||| || ||||| || ||||||||||||| || ||||||
Db          7 GACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGTCCTTCAGTC 66

Qy         82 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 141
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 126

Qy        142 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 201
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 186

Qy        202 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 261
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 246

Qy        262 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 321
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 306

Qy        322 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 381
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 366

Qy        382 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 441
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 426

Qy        442 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 501
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 486

Qy        502 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 561
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 546

Qy        562 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 621
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 606

Qy        622 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 681
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 666

Qy        682 CTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTTCAGGACGACACCAAAACCTTA 741
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 CTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTTCAGGACGACACCAAAACCTTA 726

Qy        742 ATTAAAACGATCGTTACGCGTATCAACGACATCAGTCACACCCAGTCGGTGAGCTCTAAA 801
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        727 ATTAAAACGATCGTTACGCGTATCAACGACATCAGTCACACCCAGTCGGTGAGCTCTAAA 786

Qy        802 CAGAAAGTTACAGGCCTGGACTTCATCCCGGGTCTGCACCCGATCCTGACCTTGTCCAAA 861
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 CAGAAAGTTACAGGCCTGGACTTCATCCCGGGTCTGCACCCGATCCTGACCTTGTCCAAA 846

Qy        862 ATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACCTCCATGCCGTCCCGTAACGTT 921
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 ATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACCTCCATGCCGTCCCGTAACGTT 906

Qy        922 ATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTGCTGCACGTGCTGGCATTCTCC 981
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        907 ATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTGCTGCACGTGCTGGCATTCTCC 966

Qy        982 AAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACTCTGGACTCTCTGGGCGGGGTC 1041
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        967 AAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACTCTGGACTCTCTGGGCGGGGTC 1026

Qy       1042 CTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTGTCCCGTCTGCAGGGTTCCCTT 1101
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1027 CTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTGTCCCGTCTGCAGGGTTCCCTT 1086

Qy       1102 CAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGTTAATGGATCC 1150
               ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1087 CAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGTTAATGGATCC 1135


RESULT 6
AAV32903
ID   AAV32903 standard; cDNA; 1135 BP.
XX
AC   AAV32903;
XX
DT   18-NOV-1998  (first entry)
XX
DE   Recombinant human MetFc-OB variant 3 cDNA.
XX
KW   Recombinant human MetFc-OB variant 3 cDNA; chimeric; immunoglobulin;
KW   high blood lipid level; arterial sclerosis; stroke; Fc-OB fusion protein;
KW   diabetes; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             4. .1128
FT                   /*tag= a
FT                   /product= "Recombinant human Fc-OB variant 3"
FT   mat_peptide     7. .1125
FT                   /*tag= b
FT   misc_feature    685. .1125
FT                   /*tag= c
FT                   /note= "Encodes for the OB part of the fusion protein"
XX
PN   WO9828427-A1.
XX
PD   02-JUL-1998.
XX
PF   11-DEC-1997;   97WO-US023183.
XX
PR   20-DEC-1996;   96US-00770973.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Mann MB,  Hecht RI;
XX
```

```
DR   WPI; 1998-377658/32.
DR   P-PSDB; AAW49076.
XX
PT   New fusion proteins of OB and Fc - used for treating e.g. excess weight,
PT   diabetes, arterial sclerosis, arterial plaque, high blood lipid level,
PT   gall stones or stroke.
XX
PS   Disclosure; Fig 6A-6C; 107pp; English.
XX
CC   The present sequence represents a recombinant human MetFc-OB variant 3
CC   cDNA which encodes a recombinant human Fc-OB fusion variant 3 protein
CC   having the L16E, E99A, K101A and K103A substitutions when compared with
CC   the template protein shown in AAW49075. The invention provides Fc-OB
CC   fusion proteins whereby the Fc region of an immunoglobulin or its
CC   analogue is linked, either directly or indirectly using a linker, to the
CC   N-terminus of an OB protein or its analogue. The Fc-OB fusion proteins
CC   are claimed to demonstrate increased stability and clearance rate and
CC   decreased degradation as compared to OB protein or a fusion of Fc to the
CC   C-terminus of the OB protein. These Fc-OB fusion proteins are also
CC   claimed to be useful for treating excess weight in an individual or
CC   animal or for treating co-morbidities associated with excess fat such as
CC   diabetes, high blood lipid level, arterial sclerosis and stroke
XX
SQ   Sequence 1135 BP; 270 A; 365 C; 283 G; 217 T; 0 U; 0 Other;

  Query Match             96.1%;  Score 1105;  DB 2;  Length 1135;
  Best Local Similarity   98.7%;  Pred. No. 8.8e-241;
  Matches 1114;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy         22 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC 81
              ||||||||||||||||||||||||||||||||| || ||||||   || || |||||||||
Db          7 GACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCGTCAGTC 66

Qy         82 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 141
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 126

Qy        142 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 201
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 186

Qy        202 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 261
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 246

Qy        262 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 321
              |||||||||||||||||||||||||||||||||||||||||||||||| |  |||
Db        247 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCTTACGCA 306

Qy        322 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 381
              ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 TGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 366

Qy        382 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 441
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 426

Qy        442 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 501
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 486

Qy        502 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 561
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 546

Qy        562 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 621
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 606

Qy        622 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 681
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 666

Qy        682 CTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTTCAGGACGACACCAAAACCTTA 741
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 CTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTTCAGGACGACACCAAAACCTTA 726

Qy        742 ATTAAAACGATCGTTACGCGTATCAACGACATCAGTCACACCCAGTCGGTGAGCTCTAAA 801
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        727 ATTAAAACGATCGTTACGCGTATCAACGACATCAGTCACACCCAGTCGGTGAGCTCTAAA 786

Qy        802 CAGAAAGTTACAGGCCTGGACTTCATCCCGGGTCTGCACCCGATCCTGACCTTGTCCAAA 861
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 CAGAAAGTTACAGGCCTGGACTTCATCCCGGGTCTGCACCCGATCCTGACCTTGTCCAAA 846

Qy        862 ATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACCTCCATGCCGTCCCGTAACGTT 921
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 ATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACCTCCATGCCGTCCCGTAACGTT 906

Qy        922 ATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTGCTGCACGTGCTGGCATTCTCC 981
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        907 ATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTGCTGCACGTGCTGGCATTCTCC 966

Qy        982 AAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACTCTGGACTCTCTGGGCGGGGTC 1041
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        967 AAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACTCTGGACTCTCTGGGCGGGGTC 1026

Qy       1042 CTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTGTCCCGTCTGCAGGGTTCCCTT 1101
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1027 CTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTGTCCCGTCTGCAGGGTTCCCTT 1086

Qy       1102 CAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGTTAATGGATCC 1150
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db       1087 CAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGTTAATGGATCC 1135


RESULT 7
ADD25779
ID   ADD25779 standard; DNA; 1645 BP.
XX
AC   ADD25779;
XX
DT   15-JAN-2004  (first entry)
XX
DE   Binding domain-immunoglobulin fusion protein-associated DNA #187.
XX
KW   ds; Binding domain; immunoglobulin; fusion protein; cytostatic;
KW   antiarthritic; immunosuppressive; antidiabetic; antithyroid;
KW   neuroprotective; hinge region; immunoglobulin heavy chain;
KW   CH2 constant region; CH3 constant region; IgG1;
KW   antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation;
KW   malignant condition; B-cell disorder; melanoma; carcinoma; sarcoma;
KW   rheumatoid arthritis; myasthenia gravis; Grave's disease;
KW   type I diabetes mellitus; multiple sclerosis; autoimmune disease.
XX
OS   Unidentified.
XX
PN   US2003118592-A1.
XX
PD   26-JUN-2003.
XX
PF   25-JUL-2002; 2002US-00207655.
XX
PR   17-JAN-2001; 2001US-0367358P.
PR   17-JAN-2002; 2002US-00053530.
PR   03-JUN-2002; 2002US-0385691P.
XX
PA   (GENE-) GENECRAFT INC.
XX
PI   Ledbetter JA,  Hayden-Ledbetter MS,  Thompson PA;
XX
DR   WPI; 2003-801317/75.
XX
PT   New binding domain-immunoglobulin fusion protein, useful for treating a
PT   subject having or suspected of having a malignant condition or a B-cell
PT   disorder, e.g. melanoma, Grave's disease or autoimmune disease.
```

XX
PS Disclosure; SEQ ID NO 340; 157pp; English.
XX
CC Unidentified
XX
SQ Sequence 1645 BP; 415 A; 460 C; 428 G; 342 T; 0 U; 0 Other;

Query Match 60.8%; Score 698.8; DB 10; Length 1645;
Best Local Similarity 99.7%; Pred. No. 1.2e-148;
Matches 700; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy          2 ATATGGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAAC 61
              || |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        782 ATCTGGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAAC 841

Qy         62 TCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCT 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        842 TCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCT 901

Qy        122 CCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCA 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        902 CCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCA 961

Qy        182 AGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGG 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        962 AGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGG 1021

Qy        242 AGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGC 301
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1022 AGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGC 1081

Qy        302 TGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGA 361
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1082 TGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGA 1141

Qy        362 AAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCAT 421
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1142 AAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCAT 1201

Qy        422 CCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATC 481
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1202 CCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATC 1261

Qy        482 CCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCA 541
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1262 CCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCA 1321

Qy        542 CGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACA 601
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1322 CGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACA 1381

Qy        602 AGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACA 661
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1382 AGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACA 1441

Qy        662 ACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAG 703
              |||||||||||||||||||||||||||||||||||||||||||
Db       1442 ACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAG 1483
```

RESULT 8
ADN97484
ID ADN97484 standard; DNA; 1002 BP.
XX
AC ADN97484;
XX
DT 01-JUL-2004 (first entry)
XX
DE Artificial protein construction DNA #57.
XX
KW artificial proprotein; propeptide; protein engineering; antibody; gene;
KW ds.
XX
OS Unidentified.
XX
PN WO2004031362-A2.
XX
PD 15-APR-2004.
XX
PF 03-OCT-2003; 2003WO-US031420.
XX
PR 03-OCT-2002; 2002US-0415940P.
XX
PA (LARG-) LARGE SCALE BIOLOGY CORP.
XX
PI Reini SJ, Edwards P;
XX
DR WPI; 2004-330170/30.
DR P-PSDB; ADN97485.
XX
PT New artificial proprotein comprises three peptide sequences, useful for
PT artificial multimeric protein engineering in eukaryotes.
XX
PS Example 15; SEQ ID NO 57; 244pp; English.
XX
CC The invention relates to an artificial proprotein comprising three
CC peptide sequences: a first peptide sequence of interest, a propeptide
CC sequence attached to the C-terminus of the first peptide sequence of
CC interest, and a second peptide of interest attached to the C-terminus of
CC the propeptide sequence. The artificial proprotein and polynucleotides
CC are useful for artificial multimeric protein engineering, e.g. antibodies
CC and antibody fragments in eukaryotes. This sequence corresponds to a
CC nucleic acid used in the generation of the protein of the invention.
XX
SQ Sequence 1002 BP; 235 A; 340 C; 264 G; 163 T; 0 U; 0 Other;

Query Match 60.6%; Score 697; DB 12; Length 1002;
Best Local Similarity 99.3%; Pred. No. 2.9e-148;
Matches 700; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

```
Qy          5 TGGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 64
              | || ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        293 TTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 352

Qy         65 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        353 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 412

Qy        125 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        413 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 472

Qy        185 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        473 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 532

Qy        245 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 304
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        533 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 592

Qy        305 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        593 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 652

Qy        365 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        653 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 712

Qy        425 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 484
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        713 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 772

Qy        485 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 544
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        773 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 832
```

```
Qy        545 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 604
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        833 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 892

Qy        605 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 664
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        893 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 952

Qy        665 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAGTACCGA 709
              |||||||||||||||||||||||||||||||||||||||||| ||| |
Db        953 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGACCTA 997
```

RESULT 9
ADN97490
ID ADN97490 standard; DNA; 2154 BP.
XX
AC ADN97490;
XX
DT 01-JUL-2004 (first entry)
XX
DE Artificial protein construction DNA #60.
XX
KW artificial proprotein; propeptide; protein engineering; antibody; gene;
KW ds.
XX
OS Unidentified.
XX
PN WO2004031362-A2.
XX
PD 15-APR-2004.
XX
PF 03-OCT-2003; 2003WO-US031420.
XX
PR 03-OCT-2002; 2002US-0415940P.
XX
PA (LARG-) LARGE SCALE BIOLOGY CORP.
XX
PI Reini SJ, Edwards P;
XX
DR WPI; 2004-330170/30.
DR P-PSDB; ADN97491.
XX
PT New artificial proprotein comprises three peptide sequences, useful for
PT artificial multimeric protein engineering in eukaryotes.
XX
PS Example 15; SEQ ID NO 63; 244pp; English.
XX
CC The invention relates to an artificial proprotein comprising three
CC peptide sequences: a first peptide sequence of interest, a propeptide
CC sequence attached to the C-terminus of the first peptide sequence of
CC interest, and a second peptide of interest attached to the C-terminus of
CC the propeptide sequence. The artificial proprotein and polynucleotides
CC are useful for artificial multimeric protein engineering, e.g. antibodies
CC and antibody fragments in eukaryotes. This sequence corresponds to a
CC nucleic acid used in the generation of the protein of the invention.
XX
SQ Sequence 2154 BP; 540 A; 634 C; 554 G; 426 T; 0 U; 0 Other;

```
  Query Match           60.6%;  Score 697;  DB 12;  Length 2154;
  Best Local Similarity  99.3%;  Pred. No. 3.4e-148;
  Matches  700;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          5 TGGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 64
              | || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1448 TTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 1507

Qy         65 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1508 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 1567

Qy        125 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db       1568 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 1627

Qy        185 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1628 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 1687

Qy        245 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 304
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1688 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 1747

Qy        305 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1748 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 1807

Qy        365 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1808 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 1867

Qy        425 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 484
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1868 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 1927

Qy        485 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 544
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1928 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 1987

Qy        545 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 604
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1988 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 2047

Qy        605 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 664
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2048 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 2107

Qy        665 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAGTACCGA 709
              |||||||||||||||||||||||||||||||||||||||||| ||| |
Db       2108 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGACCTA 2152
```

RESULT 10
ADN97488
ID ADN97488 standard; DNA; 2160 BP.
XX
AC ADN97488;
XX
DT 01-JUL-2004 (first entry)
XX
DE Artificial protein construction DNA #59.
XX
KW artificial proprotein; propeptide; protein engineering; antibody; gene;
KW ds.
XX
OS Unidentified.
XX
PN WO2004031362-A2.
XX
PD 15-APR-2004.
XX
PF 03-OCT-2003; 2003WO-US031420.
XX
PR 03-OCT-2002; 2002US-0415940P.
XX
PA (LARG-) LARGE SCALE BIOLOGY CORP.
XX
PI Reini SJ, Edwards P;
XX
DR WPI; 2004-330170/30.
DR P-PSDB; ADN97489.
XX
PT New artificial proprotein comprises three peptide sequences, useful for
PT artificial multimeric protein engineering in eukaryotes.
XX
PS Example 15; SEQ ID NO 61; 244pp; English.

XX
CC The invention relates to an artificial proprotein comprising three
CC peptide sequences: a first peptide sequence of interest, a propeptide
CC sequence attached to the C-terminus of the first peptide sequence of
CC interest, and a second peptide of interest attached to the C-terminus of
CC the propeptide sequence. The artificial proprotein and polynucleotides
CC are useful for artificial multimeric protein engineering, e.g. antibodies
CC and antibody fragments in eukaryotes. This sequence corresponds to a
CC nucleic acid used in the generation of the protein of the invention.
XX
SQ Sequence 2160 BP; 542 A; 633 C; 563 G; 422 T; 0 U; 0 Other;

Query Match 60.6%; Score 697; DB 12; Length 2160;
Best Local Similarity 99.3%; Pred. No. 3.4e-148;
Matches 700; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

```
Qy          5 TGGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 64
              | || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1454 TTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 1513

Qy         65 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1514 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 1573

Qy        125 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1574 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 1633

Qy        185 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1634 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 1693

Qy        245 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 304
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1694 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 1753

Qy        305 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1754 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 1813

Qy        365 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1814 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 1873

Qy        425 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 484
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1874 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 1933

Qy        485 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 544
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1934 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 1993

Qy        545 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 604
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1994 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 2053

Qy        605 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 664
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2054 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 2113

Qy        665 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAGTACCGA 709
              |||||||||||||||||||||||||||||||||||  ||| |
Db       2114 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGACCTA 2158
```

RESULT 11
ABA02694
ID ABA02694 standard; DNA; 2190 BP.
XX
AC ABA02694;
XX
DT 05-FEB-2002 (first entry)
XX
DE Humanised HMFG-1 heavy chain/DNase I fusion encoding polynucleotide 5.
XX
KW Humanised monoclonal antibody; polymorphic epithelial mucin; PEM1; ds;
KW cytotoxic; endonuclease; DNase I; human; cytostatic; cancer; apoptosis.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200174905-A1.
XX
PD 11-OCT-2001.
XX
PF 26-MAR-2001; 2001WO-GB001324.
XX
PR 03-APR-2000; 2000GB-00008049.
PR 02-OCT-2000; 2000US-0237159P.
XX
PA (ANTI-) ANTISOMA RES LTD.
XX
PI Young RJ;
XX
DR WPI; 2001-662969/76.
XX
PT Novel compound used to treat cancer has target cell-specific portion
PT comprising humanized monoclonal antibody having specificity for
PT polymorphic epithelial mucin, and cytotoxic portion having
PT endonucleolytic activity.
XX
PS Claim 24; Fig 9; 176pp; English.
XX
CC The invention relates to a compound which comprises a target cell-
CC specific portion, comprising an humanised monoclonal antibody, having
CC specificity for polymorphic epithelial mucin (PEM) or its antigen binding
CC fragment and a cytotoxic portion having endonucleolytic activity,
CC exemplified by AAM52154-AAM52168 and encoded by ABA02682-ABA02728. The
CC compound has cytostatic activity useful for treating cancer and acting as
CC a potential inducer of apoptosis
XX
SQ Sequence 2190 BP; 498 A; 678 C; 605 G; 409 T; 0 U; 0 Other;

Query Match 60.6%; Score 697; DB 4; Length 2190;
Best Local Similarity 93.6%; Pred. No. 3.4e-148;
Matches 727; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

```
Qy          5 TGGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 64
              | || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        704 TTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 763

Qy         65 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        764 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 823

Qy        125 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        824 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 883

Qy        185 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        884 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 943

Qy        245 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 304
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        944 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 1003

Qy        305 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1004 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 1063

Qy        365 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1064 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 1123

Qy        425 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 484
```

```
Db       1124 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 1183

Qy        485 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 544
Db       1184 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 1243

Qy        545 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 604
Db       1244 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 1303

Qy        605 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 664
Db       1304 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 1363

Qy        665 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTTCAGG 724
Db       1364 ACTACACGCAGAAGAGCCTCTCCCTGTCCCCGGGGAGCGGCGGGCTGAAGATCGCAGCCT 1423

Qy        725 ACGACACCAAAACCTTAATTAAAACGATCGTTACGCGTATCAACGACATCAGTCACA 781
Db       1424 TCAACATCCAGACATTTGGGGAGACCAAGATGTCCAATGCCACCCTCGTCAGCTACA 1480
```

RESULT 12
ABA02700
ID ABA02700 standard; DNA; 2220 BP.
XX
AC ABA02700;
XX
DT 05-FEB-2002 (first entry)
XX
DE Humanised HMFG-1 heavy chain/DNase I fusion encoding polynucleotide 11.
XX
KW Humanised monoclonal antibody; polymorphic epithelial mucin; PEM1; ds;
KW cytotoxic; endonuclease; DNase I; human; cytostatic; cancer; apoptosis.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200174905-A1.
XX
PD 11-OCT-2001.
XX
PF 26-MAR-2001; 2001WO-GB001324.
XX
PR 03-APR-2000; 2000GB-00008049.
PR 02-OCT-2000; 2000US-0237159P.
XX
PA (ANTI-) ANTISOMA RES LTD.
XX
PI Young RJ;
XX
DR WPI; 2001-662969/76.
XX
PT Novel compound used to treat cancer has target cell-specific portion
PT comprising humanized monoclonal antibody having specificity for
PT polymorphic epithelial mucin, and cytotoxic portion having
PT endonucleolytic activity.
XX
PS Claim 24; Fig 12; 176pp; English.
XX
CC The invention relates to a compound which comprises a target cell-
CC specific portion, comprising an humanised monoclonal antibody, having
CC specificity for polymorphic epithelial mucin (PEM) or its antigen binding
CC fragment and a cytotoxic portion having endonucleolytic activity,
CC exemplified by AAM52154-AAM52168 and encoded by ABA02682-ABA02728. The
CC compound has cytostatic activity useful for treating cancer and acting as
CC a potential inducer of apoptosis
XX
SQ Sequence 2220 BP; 508 A; 684 C; 617 G; 411 T; 0 U; 0 Other;

Query Match 60.6%; Score 697; DB 4; Length 2220;

Best Local Similarity 93.6%; Pred. No. 3.4e-148;
Matches 727; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

```
Qy          5 TGGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 64
Db        704 TTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 763

Qy         65 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 124
Db        764 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 823

Qy        125 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 184
Db        824 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 883

Qy        185 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 244
Db        884 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 943

Qy        245 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 304
Db        944 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 1003

Qy        305 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 364
Db       1004 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 1063

Qy        365 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 424
Db       1064 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 1123

Qy        425 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 484
Db       1124 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 1183

Qy        485 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 544
Db       1184 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 1243

Qy        545 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 604
Db       1244 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 1303

Qy        605 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 664
Db       1304 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 1363

Qy        665 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTTCAGG 724
Db       1364 ACTACACGCAGAAGAGCCTCTCCCTGTCCCCGGGGAGCGGCGGGCTGAAGATCGCAGCCT 1423

Qy        725 ACGACACCAAAACCTTAATTAAAACGATCGTTACGCGTATCAACGACATCAGTCACA 781
Db       1424 TCAACATCCAGACATTTGGGGAGACCAAGATGTCCAATGCCACCCTCGTCAGCTACA 1480
```

RESULT 13
AAC67833
ID AAC67833 standard; cDNA; 1288 BP.
XX
AC AAC67833;
XX
DT 14-FEB-2001 (first entry)
XX
DE Fc-huAGP-1 (114-281) nucleotide sequence.
XX
KW Human; AGP-1; type II transmembrane protein; cytostatic; antiviral;
KW antiinflammatory; hepatotropic; antiarteriosclerotic; anti-HIV; HIV;
KW human immunodeficiency virus; apoptosis; proliferative disorder; cancer;
KW hepatitis; acquired immunodeficiency syndrome; AIDS; autoimmune disorder;
KW transplant rejection; cardiovascular disease; arteriosclerosis;
KW Fc-huAGP-1; fusion protein; ss.
XX

OS Homo sapiens.
XX
PN WO200063253-A1.
XX
PD 26-OCT-2000.
XX
PF 24-MAR-2000; 2000WO-US008004.
XX
PR 16-APR-1999; 99US-00293245.
XX
PA (AMGE-) AMGEN INC.
XX
PI Hsu H, Meng S;
XX
DR WPI; 2000-665240/64.
DR P-PSDB; AAB28693.
XX
PT Fusion protein of AGP-1 protein and an Fc region, used to treat
PT proliferative disorders, immune disorders, and virally-induced disorders.
XX
PS Disclosure; Fig 4; 93pp; English.
XX
CC The present sequence encodes an AGP-1 fusion protein. AGP-1 is a type II
CC transmembrane protein. The fusion proteins comprise an Fc immunoglobulin
CC region fused to the N-terminal portion of the AGP-1 protein. The fusion
CC proteins can be used to induce apoptosis in a tissue, and to treat
CC proliferative disorders, immune disorders, or virally-induced disorders.
CC The proliferative disorders include cancers, such as breast, prostate,
CC lung or colon cancer. The viral infections include hepatitis, and
CC acquired immunodeficiency syndrome (AIDS), and the immune disorders may
CC be autoimmune disorders or transplant rejection. Cardiovascular diseases
CC such as arteriosclerosis may also be treated. The AGP-1 containing fusion
CC proteins have increased biological activity compared to the soluble AGP-1
CC proteins used in prior art therapies
XX
SQ Sequence 1288 BP; 371 A; 346 C; 313 G; 258 T; 0 U; 0 Other;

Query Match 60.6%; Score 696.8; DB 3; Length 1288;
Best Local Similarity 99.7%; Pred. No. 3.4e-148;
Matches 698; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy          5 TGGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 64
              | || ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         78 TTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 137

Qy         65 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        138 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 197

Qy        125 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        198 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 257

Qy        185 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        258 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 317

Qy        245 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 304
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        318 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 377

Qy        305 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        378 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 437

Qy        365 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        438 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 497

Qy        425 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 484
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        498 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 557
```

```
Qy        485 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 544
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        558 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 617

Qy        545 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 604
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        618 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 677

Qy        605 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 664
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        678 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 737

Qy        665 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAGT 704
              |||||||||||||||||||||||||||||||||||||||
Db        738 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAGT 777
```

RESULT 14
ADM97512
ID ADM97512 standard; DNA; 1435 BP.
XX
AC ADM97512;
XX
DT 01-JUL-2004 (first entry)
XX
DE CD1d-IgG-B2M complex IgG1-beta2-microglobulin DNA SEQ ID NO: 35.
XX
KW CD1d complex; cytostatic; antiinflammatory; cancer; autoimmune disease;
KW inflammatory disease; immunosuppressive; antimicrobial; neuroprotective;
KW antidiabetic; antiarthritic; antirheumatic; ophthalmological;
KW gastrointestinal; nephrotropic; dermatological; hepatotropic;
KW beta2-microglobulin; ds; gene.
XX
OS Synthetic.
OS Unidentified.
XX
FH Key Location/Qualifiers
FT CDS 14. .1435
FT /*tag= a
FT /product= "IgG1-beta2 microglobulin"
FT /transl_except
FT /note= "(pos:1274. .1276, aa: Val)"
XX
PN WO2004029206-A2.
XX
PD 08-APR-2004.
XX
PF 26-SEP-2003; 2003WO-US030238.
XX
PR 27-SEP-2002; 2002EP-00405838.
XX
PA (VACC-) VACCINEX INC.
PA (ROBE/) ROBERT B.
PA (DOND/) DONDA A.
PA (CESS/) CESSON V.
PA (MACH/) MACH J.
XX
PI Robert B, Donda A, Cesson V, Mach J, Zauderer M;
XX
DR WPI; 2004-316095/29.
DR P-PSDB; ADM97513.
XX
PT New compound comprising CD1d complexes and an antibody specific for a
PT cell surface marker, useful for preventing or treating tumors and
PT autoimmune/inflammatory or infectious diseases, e.g. multiple sclerosis,
PT diabetes or psoriasis.
XX
PS Example 10; Page 88-89; 152pp; English.
XX
CC The present invention relates to a compound comprising one or more CD1d
CC complexes and an antibody or its fragment specific for a cell surface
CC marker. The CD1d complexes comprise a CD1d and a beta2-microglobulin
CC molecule, and are linked to the antibody or its fragment. The composition

CC and methods are useful for preventing or treating tumours and
CC autoimmune/inflammatory or infectious diseases, such as multiple
CC sclerosis, type I diabetes, ankylosing spondylitis, acute anterior
CC uveitis, atrophic gastritis, Goodpasture's syndrome, Grave's disease,
CC Hashimoto's thyroiditis, myasthenia gravis, psoriasis, psoriatic
CC arthritis, rheumatoid arthritis, systemic lupus erythematosus, systemic
CC sclerosis, pemphigus vulgaris, pernicious anemia, primary biliary
CC cirrhosis, ulcerative colitis or autoimmune hepatitis. The present
CC sequence is a coding sequence used in the exemplification of the
CC invention.
XX
SQ Sequence 1435 BP; 351 A; 444 C; 368 G; 272 T; 0 U; 0 Other;

Query Match 60.5%; Score 696.2; DB 12; Length 1435;
Best Local Similarity 99.6%; Pred. No. 4.7e-148;
Matches 698; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy        5 TGGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 64
          | || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      378 TTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 437

Qy       65 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 124
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      438 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 497

Qy      125 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 184
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      498 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 557

Qy      185 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 244
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      558 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 617

Qy      245 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 304
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      618 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 677

Qy      305 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 364
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      678 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 737

Qy      365 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 424
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      738 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 797

Qy      425 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 484
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      798 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 857

Qy      485 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 544
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      858 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 917

Qy      545 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 604
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      918 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 977

Qy      605 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 664
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      978 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 1037

Qy      665 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAGTA 705
           |||||||||||||||||||||||||||||||||||||||| |
Db     1038 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAGGA 1078
```

RESULT 15
ADM97492
ID ADM97492 standard; DNA; 1522 BP.
XX
AC ADM97492;
XX
DT 01-JUL-2004 (first entry)
XX
DE CD1d-IgG-avidin complex IgG1 fragment coding sequence SEQ ID NO: 15.
XX
KW CD1d complex; cytostatic; antiinflammatory; cancer; autoimmune disease;
KW inflammatory disease; immunosuppressive; antimicrobial; neuroprotective;
KW antidiabetic; antiarthritic; antirheumatic; ophthalmological;
KW gastrointestinal; nephrotropic; dermatological; hepatotropic;
KW beta2-microglobulin; ds; gene.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT CDS 14. .1522
FT /*tag= a
FT /product= "IgG1"
XX
PN WO2004029206-A2.
XX
PD 08-APR-2004.
XX
PF 26-SEP-2003; 2003WO-US030238.
XX
PR 27-SEP-2002; 2002EP-00405838.
XX
PA (VACC-) VACCINEX INC.
PA (ROBE/) ROBERT B.
PA (DOND/) DONDA A.
PA (CESS/) CESSON V.
PA (MACH/) MACH J.
XX
PI Robert B, Donda A, Cesson V, Mach J, Zauderer M;
XX
DR WPI; 2004-316095/29.
DR P-PSDB; ADM97493.
XX
PT New compound comprising CD1d complexes and an antibody specific for a
PT cell surface marker, useful for preventing or treating tumors and
PT autoimmune/inflammatory or infectious diseases, e.g. multiple sclerosis,
PT diabetes or psoriasis.
XX
PS Example 4; Page 77-78; 152pp; English.
XX
CC The present invention relates to a compound comprising one or more CD1d
CC complexes and an antibody or its fragment specific for a cell surface
CC marker. The CD1d complexes comprise a CD1d and a beta2-microglobulin
CC molecule, and are linked to the antibody or its fragment. The composition
CC and methods are useful for preventing or treating tumours and
CC autoimmune/inflammatory or infectious diseases, such as multiple
CC sclerosis, type I diabetes, ankylosing spondylitis, acute anterior
CC uveitis, atrophic gastritis, Goodpasture's syndrome, Grave's disease,
CC Hashimoto's thyroiditis, myasthenia gravis, psoriasis, psoriatic
CC arthritis, rheumatoid arthritis, systemic lupus erythematosus, systemic
CC sclerosis, pemphigus vulgaris, pernicious anemia, primary biliary
CC cirrhosis, ulcerative colitis or autoimmune hepatitis. The present
CC sequence is a coding sequence used in the exemplification of the
CC invention.
XX
SQ Sequence 1522 BP; 376 A; 484 C; 401 G; 261 T; 0 U; 0 Other;

Query Match 60.5%; Score 696.2; DB 12; Length 1522;
Best Local Similarity 99.6%; Pred. No. 4.8e-148;
Matches 698; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy        5 TGGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 64
          | || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      378 TTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 437

Qy       65 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 124
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      438 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 497

Qy      125 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 184
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        498 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 557

Qy        185 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        558 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 617

Qy        245 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 304
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        618 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 677

Qy        305 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        678 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 737

Qy        365 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        738 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 797

Qy        425 GCGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 484
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        798 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 857

Qy        485 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 544
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        858 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 917

Qy        545 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 604
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        918 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 977

Qy        605 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 664
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        978 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 1037

Qy        665 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAGTA 705
              |||||||||||||||||||||||||||||||||||||||| |
Db       1038 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAGGA 1078
```

Search completed: October 17, 2004, 16:46:27
Job time : 601.515 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 17, 2004, 15:27:13 ; Search time 586.198 Seconds (without alignments) 10035.691 Million cell updates/sec

Title: US-10-679-999-7
Perfect score: 1150
Sequence: 1 CATATGGAACCCAAATCTTG.....TCCGGGTTGTTAATGGATCC 1150

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3403857 seqs, 2557783690 residues

Total number of hits satisfying chosen parameters: 6807714

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
18: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
19: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
20: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1150	100.0	1150	16	US-10-679-999-7	Sequence 7, Appli
2	1134	98.6	1150	16	US-10-679-999-10	Sequence 10, Appl
3	1117.8	97.2	1135	16	US-10-679-999-13	Sequence 13, Appl
4	1105	96.1	1135	16	US-10-679-999-16	Sequence 16, Appl
5	698.8	60.8	1645	15	US-10-207-655-340	Sequence 340, App
6	697	60.6	1002	17	US-10-679-620-57	Sequence 57, Appl
7	697	60.6	2154	17	US-10-679-620-63	Sequence 63, Appl
8	697	60.6	2160	17	US-10-679-620-61	Sequence 61, Appl
9	697	60.6	2190	9	US-09-825-012-50	Sequence 50, Appl
10	697	60.6	2190	9	US-09-825-012-51	Sequence 51, Appl
11	697	60.6	2220	9	US-09-825-012-59	Sequence 59, Appl
12	697	60.6	2220	9	US-09-825-012-60	Sequence 60, Appl
13	696.2	60.5	1580	16	US-10-449-566-5	Sequence 5, Appli
14	696.2	60.5	1580	16	US-10-449-566-17	Sequence 17, Appl
15	696.2	60.5	1580	16	US-10-449-566-105	Sequence 105, App
16	695.8	60.5	2196	9	US-09-825-012-44	Sequence 44, Appl
17	695.8	60.5	2196	9	US-09-825-012-45	Sequence 45, Appl
18	695.8	60.5	2226	9	US-09-825-012-53	Sequence 53, Appl
19	695.8	60.5	2226	9	US-09-825-012-54	Sequence 54, Appl
20	695.6	60.5	1714	16	US-10-471-151-30	Sequence 30, Appl
21	695.6	60.5	1720	9	US-09-746-359A-52	Sequence 52, Appl
22	695.6	60.5	1720	9	US-09-951-268-29	Sequence 29, Appl
23	695.6	60.5	1720	16	US-10-424-658-52	Sequence 52, Appl
24	695.4	60.5	1012	16	US-10-272-899A-7	Sequence 7, Appli
25	695.4	60.5	1094	16	US-10-272-899A-71	Sequence 71, Appl
26	695.4	60.5	1443	9	US-09-875-338-4	Sequence 4, Appli
27	695.4	60.5	1443	14	US-10-077-023-4	Sequence 4, Appli
28	695.4	60.5	1494	16	US-10-683-255-5	Sequence 5, Appli
29	695.4	60.5	1578	16	US-10-683-255-3	Sequence 3, Appli
30	695.4	60.5	1869	16	US-10-683-255-1	Sequence 1, Appli
31	695.2	60.5	714	15	US-10-207-655-207	Sequence 207, App
32	695.2	60.5	1080	9	US-09-949-713-14	Sequence 14, Appl
33	695.2	60.5	1182	9	US-09-949-713-18	Sequence 18, Appl
34	695.2	60.5	1182	15	US-10-084-139-9	Sequence 9, Appli
35	695.2	60.5	1491	15	US-10-207-655-338	Sequence 338, App
36	695.2	60.5	1518	15	US-10-207-655-2	Sequence 2, Appli
37	695.2	60.5	1518	15	US-10-207-655-147	Sequence 147, App
38	695.2	60.5	1518	15	US-10-053-530-2	Sequence 2, Appli
39	695.2	60.5	1521	15	US-10-207-655-239	Sequence 239, App
40	695.2	60.5	1527	15	US-10-207-655-347	Sequence 347, App
41	694.8	60.4	990	10	US-09-995-898A-14	Sequence 14, Appl
42	694.8	60.4	990	10	US-09-892-949-37	Sequence 37, Appl
43	694.8	60.4	990	16	US-10-420-034A-14	Sequence 14, Appl
44	694.8	60.4	990	17	US-10-772-531-37	Sequence 37, Appl
45	694.8	60.4	993	15	US-10-383-902A-4	Sequence 4, Appli

ALIGNMENTS

```
RESULT 1
US-10-679-999-7
; Sequence 7, Application US/10679999
; Publication No. US20040067520A1
;  GENERAL INFORMATION:
;       APPLICANT: Mann, Michael B.
;                  Hecht, Randy I.
;       TITLE OF INVENTION: OB FUSION PROTEIN COMPOSITIONS AND
;                           METHODS
;       NUMBER OF SEQUENCES: 18
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Amgen Inc.
;            STREET: 1840 DeHavilland Drive
;            CITY: Thousand Oaks
;            STATE: CA
;            COUNTRY: USA
;            ZIP: 91320-1789
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/679,999
;            FILING DATE: 06-Oct-2003
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/09/568,528
;            FILING DATE: 09-May-2000
;            APPLICATION NUMBER: 09/267,517
;            FILING DATE: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Knight, Matthew W.
;            REGISTRATION NUMBER: 36,846
;            REFERENCE/DOCKET NUMBER: A-416
;  INFORMATION FOR SEQ ID NO: 7:
```

```
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 1150 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: double
;            TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       FEATURE:
;            NAME/KEY:  misc_feature
;            LOCATION:  4
;            OTHER INFORMATION:  /note= "Met = ATG"
;       SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-679-999-7

  Query Match             100.0%;  Score 1150;  DB 16;  Length 1150;
  Best Local Similarity   100.0%;  Pred. No. 7.8e-313;
  Matches 1150;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CATATGGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CATATGGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAA 60

Qy         61 CTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATC 120

Qy        121 TCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTC 180

Qy        181 AAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAG 240

Qy        241 GAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGG 300

Qy        301 CTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAG 360

Qy        361 AAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCA 420

Qy        421 TCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTAT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTAT 480

Qy        481 CCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACC 540

Qy        541 ACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGAC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 ACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGAC 600

Qy        601 AAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCAC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCAC 660

Qy        661 AACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTT 720

Qy        721 CAGGACGACACCAAAACCTTAATTAAAACGATCGTTACGCGTATCAACGACATCAGTCAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CAGGACGACACCAAAACCTTAATTAAAACGATCGTTACGCGTATCAACGACATCAGTCAC 780

Qy        781 ACCCAGTCGGTGAGCTCTAAACAGAAAGTTACAGGCCTGGACTTCATCCCGGGTCTGCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 ACCCAGTCGGTGAGCTCTAAACAGAAAGTTACAGGCCTGGACTTCATCCCGGGTCTGCAC 840

Qy        841 CCGATCCTGACCTTGTCCAAAATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CCGATCCTGACCTTGTCCAAAATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACC 900

Qy        901 TCCATGCCGTCCCGTAACGTTATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TCCATGCCGTCCCGTAACGTTATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTG 960

Qy        961 CTGCACGTGCTGGCATTCTCCAAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CTGCACGTGCTGGCATTCTCCAAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACT 1020

Qy       1021 CTGGACTCTCTGGGCGGGGTCCTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTG 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 CTGGACTCTCTGGGCGGGGTCCTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTG 1080

Qy       1081 TCCCGTCTGCAGGGTTCCCTTCAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TCCCGTCTGCAGGGTTCCCTTCAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGT 1140

Qy       1141 TAATGGATCC 1150
              ||||||||||
Db       1141 TAATGGATCC 1150


RESULT 2
US-10-679-999-10
; Sequence 10, Application US/10679999
; Publication No. US20040067520A1
;   GENERAL INFORMATION:
;        APPLICANT: Mann, Michael B.
;                   Hecht, Randy I.
;        TITLE OF INVENTION: OB FUSION PROTEIN COMPOSITIONS AND
;                            METHODS
;        NUMBER OF SEQUENCES: 18
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Amgen Inc.
;             STREET: 1840 DeHavilland Drive
;             CITY: Thousand Oaks
;             STATE: CA
;             COUNTRY: USA
;             ZIP: 91320-1789
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/679,999
;             FILING DATE: 06-Oct-2003
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/568,528
;             FILING DATE: 09-May-2000
;             APPLICATION NUMBER: 09/267,517
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Knight, Matthew W.
;             REGISTRATION NUMBER: 36,846
;             REFERENCE/DOCKET NUMBER: A-416
;   INFORMATION FOR SEQ ID NO: 10:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1150 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        FEATURE:
;             NAME/KEY:  misc_feature
;             LOCATION:  4
;             OTHER INFORMATION:  /note= "Met = ATG"
;        SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-679-999-10
```

```
Query Match             98.6%;  Score 1134;  DB 16;  Length 1150;
Best Local Similarity   99.1%;  Pred. No. 2.4e-308;
Matches 1140;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          1 CATATGGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAA 60
              ||||||||||| |||||| |||||||||||||||||| ||||| || ||||| || |||
Db          1 CATATGGAACCAAAATCTGCTGACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAA 60

Qy         61 CTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATC 120
              |||||||||||  || ||||||||||||||||||||||||||||||||||||||||||||
Db         61 CTCCTGGGGGGTCCTTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATC 120

Qy        121 TCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTC 180

Qy        181 AAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAG 240

Qy        241 GAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGG 300

Qy        301 CTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAG 360

Qy        361 AAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCA 420

Qy        421 TCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTAT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTAT 480

Qy        481 CCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACC 540

Qy        541 ACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGAC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 ACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGAC 600

Qy        601 AAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCAC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCAC 660

Qy        661 AACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTT 720

Qy        721 CAGGACGACACCAAAACCTTAATTAAAACGATCGTTACGCGTATCAACGACATCAGTCAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CAGGACGACACCAAAACCTTAATTAAAACGATCGTTACGCGTATCAACGACATCAGTCAC 780

Qy        781 ACCCAGTCGGTGAGCTCTAAACAGAAAGTTACAGGCCTGGACTTCATCCCGGGTCTGCAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 ACCCAGTCGGTGAGCTCTAAACAGAAAGTTACAGGCCTGGACTTCATCCCGGGTCTGCAC 840

Qy        841 CCGATCCTGACCTTGTCCAAAATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CCGATCCTGACCTTGTCCAAAATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACC 900

Qy        901 TCCATGCCGTCCCGTAACGTTATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TCCATGCCGTCCCGTAACGTTATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTG 960

Qy        961 CTGCACGTGCTGGCATTCTCCAAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CTGCACGTGCTGGCATTCTCCAAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACT 1020

Qy       1021 CTGGACTCTCTGGGCGGGGTCCTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTG 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 CTGGACTCTCTGGGCGGGGTCCTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTG 1080

Qy       1081 TCCCGTCTGCAGGGTTCCCTTCAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TCCCGTCTGCAGGGTTCCCTTCAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGT 1140

Qy       1141 TAATGGATCC 1150
              ||||||||||
Db       1141 TAATGGATCC 1150
```

RESULT 3
US-10-679-999-13
; Sequence 13, Application US/10679999
; Publication No. US20040067520A1
; GENERAL INFORMATION:
; APPLICANT: Mann, Michael B.
; Hecht, Randy I.
; TITLE OF INVENTION: OB FUSION PROTEIN COMPOSITIONS AND
; METHODS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: CA
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/679,999
; FILING DATE: 06-Oct-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/568,528
; FILING DATE: 09-May-2000
; APPLICATION NUMBER: 09/267,517
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Knight, Matthew W.
; REGISTRATION NUMBER: 36,846
; REFERENCE/DOCKET NUMBER: A-416
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1135 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 4
; OTHER INFORMATION: /note= "Met = ATG"
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-10-679-999-13

```
Query Match             97.2%;  Score 1117.8;  DB 16;  Length 1135;
Best Local Similarity   99.4%;  Pred. No. 8.6e-304;
Matches 1122;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy         22 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC 81
              ||||||||||||||| ||||| || ||||| || ||||||||||||| || ||||||
Db          7 GACAAAACTCACACATGTCCACCTTGTCCAGCTCCGGAACTCCTGGGGGGTCCTTCAGTC 66

Qy         82 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 141
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 126
```

```
Qy        142 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 201
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 186

Qy        202 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 261
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 246

Qy        262 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 321
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 306

Qy        322 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 381
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 366

Qy        382 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 441
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 426

Qy        442 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 501
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 486

Qy        502 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 561
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 546

Qy        562 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 621
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 606

Qy        622 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 681
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 666

Qy        682 CTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTTCAGGACGACACCAAAACCTTA 741
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 CTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTTCAGGACGACACCAAAACCTTA 726

Qy        742 ATTAAAACGATCGTTACGCGTATCAACGACATCAGTCACACCCAGTCGGTGAGCTCTAAA 801
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        727 ATTAAAACGATCGTTACGCGTATCAACGACATCAGTCACACCCAGTCGGTGAGCTCTAAA 786

Qy        802 CAGAAAGTTACAGGCCTGGACTTCATCCCGGGTCTGCACCCGATCCTGACCTTGTCCAAA 861
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 CAGAAAGTTACAGGCCTGGACTTCATCCCGGGTCTGCACCCGATCCTGACCTTGTCCAAA 846

Qy        862 ATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACCTCCATGCCGTCCCGTAACGTT 921
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 ATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACCTCCATGCCGTCCCGTAACGTT 906

Qy        922 ATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTGCTGCACGTGCTGGCATTCTCC 981
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        907 ATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTGCTGCACGTGCTGGCATTCTCC 966

Qy        982 AAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACTCTGGACTCTCTGGGCGGGGTC 1041
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        967 AAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACTCTGGACTCTCTGGGCGGGGTC 1026

Qy       1042 CTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTGTCCCGTCTGCAGGGTTCCCTT 1101
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1027 CTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTGTCCCGTCTGCAGGGTTCCCTT 1086

Qy       1102 CAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGTTAATGGATCC 1150
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1087 CAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGTTAATGGATCC 1135

RESULT 4
US-10-679-999-16
; Sequence 16, Application US/10679999
; Publication No. US20040067520A1
;  GENERAL INFORMATION:
;       APPLICANT: Mann, Michael B.
;                  Hecht, Randy I.
;       TITLE OF INVENTION: OB FUSION PROTEIN COMPOSITIONS AND
;                           METHODS
;       NUMBER OF SEQUENCES: 18
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Amgen Inc.
;            STREET: 1840 DeHavilland Drive
;            CITY: Thousand Oaks
;            STATE: CA
;            COUNTRY: USA
;            ZIP: 91320-1789
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/679,999
;            FILING DATE: 06-Oct-2003
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/09/568,528
;            FILING DATE: 09-May-2000
;            APPLICATION NUMBER: 09/267,517
;            FILING DATE: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Knight, Matthew W.
;            REGISTRATION NUMBER: 36,846
;            REFERENCE/DOCKET NUMBER: A-416
;  INFORMATION FOR SEQ ID NO: 16:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 1135 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: double
;            TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       FEATURE:
;            NAME/KEY:  misc_feature
;            LOCATION:  4
;            OTHER INFORMATION:  /note= "Met = ATG"
;        SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-10-679-999-16

  Query Match             96.1%;  Score 1105;  DB 16;  Length 1135;
  Best Local Similarity   98.7%;  Pred. No. 3.4e-300;
  Matches 1114;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy         22 GACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTC 81
              ||||||||||||||||||||||||||||||||||| || ||||||  || || |||||||||
Db          7 GACAAAACTCACACATGCCCACCGTGCCCAGCTCCGGAACTCGAAGGTGGTCCGTCAGTC 66

Qy         82 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 141
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 TTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACA 126

Qy        142 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 201
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 TGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGAC 186

Qy        202 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 261
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAC 246

Qy        262 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAAGCTTACGCA 321
              |||||||||||||||||||||||||||||||||||||||||||||||||| | |||||||
Db        247 CGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAG 306

Qy        322 TGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 381
              ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 TGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAA 366
```

```
Qy        382 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 441
Db        367 GGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAG 426

Qy        442 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 501
Db        427 AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG 486

Qy        502 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 561
Db        487 TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCC 546

Qy        562 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 621
Db        547 GACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 606

Qy        622 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 681
Db        607 AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC 666

Qy        682 CTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTTCAGGACGACACCAAAACCTTA 741
Db        667 CTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTTCAGGACGACACCAAAACCTTA 726

Qy        742 ATTAAAACGATCGTTACGCGTATCAACGACATCAGTCACACCCAGTCGGTGAGCTCTAAA 801
Db        727 ATTAAAACGATCGTTACGCGTATCAACGACATCAGTCACACCCAGTCGGTGAGCTCTAAA 786

Qy        802 CAGAAAGTTACAGGCCTGGACTTCATCCCGGGTCTGCACCCGATCCTGACCTTGTCCAAA 861
Db        787 CAGAAAGTTACAGGCCTGGACTTCATCCCGGGTCTGCACCCGATCCTGACCTTGTCCAAA 846

Qy        862 ATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACCTCCATGCCGTCCCGTAACGTT 921
Db        847 ATGGACCAGACCCTGGCTGTATACCAGCAGATCTTAACCTCCATGCCGTCCCGTAACGTT 906

Qy        922 ATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTGCTGCACGTGCTGGCATTCTCC 981
Db        907 ATCCAGATCTCTAACGACCTCGAGAACCTTCGCGACCTGCTGCACGTGCTGGCATTCTCC 966

Qy        982 AAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACTCTGGACTCTCTGGGCGGGGTC 1041
Db        967 AAATCCTGCCACCTGCCATGGGCTTCAGGTCTTGAGACTCTGGACTCTCTGGGCGGGGTC 1026

Qy       1042 CTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTGTCCCGTCTGCAGGGTTCCCTT 1101
Db       1027 CTGGAAGCATCCGGTTACAGCACCGAAGTTGTTGCTCTGTCCCGTCTGCAGGGTTCCCTT 1086

Qy       1102 CAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGTTAATGGATCC 1150
Db       1087 CAGGACATGCTTTGGCAGCTGGACCTGTCTCCGGGTTGTTAATGGATCC 1135
```

RESULT 5
US-10-207-655-340
; Sequence 340, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Hayden-Ledbetter, Martha S.
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
; FILE REFERENCE: 390069.401C1
; CURRENT APPLICATION NUMBER: US/10/207,655
; CURRENT FILING DATE: 2002-07-25
; NUMBER OF SEQ ID NOS: 426
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 340
; LENGTH: 1645
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion polynucleotide

US-10-207-655-340

Query Match 60.8%; Score 698.8; DB 15; Length 1645;
Best Local Similarity 99.7%; Pred. No. 5.1e-186;
Matches 700; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy          2 ATATGGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAAC 61
Db        782 ATCTGGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAAC 841

Qy         62 TCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCT 121
Db        842 TCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCT 901

Qy        122 CCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCA 181
Db        902 CCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCA 961

Qy        182 AGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGG 241
Db        962 AGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGG 1021

Qy        242 AGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGC 301
Db       1022 AGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGC 1081

Qy        302 TGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGA 361
Db       1082 TGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGA 1141

Qy        362 AAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCAT 421
Db       1142 AAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCAT 1201

Qy        422 CCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATC 481
Db       1202 CCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATC 1261

Qy        482 CCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCA 541
Db       1262 CCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCA 1321

Qy        542 CGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACA 601
Db.      1322 CGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACA 1381

Qy        602 AGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACA 661
Db       1382 AGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACA 1441

Qy        662 ACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAG 703
Db       1442 ACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAG 1483
```

RESULT 6
US-10-679-620-57
; Sequence 57, Application US/10679620
; Publication No. US20040110930A1
; GENERAL INFORMATION:
; APPLICANT: Large Scale Biology
; APPLICANT: Reinl, Stephen J.
; APPLICANT: Edwards, Patricia C.
; TITLE OF INVENTION: MULTIMERIC PROTEIN ENGINEERING
; FILE REFERENCE: 34150-004A
; CURRENT APPLICATION NUMBER: US/10/679,620
; CURRENT FILING DATE: 2003-10-03
; PRIOR APPLICATION NUMBER: 60/415,940
; PRIOR FILING DATE: 2002-10-03
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 57
; LENGTH: 1002

```
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: phCHTOPO , see Example 15
US-10-679-620-57

  Query Match             60.6%;  Score 697;  DB 17;  Length 1002;
  Best Local Similarity   99.3%;  Pred. No. 1.5e-185;
  Matches  700;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          5 TGGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 64
              | || |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        293 TTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 352

Qy         65 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        353 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 412

Qy        125 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        413 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 472

Qy        185 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        473 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 532

Qy        245 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 304
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        533 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 592

Qy        305 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        593 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 652

Qy        365 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        653 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 712

Qy        425 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 484
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        713 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 772

Qy        485 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 544
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        773 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 832

Qy        545 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 604
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        833 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 892

Qy        605 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 664
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        893 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 952

Qy        665 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAGTACCGA 709
              |||||||||||||||||||||||||||||||||||||  ||| |
Db        953 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGACCTA 997


RESULT 7
US-10-679-620-63
; Sequence 63, Application US/10679620
; Publication No. US20040110930A1
; GENERAL INFORMATION:
;  APPLICANT: Large Scale Biology
;  APPLICANT:  Reinl, Stephen J.
;  APPLICANT:  Edwards, Patricia C.
;  TITLE OF INVENTION: MULTIMERIC PROTEIN ENGINEERING
;  FILE REFERENCE: 34150-004A
;  CURRENT APPLICATION NUMBER: US/10/679,620
;  CURRENT FILING DATE:  2003-10-03
;  PRIOR APPLICATION NUMBER: 60/415,940
;  PRIOR FILING DATE: 2002-10-03
;  NUMBER OF SEQ ID NOS: 122
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 63
;   LENGTH: 2154
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: p9E10chimericv2-1, see Example 15
US-10-679-620-63

  Query Match             60.6%;  Score 697;  DB 17;  Length 2154;
  Best Local Similarity   99.3%;  Pred. No. 1.7e-185;
  Matches  700;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          5 TGGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 64
              | || |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1448 TTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 1507

Qy         65 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1508 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 1567

Qy        125 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1568 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 1627

Qy        185 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1628 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 1687

Qy        245 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 304
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1688 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 1747

Qy        305 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1748 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 1807

Qy        365 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1808 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 1867

Qy        425 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 484
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1868 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 1927

Qy        485 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 544
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1928 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 1987

Qy        545 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 604
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1988 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 2047

Qy        605 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 664
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2048 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 2107

Qy        665 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAGTACCGA 709
              |||||||||||||||||||||||||||||||||||||  ||| |
Db       2108 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGACCTA 2152


RESULT 8
US-10-679-620-61
; Sequence 61, Application US/10679620
; Publication No. US20040110930A1
; GENERAL INFORMATION:
;  APPLICANT: Large Scale Biology
;  APPLICANT:  Reinl, Stephen J.
;  APPLICANT:  Edwards, Patricia C.
;  TITLE OF INVENTION: MULTIMERIC PROTEIN ENGINEERING
;  FILE REFERENCE: 34150-004A
```

```
;  CURRENT APPLICATION NUMBER: US/10/679,620
;  CURRENT FILING DATE:  2003-10-03
;  PRIOR APPLICATION NUMBER: 60/415,940
;  PRIOR FILING DATE: 2002-10-03
;  NUMBER OF SEQ ID NOS: 122
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 61
;   LENGTH: 2160
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: p9E10chimericv1-1, see Example 15
US-10-679-620-61

  Query Match             60.6%;  Score 697;  DB 17;  Length 2160;
  Best Local Similarity   99.3%;  Pred. No. 1.7e-185;
  Matches  700;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          5 TGGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 64
              | || ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1454 TTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 1513

Qy         65 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1514 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 1573

Qy         125 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1574 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 1633

Qy         185 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1634 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 1693

Qy         245 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 304
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1694 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 1753

Qy         305 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1754 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 1813

Qy         365 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1814 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 1873

Qy         425 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 484
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1874 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 1933

Qy         485 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 544
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1934 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 1993

Qy         545 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 604
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1994 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 2053

Qy         605 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 664
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2054 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 2113

Qy         665 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAGTACCGA 709
              |||||||||||||||||||||||||||||||||||||||||||| |||
Db       2114 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGACCTA 2158


RESULT 9
US-09-825-012-50
; Sequence 50, Application US/09825012
; Patent No. US20020122798A1
; GENERAL INFORMATION:
;  APPLICANT: Young, Robert
;  TITLE OF INVENTION: Compounds for Targeting
;  FILE REFERENCE: 43191-256808
;  CURRENT APPLICATION NUMBER: US/09/825,012
;  CURRENT FILING DATE:  2001-04-03
;  PRIOR APPLICATION NUMBER: US 60/237,159
;  PRIOR FILING DATE: 2000-10-02
;  PRIOR APPLICATION NUMBER: GB 0008049.9
;  PRIOR FILING DATE: 2000-04-03
;  NUMBER OF SEQ ID NOS: 102
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 50
;   LENGTH: 2190
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Humanised HMFG1 heavy chain - DNase I fusion
US-09-825-012-50

  Query Match             60.6%;  Score 697;  DB 9;  Length 2190;
  Best Local Similarity   93.6%;  Pred. No. 1.7e-185;
  Matches  727;  Conservative    0;  Mismatches   50;  Indels    0;  Gaps    0;

Qy          5 TGGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 64
              | || ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        704 TTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 763

Qy         65 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        764 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 823

Qy         125 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 184
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        824 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 883

Qy         185 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 244
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        884 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 943

Qy         245 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 304
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        944 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 1003

Qy         305 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 364
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1004 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 1063

Qy         365 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 424
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1064 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 1123

Qy         425 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 484
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1124 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 1183

Qy         485 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 544
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1184 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 1243

Qy         545 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 604
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1244 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 1303

Qy         605 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 664
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1304 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 1363

Qy         665 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTTCAGG 724
               |||||||||||||||||||||||||||||| ||||| |  |    | |  ||| |
Db       1364 ACTACACGCAGAAGAGCCTCTCCCTGTCCCCGGGGAGCGGCGGGCTGAAGATCGCAGCCT 1423

Qy         725 ACGACACCAAAACCTTAATTAAAACGATCGTTACGCGTATCAACGACATCAGTCACA 781
               | ||| | | ||  ||      | || |   |  |  | || |  | ||||  |||
Db       1424 TCAACATCCAGACATTTGGGGAGACCAAGATGTCCAATGCCACCCTCGTCAGCTACA 1480
```

```
RESULT 10
US-09-825-012-51
; Sequence 51, Application US/09825012
; Patent No. US20020122798A1
; GENERAL INFORMATION:
;  APPLICANT: Young, Robert
;  TITLE OF INVENTION: Compounds for Targeting
;  FILE REFERENCE: 43191-256808
;  CURRENT APPLICATION NUMBER: US/09/825,012
;  CURRENT FILING DATE:  2001-04-03
;  PRIOR APPLICATION NUMBER: US 60/237,159
;  PRIOR FILING DATE: 2000-10-02
;  PRIOR APPLICATION NUMBER: GB 0008049.9
;  PRIOR FILING DATE: 2000-04-03
;  NUMBER OF SEQ ID NOS: 102
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 51
;   LENGTH: 2190
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Humanised HMFG1 heavy chain - DNase I fusion
;   NAME/KEY: CDS
;   LOCATION: (1)..(2190)
;   OTHER INFORMATION:
US-09-825-012-51

  Query Match             60.6%;  Score 697;  DB 9;  Length 2190;
  Best Local Similarity   93.6%;  Pred. No. 1.7e-185;
  Matches  727;  Conservative    0;  Mismatches   50;  Indels    0;  Gaps    0;

Qy          5 TGGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 64
              | || ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        704 TTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 763

Qy         65 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        764 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 823

Qy        125 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        824 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 883

Qy        185 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        884 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 943

Qy        245 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 304
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        944 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 1003

Qy        305 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1004 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 1063

Qy        365 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1064 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 1123

Qy        425 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 484
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1124 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 1183

Qy        485 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 544
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1184 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 1243

Qy        545 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 604
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1244 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 1303

Qy        605 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 664
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1304 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 1363

Qy        665 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTTCAGG 724
              ||||||||||||||||||||||||||||||| ||||| |  |    ||  ||| |
Db       1364 ACTACACGCAGAAGAGCCTCTCCCTGTCCCCGGGGAGCGGCGGGCTGAAGATCGCAGCCT 1423

Qy        725 ACGACACCAAAACCTTAATTAAAACGATCGTTACGCGTATCAACGACATCAGTCACA 781
              | ||| | | || ||      | || |  |  |  |  || | | |||| |||
Db       1424 TCAACATCCAGACATTTGGGGAGACCAAGATGTCCAATGCCACCCTCGTCAGCTACA 1480


RESULT 11
US-09-825-012-59
; Sequence 59, Application US/09825012
; Patent No. US20020122798A1
; GENERAL INFORMATION:
;  APPLICANT: Young, Robert
;  TITLE OF INVENTION: Compounds for Targeting
;  FILE REFERENCE: 43191-256808
;  CURRENT APPLICATION NUMBER: US/09/825,012
;  CURRENT FILING DATE:  2001-04-03
;  PRIOR APPLICATION NUMBER: US 60/237,159
;  PRIOR FILING DATE: 2000-10-02
;  PRIOR APPLICATION NUMBER: GB 0008049.9
;  PRIOR FILING DATE: 2000-04-03
;  NUMBER OF SEQ ID NOS: 102
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 59
;   LENGTH: 2220
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Humanised HMFG1 heavy chain - DNase I fusion
US-09-825-012-59

  Query Match             60.6%;  Score 697;  DB 9;  Length 2220;
  Best Local Similarity   93.6%;  Pred. No. 1.7e-185;
  Matches  727;  Conservative    0;  Mismatches   50;  Indels    0;  Gaps    0;

Qy          5 TGGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 64
              | || ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        704 TTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 763

Qy         65 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        764 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 823

Qy        125 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        824 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 883

Qy        185 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        884 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 943

Qy        245 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 304
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        944 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 1003

Qy        305 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1004 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 1063

Qy        365 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1064 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 1123

Qy        425 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 484
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1124 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 1183
```

```
Qy        485 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 544
Db       1184 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 1243

Qy        545 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 604
Db       1244 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 1303

Qy        605 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 664
Db       1304 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 1363

Qy        665 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTTCAGG 724
Db       1364 ACTACACGCAGAAGAGCCTCTCCCTGTCCCCGGGGAGCGGCGGGCTGAAGATCGCAGCCT 1423

Qy        725 ACGACACCAAAACCTTAATTAAAACGATCGTTACGCGTATCAACGACATCAGTCACA 781
Db       1424 TCAACATCCAGACATTTGGGGAGACCAAGATGTCCAATGCCACCCTCGTCAGCTACA 1480
```

RESULT 12
US-09-825-012-60
; Sequence 60, Application US/09825012
; Patent No. US20020122798A1
; GENERAL INFORMATION:
; APPLICANT: Young, Robert
; TITLE OF INVENTION: Compounds for Targeting
; FILE REFERENCE: 43191-256808
; CURRENT APPLICATION NUMBER: US/09/825,012
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/237,159
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: GB 0008049.9
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 60
; LENGTH: 2220
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanised HMFG1 heavy chain - DNase I fusion
; NAME/KEY: CDS
; LOCATION: (1)..(2220)
; OTHER INFORMATION:
US-09-825-012-60

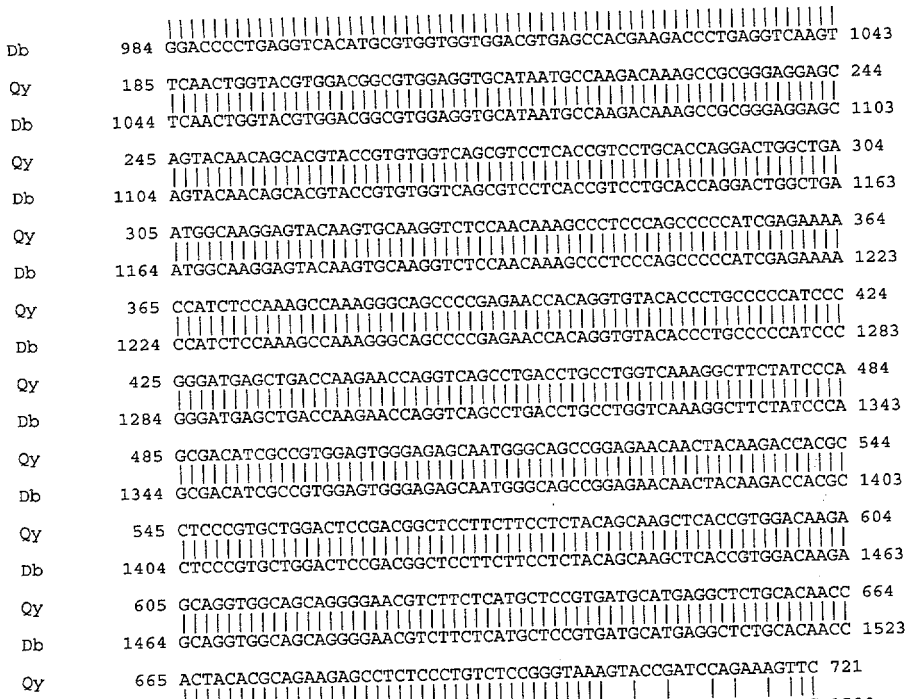
Query Match 60.6%; Score 697; DB 9; Length 2220;
Best Local Similarity 93.6%; Pred. No. 1.7e-185;
Matches 727; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

```
Qy          5 TGGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 64
Db        704 TTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 763

Qy         65 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 124
Db        764 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 823

Qy        125 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 184
Db        824 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 883

Qy        185 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 244
Db        884 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 943

Qy        245 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 304
Db        944 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 1003

Qy        305 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 364
Db       1004 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 1063

Qy        365 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 424
Db       1064 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 1123

Qy        425 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 484
Db       1124 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 1183

Qy        485 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 544
Db       1184 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 1243

Qy        545 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 604
Db       1244 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 1303

Qy        605 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 664
Db       1304 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 1363

Qy        665 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTTCAGG 724
Db       1364 ACTACACGCAGAAGAGCCTCTCCCTGTCCCCGGGGAGCGGCGGGCTGAAGATCGCAGCCT 1423

Qy        725 ACGACACCAAAACCTTAATTAAAACGATCGTTACGCGTATCAACGACATCAGTCACA 781
Db       1424 TCAACATCCAGACATTTGGGGAGACCAAGATGTCCAATGCCACCCTCGTCAGCTACA 1480
```

RESULT 13
US-10-449-566-5
; Sequence 5, Application US/10449566
; Publication No. US20040010124A1
; GENERAL INFORMATION:
; APPLICANT: JOHNSON, Leslie S.
; APPLICANT: HUANG, Ling
; APPLICANT: LI, Hua
; APPLICANT: TUAILLON, Nadine
; TITLE OF INVENTION: CD16A BINDING PROTEINS AND USE FOR THE
; TITLE OF INVENTION: TREATMENT OF IMMUNE DISORDERS
; FILE REFERENCE: 529392000100
; CURRENT APPLICATION NUMBER: US/10/449,566
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: 60/384,689
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/439,320
; PRIOR FILING DATE: 2003-01-10
; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1580
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-449-566-5

Query Match 60.5%; Score 696.2; DB 16; Length 1580;
Best Local Similarity 98.2%; Pred. No. 2.7e-185;
Matches 704; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

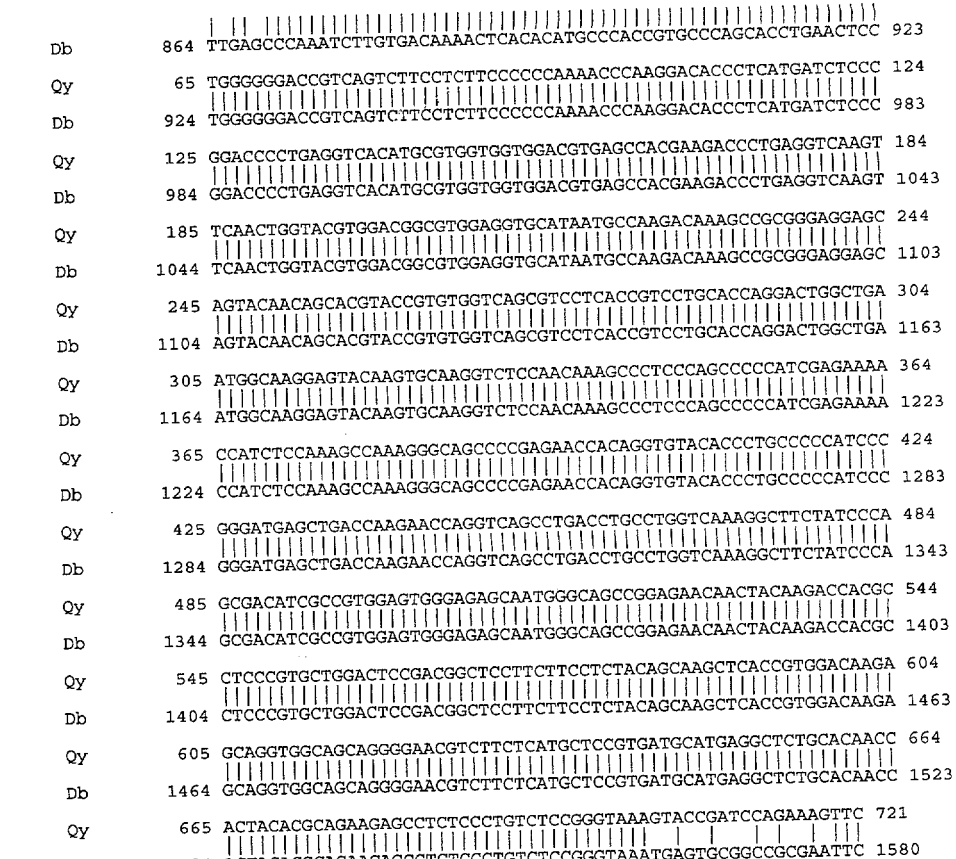
```
Qy          5 TGGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 64
Db        864 TTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 923

Qy         65 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 124
Db        924 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 983

Qy        125 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 184
```


Db 984 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 1043
Qy 185 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 244
Db 1044 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 1103
Qy 245 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 304
Db 1104 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 1163
Qy 305 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 364
Db 1164 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 1223
Qy 365 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 424
Db 1224 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 1283
Qy 425 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 484
Db 1284 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 1343
Qy 485 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 544
Db 1344 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 1403
Qy 545 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 604
Db 1404 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 1463
Qy 605 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 664
Db 1464 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 1523
Qy 665 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTTC 721
Db 1524 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGAGTGCGGCCGCGAATTC 1580

RESULT 14
US-10-449-566-17
; Sequence 17, Application US/10449566
; Publication No. US20040010124A1
; GENERAL INFORMATION:
; APPLICANT: JOHNSON, Leslie S.
; APPLICANT: HUANG, Ling
; APPLICANT: LI, Hua
; APPLICANT: TUAILLON, Nadine
; TITLE OF INVENTION: CD16A BINDING PROTEINS AND USE FOR THE
; TITLE OF INVENTION: TREATMENT OF IMMUNE DISORDERS
; FILE REFERENCE: 529392000100
; CURRENT APPLICATION NUMBER: US/10/449,566
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: 60/384,689
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/439,320
; PRIOR FILING DATE: 2003-01-10
; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 1580
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-449-566-17

Query Match 60.5%; Score 696.2; DB 16; Length 1580;
Best Local Similarity 98.2%; Pred. No. 2.7e-185;
Matches 704; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy 5 TGGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 64


Db 864 TTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 923
Qy 65 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 124
Db 924 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 983
Qy 125 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 184
Db 984 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 1043
Qy 185 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 244
Db 1044 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 1103
Qy 245 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 304
Db 1104 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 1163
Qy 305 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 364
Db 1164 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 1223
Qy 365 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 424
Db 1224 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 1283
Qy 425 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 484
Db 1284 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 1343
Qy 485 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 544
Db 1344 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 1403
Qy 545 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 604
Db 1404 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 1463
Qy 605 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 664
Db 1464 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 1523
Qy 665 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTTC 721
Db 1524 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGAGTGCGGCCGCGAATTC 1580

RESULT 15
US-10-449-566-105
; Sequence 105, Application US/10449566
; Publication No. US20040010124A1
; GENERAL INFORMATION:
; APPLICANT: JOHNSON, Leslie S.
; APPLICANT: HUANG, Ling
; APPLICANT: LI, Hua
; APPLICANT: TUAILLON, Nadine
; TITLE OF INVENTION: CD16A BINDING PROTEINS AND USE FOR THE
; TITLE OF INVENTION: TREATMENT OF IMMUNE DISORDERS
; FILE REFERENCE: 529392000100
; CURRENT APPLICATION NUMBER: US/10/449,566
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: 60/384,689
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/439,320
; PRIOR FILING DATE: 2003-01-10
; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 105
; LENGTH: 1580
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: Synthetic Construct
US-10-449-566-105

Query Match 60.5%; Score 696.2; DB 16; Length 1580;
Best Local Similarity 98.2%; Pred. No. 2.7e-185;
Matches 704; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

```
Qy          5 TGGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 64
              | || ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        864 TTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 923

Qy         65 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        924 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 983

Qy        125 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        984 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 1043

Qy        185 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1044 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 1103

Qy        245 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 304
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1104 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 1163

Qy        305 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1164 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 1223

Qy        365 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1224 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 1283

Qy        425 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 484
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1284 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 1343

Qy        485 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 544
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1344 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 1403

Qy        545 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 604
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1404 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 1463

Qy        605 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 664
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1464 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 1523

Qy        665 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAGTACCGATCCAGAAAGTTC 721
              |||||||||||||||||||||||||||||||||||  |  |   | |  | |||
Db       1524 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGAGTGCGGCCGCGAATTC 1580
```

Search completed: October 17, 2004, 18:18:17
Job time : 595.198 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 17, 2004, 15:27:13 ; Search time 104.054 Seconds
(without alignments)
7855.635 Million cell updates/sec

Title: US-10-679-999-7
Perfect score: 1150
Sequence: 1 CATATGGAACCCAAATCTTG.....TCCGGGTTGTTAATGGATCC 1150

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	695.6	60.5	1720	4	US-09-746-359A-52	Sequence 52, Appl
2	695.4	60.5	1494	4	US-09-499-846-5	Sequence 5, Appli
3	695.4	60.5	1578	4	US-09-499-846-3	Sequence 3, Appli
4	695.4	60.5	1869	4	US-09-499-846-1	Sequence 1, Appli
5	695.2	60.5	1080	3	US-09-180-100-14	Sequence 14, Appl
6	695.2	60.5	1182	3	US-09-180-100-18	Sequence 18, Appl
7	694.8	60.4	1458	4	US-08-030-175-6	Sequence 6, Appli
8	694.8	60.4	1458	4	US-08-030-175-7	Sequence 7, Appli
9	694.8	60.4	1467	4	US-08-030-175-5	Sequence 5, Appli
10	694.8	60.4	1599	4	US-09-023-655-1120	Sequence 1120, Ap
11	694.8	60.4	1617	2	US-08-378-939-9	Sequence 9, Appli
12	694.8	60.4	1701	4	US-09-825-561A-15	Sequence 15, Appl
13	694.8	60.4	19040	4	US-09-343-485A-3	Sequence 3, Appli
14	694.6	60.4	1272	5	PCT-US95-03866-11	Sequence 11, Appl
15	694.6	60.4	1272	5	PCT-US95-03866-13	Sequence 13, Appl
16	694.4	60.4	1019	3	US-09-178-869-1	Sequence 1, Appli
17	694.4	60.4	1019	4	US-09-761-413-1	Sequence 1, Appli
18	694.4	60.4	1428	1	US-08-488-376-19	Sequence 19, Appl
19	694.4	60.4	1428	2	US-08-634-223-19	Sequence 19, Appl
20	694.4	60.4	1428	2	US-08-634-224-19	Sequence 19, Appl
21	694.4	60.4	1428	2	US-08-634-400-19	Sequence 19, Appl
22	694.4	60.4	1428	2	US-08-635-878-19	Sequence 19, Appl
23	694.4	60.4	1428	2	US-08-770-057-19	Sequence 19, Appl
24	694.4	60.4	1428	3	US-09-335-697B-19	Sequence 19, Appl
25	694.4	60.4	1428	4	US-09-335-697B-19	Sequence 19, Appl
26	694.4	60.4	1428	4	US-09-740-002-19	Sequence 19, Appl
27	694.4	60.4	1431	3	US-08-487-550-3	Sequence 3, Appli
28	694.4	60.4	1431	3	US-08-487-550-11	Sequence 11, Appl
29	694.4	60.4	1431	4	US-09-526-098-3	Sequence 3, Appli
30	694.4	60.4	1431	4	US-09-526-098-11	Sequence 11, Appl
31	694.4	60.4	1431	4	US-09-383-916-3	Sequence 3, Appli
32	694.4	60.4	1431	4	US-09-383-916-11	Sequence 11, Appl
33	694.4	60.4	1437	3	US-08-487-550-7	Sequence 7, Appli
34	694.4	60.4	1437	4	US-09-526-098-7	Sequence 7, Appli
35	694.4	60.4	1437	4	US-09-383-916-7	Sequence 7, Appli
36	694.4	60.4	9209	1	US-08-149-099C-3	Sequence 3, Appli
37	694.4	60.4	9209	1	US-08-476-275-2	Sequence 2, Appli
38	694.4	60.4	9209	2	US-08-478-967A-3	Sequence 3, Appli
39	694.4	60.4	9209	3	US-08-475-815B-3	Sequence 3, Appli
40	694.4	60.4	9209	4	US-08-475-813-2	Sequence 2, Appli
41	694.4	60.4	18986	2	US-08-819-866-2	Sequence 2, Appli
42	694.4	60.4	18986	2	US-09-023-715-2	Sequence 2, Appli
43	694.4	60.4	18986	4	US-09-343-485A-2	Sequence 2, Appli
44	693.2	60.3	1350	1	US-08-157-101A-9	Sequence 9, Appli
45	693.2	60.3	1576	1	US-08-157-101A-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-09-746-359A-52
; Sequence 52, Application US/09746359A
; Patent No. 6610286
; GENERAL INFORMATION:
; APPLICANT: Thompson, Penny
; APPLICANT: Foster, Donald C.
; APPLICANT: Xu, Wenfeng
; APPLICANT: Madden, Karen L.
; APPLICANT: Kelly, James D.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Blumberg, Hal
; APPLICANT: Eagan, Maribeth A.
; APPLICANT: Jaspers, Stephen R.
; APPLICANT: Chandrasekher, Yasmin A.
; APPLICANT: No. 6610286ak, Julia E.
; TITLE OF INVENTION: Method for Treating Inflammation
; FILE REFERENCE: 99-108
; CURRENT APPLICATION NUMBER: US/09/746,359A
; CURRENT FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/171,969
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/213,341
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 52
; LENGTH: 1720
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1713)
US-09-746-359A-52

Query Match 60.5%; Score 695.6; DB 4; Length 1720;
Best Local Similarity 99.4%; Pred. No. 2.6e-171;
Matches 698; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
Qy          5 TGGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 64
              || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1016 TTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 1075

Qy         65 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1076 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 1135

Qy        125 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1136 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 1195
```

```
Qy       185 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 244
Db      1196 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 1255

Qy       245 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 304
Db      1256 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 1315

Qy       305 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 364
Db      1316 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 1375

Qy       365 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 424
Db      1376 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 1435

Qy       425 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 484
Db      1436 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 1495

Qy       485 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 544
Db      1496 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 1555

Qy       545 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 604
Db      1556 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 1615

Qy       605 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 664
Db      1616 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 1675

Qy       665 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAGTAC 706
Db      1676 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGAC 1717
```

RESULT 2
US-09-499-846-5
; Sequence 5, Application US/09499846
; Patent No. 6656728
; GENERAL INFORMATION:
; APPLICANT: Kavanaugh et al.
; TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR
; TITLE OF INVENTION: RECEPTOR-IMMUNOGLOBULIN FUSION
; FILE REFERENCE: 035784/195012 (5784-
; CURRENT APPLICATION NUMBER: US/09/499,846
; CURRENT FILING DATE: 2000-02-07
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 1494
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1494)
US-09-499-846-5

Query Match 60.5%; Score 695.4; DB 4; Length 1494;
Best Local Similarity 99.9%; Pred. No. 2.8e-171;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy         6 GGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCT 65
Db       795 GGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCT 854

Qy        66 GGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCG 125
Db       855 GGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCG 914

Qy       126 GACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTT 185
Db       915 GACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTT 974

Qy       186 CAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCA 245
Db       975 CAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCA 1034

Qy       246 GTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAA 305
Db      1035 GTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAA 1094

Qy       306 TGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAAC 365
Db      1095 TGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAAC 1154

Qy       366 CATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCG 425
Db      1155 CATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCG 1214

Qy       426 GGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAG 485
Db      1215 GGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAG 1274

Qy       486 CGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCC 545
Db      1275 CGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCC 1334

Qy       546 TCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAG 605
Db      1335 TCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAG 1394

Qy       606 CAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCA 665
Db      1395 CAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCA 1454

Qy       666 CTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 702
Db      1455 CTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 1491
```

RESULT 3
US-09-499-846-3
; Sequence 3, Application US/09499846
; Patent No. 6656728
; GENERAL INFORMATION:
; APPLICANT: Kavanaugh et al.
; TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR
; TITLE OF INVENTION: RECEPTOR-IMMUNOGLOBULIN FUSION
; FILE REFERENCE: 035784/195012 (5784-
; CURRENT APPLICATION NUMBER: US/09/499,846
; CURRENT FILING DATE: 2000-02-07
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 1578
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1578)
US-09-499-846-3

Query Match 60.5%; Score 695.4; DB 4; Length 1578;
Best Local Similarity 99.9%; Pred. No. 2.9e-171;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy         6 GGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCT 65
Db       879 GGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCT 938

Qy        66 GGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCG 125
Db       939 GGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCG 998
```

```
Qy        126 GACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTT 185
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        999 GACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTT 1058

Qy        186 CAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCA 245
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1059 CAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCA 1118

Qy        246 GTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAA 305
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1119 GTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAA 1178

Qy        306 TGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAAC 365
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1179 TGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAAC 1238

Qy        366 CATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCG 425
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1239 CATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCG 1298

Qy        426 GGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAG 485
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1299 GGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAG 1358

Qy        486 CGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCC 545
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1359 CGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCC 1418

Qy        546 TCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAG 605
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1419 TCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAG 1478

Qy        606 CAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCA 665
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1479 CAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCA 1538

Qy        666 CTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 702
              ||||||||||||||||||||||||||||||||||||
Db       1539 CTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 1575
```

RESULT 4
US-09-499-846-1
; Sequence 1, Application US/09499846
; Patent No. 6656728
; GENERAL INFORMATION:
; APPLICANT: Kavanaugh et al.
; TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR
; TITLE OF INVENTION: RECEPTOR-IMMUNOGLOBULIN FUSION
; FILE REFERENCE: 035784/195012 (5784-
; CURRENT APPLICATION NUMBER: US/09/499,846
; CURRENT FILING DATE: 2000-02-07
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1869
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1869)
US-09-499-846-1

Query Match 60.5%; Score 695.4; DB 4; Length 1869;
Best Local Similarity 99.9%; Pred. No. 3.1e-171;
Matches 696; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          6 GGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCT 65
              ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1170 GGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCT 1229

Qy         66 GGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCG 125
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1230 GGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCG 1289

Qy        126 GACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTT 185
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1290 GACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTT 1349

Qy        186 CAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCA 245
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1350 CAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCA 1409

Qy        246 GTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAA 305
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1410 GTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAA 1469

Qy        306 TGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAAC 365
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1470 TGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAAC 1529

Qy        366 CATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCG 425
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1530 CATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCG 1589

Qy        426 GGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAG 485
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1590 GGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAG 1649

Qy        486 CGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCC 545
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1650 CGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCC 1709

Qy        546 TCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAG 605
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1710 TCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAG 1769

Qy        606 CAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCA 665
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1770 CAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCA 1829

Qy        666 CTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 702
              ||||||||||||||||||||||||||||||||||||
Db       1830 CTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 1866
```

RESULT 5
US-09-180-100-14
; Sequence 14, Application US/09180100
; Patent No. 6306395
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, No. 6306395io
; APPLICANT: NAGATA, Shigekazu
; TITLE OF INVENTION: NOVEL Fas ANTIGEN DERIVATIVE
; FILE REFERENCE: 1110-207P
; CURRENT APPLICATION NUMBER: US/09/180,100
; CURRENT FILING DATE: 1998-11-02
; EARLIER APPLICATION NUMBER: PCT/JP97/01502
; EARLIER FILING DATE: 1997-05-01
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 1080
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-180-100-14

Query Match 60.5%; Score 695.2; DB 3; Length 1080;
Best Local Similarity 99.6%; Pred. No. 2.8e-171;
Matches 697; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy          3 TATGGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACT 62
              || || ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 TAACGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACT 440
```

```
Qy          63 CCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTC 122
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         441 CCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTC 500

Qy         123 CCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAA 182
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         501 CCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAA 560

Qy         183 GTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGA 242
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         561 GTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGA 620

Qy         243 GCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCT 302
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         621 GCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCT 680

Qy         303 GAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAA 362
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         681 GAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAA 740

Qy         363 AACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATC 422
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         741 AACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATC 800

Qy         423 CCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCC 482
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         801 CCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCC 860

Qy         483 CAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCAC 542
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         861 CAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCAC 920

Qy         543 GCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAA 602
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         921 GCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAA 980

Qy         603 GAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAA 662
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         981 GAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAA 1040

Qy         663 CCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 702
               |||||||||||||||||||||||||||||||||||||||
Db        1041 CCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 1080
```

RESULT 6
US-09-180-100-18
; Sequence 18, Application US/09180100
; Patent No. 6306395
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, No. 6306395io
; APPLICANT: NAGATA, Shigekazu
; TITLE OF INVENTION: NOVEL Fas ANTIGEN DERIVATIVE
; FILE REFERENCE: 1110-207P
; CURRENT APPLICATION NUMBER: US/09/180,100
; CURRENT FILING DATE: 1998-11-02
; EARLIER APPLICATION NUMBER: PCT/JP97/01502
; EARLIER FILING DATE: 1997-05-01
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 1182
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-180-100-18

Query Match 60.5%; Score 695.2; DB 3; Length 1182;
Best Local Similarity 99.6%; Pred. No. 2.9e-171;
Matches 697; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy           3 TATGGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACT 62
               ||  || ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         464 TAACGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACT 523
```

```
Qy          63 CCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTC 122
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         524 CCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTC 583

Qy         123 CCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAA 182
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         584 CCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAA 643

Qy         183 GTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGA 242
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         644 GTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGA 703

Qy         243 GCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCT 302
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         704 GCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCT 763

Qy         303 GAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAA 362
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         764 GAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAA 823

Qy         363 AACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATC 422
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         824 AACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATC 883

Qy         423 CCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCC 482
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         884 CCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCC 943

Qy         483 CAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCAC 542
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         944 CAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCAC 1003

Qy         543 GCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAA 602
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1004 GCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAA 1063

Qy         603 GAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAA 662
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1064 GAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAA 1123

Qy         663 CCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 702
               |||||||||||||||||||||||||||||||||||||||
Db        1124 CCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 1163
```

RESULT 7
US-08-030-175-6
; Sequence 6, Application US/08030175
; Patent No. 6767996
; GENERAL INFORMATION:
; APPLICANT: Gorman, Scott D.
; APPLICANT: Clark, Michael R.
; APPLICANT: Cobbold, Stephen P.
; APPLICANT: Waldmann, Herman
; TITLE OF INVENTION: ALTERED ANTIBODIES AND THEIR PREPARATION
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P. C.
; STREET: 555 13TH ST., NW Suite 701 East
; CITY: Washington
; STATE: D. C.
; COUNTRY: U.S.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk, 5.25 inch, 360 Kb storage
; COMPUTER: IBM AT compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS V 3.2
; SOFTWARE: WordPerfect 5.0 (Dos Text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/030,175
; FILING DATE: 17-MAY-1993
; CLASSIFICATION: 424

```
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/GB91/01578
;      FILING DATE:  13-SEP-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ernst, Barbara G.
;      REGISTRATION NUMBER:  30,377
;      REFERENCE/DOCKET NUMBER:  1768-113
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)783-6040
;      TELEFAX:  (202)783-6031
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1458 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  both
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  36..1439
US-08-030-175-6

  Query Match           60.4%;  Score 694.8;  DB 4;  Length 1458;
  Best Local Similarity  99.7%;  Pred. No. 4e-171;
  Matches  696;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 TGGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 64
              | || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        739 TTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 798

Qy         65 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        799 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 858

Qy        125 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        859 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 918

Qy        185 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        919 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 978

Qy        245 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 304
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        979 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 1038

Qy        305 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1039 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 1098

Qy        365 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1099 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 1158

Qy        425 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 484
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1159 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 1218

Qy        485 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 544
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1219 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 1278

Qy        545 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 604
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1279 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 1338

Qy        605 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 664
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1339 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 1398

Qy        665 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 702
              ||||||||||||||||||||||||||||||||||||||
Db       1399 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 1436


RESULT 8
US-08-030-175-7
; Sequence 7, Application US/08030175
; Patent No. 6767996
;  GENERAL INFORMATION:
;    APPLICANT:  Gorman, Scott D.
;    APPLICANT:  Clark, Michael R.
;    APPLICANT:  Cobbold, Stephen P.
;    APPLICANT:  Waldmann, Herman
;    TITLE OF INVENTION:  ALTERED ANTIBODIES AND THEIR PREPARATION
;    NUMBER OF SEQUENCES:  43
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Rothwell, Figg, Ernst & Kurz, P. C.
;      STREET:  555 13TH ST., NW  Suite 701 East
;      CITY:  Washington
;      STATE:  D. C.
;      COUNTRY:  U.S.
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk, 5.25 inch, 360 Kb storage
;      COMPUTER:  IBM AT compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS V 3.2
;      SOFTWARE:  WordPerfect 5.0 (Dos Text)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/030,175
;      FILING DATE:  17-MAY-1993
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/GB91/01578
;      FILING DATE:  13-SEP-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ernst, Barbara G.
;      REGISTRATION NUMBER:  30,377
;      REFERENCE/DOCKET NUMBER:  1768-113
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)783-6040
;      TELEFAX:  (202)783-6031
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1458 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  both
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  36..1439
US-08-030-175-7

  Query Match           60.4%;  Score 694.8;  DB 4;  Length 1458;
  Best Local Similarity  99.7%;  Pred. No. 4e-171;
  Matches  696;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 TGGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 64
              | || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        739 TTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 798

Qy         65 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        799 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 858

Qy        125 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        859 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 918

Qy        185 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        919 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 978

Qy        245 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 304
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        979 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 1038

Qy        305 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1039 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 1098

Qy        365 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1099 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 1158

Qy        425 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 484
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1159 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 1218

Qy        485 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 544
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1219 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 1278

Qy        545 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 604
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1279 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 1338

Qy        605 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 664
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1339 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 1398

Qy        665 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 702
              |||||||||||||||||||||||||||||||||||||||
Db       1399 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 1436


RESULT 9
US-08-030-175-5
; Sequence 5, Application US/08030175
; Patent No. 6767996
;  GENERAL INFORMATION:
;    APPLICANT:  Gorman, Scott D.
;    APPLICANT:  Clark, Michael R.
;    APPLICANT:  Cobbold, Stephen P.
;    APPLICANT:  Waldmann, Herman
;    TITLE OF INVENTION:  ALTERED ANTIBODIES AND THEIR PREPARATION
;    NUMBER OF SEQUENCES:  43
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Rothwell, Figg, Ernst & Kurz, P. C.
;      STREET:  555 13TH ST., NW  Suite 701 East
;      CITY:  Washington
;      STATE:  D. C.
;      COUNTRY:  U.S.
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk, 5.25 inch, 360 Kb storage
;      COMPUTER:  IBM AT compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS V 3.2
;      SOFTWARE:  WordPerfect 5.0 (Dos Text)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/030,175
;      FILING DATE:  17-MAY-1993
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/GB91/01578
;      FILING DATE:  13-SEP-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ernst, Barbara G.
;      REGISTRATION NUMBER:  30,377
;      REFERENCE/DOCKET NUMBER:  1768-113
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)783-6040
;      TELEFAX:  (202)783-6031
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1467 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  both
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-030-175-5

  Query Match             60.4%;  Score 694.8;  DB 4;  Length 1467;
  Best Local Similarity   99.7%;  Pred. No. 4e-171;
  Matches  696;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 TGGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 64
              | || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        748 TTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 807

Qy         65 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        808 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 867

Qy        125 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        868 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 927

Qy        185 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        928 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 987

Qy        245 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 304
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        988 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 1047

Qy        305 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1048 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 1107

Qy        365 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1108 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 1167

Qy        425 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 484
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1168 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 1227

Qy        485 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 544
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1228 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 1287

Qy        545 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 604
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1288 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 1347

Qy        605 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 664
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1348 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 1407

Qy        665 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 702
              |||||||||||||||||||||||||||||||||||||||
Db       1408 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 1445


RESULT 10
US-09-023-655-1120
; Sequence 1120, Application US/09023655
; Patent No. 6607879
;  GENERAL INFORMATION:
;    APPLICANT:  Cocks, Benjamin G.
;    APPLICANT:  Susan G. Stuart
;    APPLICANT:  Jeffrey J. Seilhamer
;    TITLE OF INVENTION:  COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
;    TITLE OF INVENTION:  EXPRESSION
;    NUMBER OF SEQUENCES:  1508
;    CORRESPONDENCE ADDRESS:
```

```
;       ADDRESSEE:  INCYTE PHARMACEUTICALS, INC.
;       STREET:  3174 PORTER DRIVE
;       CITY:  PALO ALTO
;       STATE:  CALIFORNIA
;       COUNTRY:  USA
;       ZIP:  94304
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  Word Perfect 6.1 for Windows/MS-DOS 6.2
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/09/023,655
;       FILING DATE:  HEREWITH
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:
;       FILING DATE:
;       CLASSIFICATION:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Zeller, Karen J.
;       REGISTRATION NUMBER:  37,071
;       REFERENCE/DOCKET NUMBER:  PA-0001 US
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (650) 855-0555
;       TELEFAX:  (650) 845-4166
;   INFORMATION FOR SEQ ID NO:  1120:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1599 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     IMMEDIATE SOURCE:
;       LIBRARY:  GENBANK
;       CLONE:  g185361
US-09-023-655-1120

  Query Match             60.4%;  Score 694.8;  DB 4;  Length 1599;
  Best Local Similarity   99.7%;  Pred. No. 4.2e-171;
  Matches  696;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 TGGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 64
              | || ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        765 TTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 824

Qy         65 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        825 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 884

Qy        125 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        885 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 944

Qy        185 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        945 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 1004

Qy        245 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 304
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1005 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 1064

Qy        305 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1065 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 1124

Qy        365 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1125 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 1184

Qy        425 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 484
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1185 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 1244

Qy        485 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 544
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1245 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 1304

Qy        545 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 604
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1305 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 1364

Qy        605 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 664
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1365 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 1424

Qy        665 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 702
              |||||||||||||||||||||||||||||||||||||
Db       1425 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 1462


RESULT 11
US-08-378-939-9
; Sequence 9, Application US/08378939
; Patent No. 5876961
;  GENERAL INFORMATION:
;    APPLICANT:  CROWE, JAMES SCOTT
;    APPLICANT:  LEWIS, ALAN PETER
;    TITLE OF INVENTION:  PRODUCTION OF ANTIBODIES
;    NUMBER OF SEQUENCES:  46
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ROTHWELL, FIGG, ERNST & KURZ
;      STREET:  555 THIRTEENTH ST. N.W.
;      CITY:  WASHINGTON
;      STATE:  D. C.
;      COUNTRY:  U.S.
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/378,939
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/952640
;      FILING DATE:  01-DEC-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  ERNST, BARBARA G
;      REGISTRATION NUMBER:  30,377
;      REFERENCE/DOCKET NUMBER:  1808-118
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 783-6040
;      TELEFAX:  (202) 783-6031
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1617 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  both
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FEATURE:
;      NAME/KEY:  sig_peptide
;      LOCATION:  35..92
;    FEATURE:
;      NAME/KEY:  mat_peptide
;      LOCATION:  93..1465
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  35..1465
US-08-378-939-9

  Query Match             60.4%;  Score 694.8;  DB 2;  Length 1617;
```

```
 Best Local Similarity   99.7%;  Pred. No. 4.2e-171;
 Matches  696;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 TGGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 64
              | || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        765 TTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 824

Qy         65 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        825 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 884

Qy        125 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        885 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 944

Qy        185 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        945 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 1004

Qy        245 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 304
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1005 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 1064

Qy        305 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1065 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 1124

Qy        365 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1125 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 1184

Qy        425 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 484
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1185 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 1244

Qy        485 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 544
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1245 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 1304

Qy        545 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 604
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1305 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 1364

Qy        605 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 664
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1365 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 1424

Qy        665 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 702
              |||||||||||||||||||||||||||||||||||||
Db       1425 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 1462


RESULT 12
US-09-825-561A-15
; Sequence 15, Application US/09825561A
; Patent No. 6777539
; GENERAL INFORMATION:
;  APPLICANT: Sprecher, Cindy A.
;  APPLICANT:  No. 6777539ak, Julia E.
;  APPLICANT:  West, James W.
;  APPLICANT:  Presnell, Scott R.
;  APPLICANT:  Holly, Richard D.
;  APPLICANT:  Nelson, Andrew J.
;  TITLE OF INVENTION: SOLUBLE ZALPHA11 CYTOKINE RECEPTORS
;  FILE REFERENCE: 00-22
;  CURRENT APPLICATION NUMBER: US/09/825,561A
;  CURRENT FILING DATE:  2000-04-05
;  PRIOR APPLICATION NUMBER: US 60/194,731
;  PRIOR FILING DATE: 2000-04-05
;  PRIOR APPLICATION NUMBER: US 60/222,121
;  PRIOR FILING DATE: 2000-07-28
;  NUMBER OF SEQ ID NOS: 86
;  SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 15
;   LENGTH: 1701
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: soluble zalpha11R/IgGgamma1 construct
;   NAME/KEY: CDS
;   LOCATION: (1)...(1701)
US-09-825-561A-15

  Query Match             60.4%;  Score 694.8;  DB 4;  Length 1701;
  Best Local Similarity   99.7%;  Pred. No. 4.3e-171;
  Matches  696;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 TGGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 64
              | || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1004 TTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 1063

Qy         65 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1064 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 1123

Qy        125 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1124 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 1183

Qy        185 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1184 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 1243

Qy        245 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 304
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1244 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 1303

Qy        305 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1304 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 1363

Qy        365 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1364 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 1423

Qy        425 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 484
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1424 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 1483

Qy        485 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 544
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1484 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 1543

Qy        545 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 604
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1544 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 1603

Qy        605 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 664
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1604 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 1663

Qy        665 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 702
              |||||||||||||||||||||||||||||||||||||
Db       1664 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 1701


RESULT 13
US-09-343-485A-3
; Sequence 3, Application US/09343485A
; Patent No. 6413777
; GENERAL INFORMATION:
;  APPLICANT: REFF, MITCHELL R.
;  APPLICANT:  BARNETT, RICHARD S.
;  APPLICANT:  MCLACHLAN, KAREN R.
;  TITLE OF INVENTION: NOVEL METHOD FOR INTEGRATING GENES AT SPECIFIC SITES IN
;  TITLE OF INVENTION:  MAMMALIAN CELLS VIA HOMOLOGOUS RECOMBINATION AND
```

```
;  TITLE OF INVENTION:  VECTORS FOR ACCOMPLISHING THE SAME
;  FILE REFERENCE: 037003-0275807
;  CURRENT APPLICATION NUMBER: US/09/343,485A
;  CURRENT FILING DATE:  1999-06-30
;  PRIOR APPLICATION NUMBER: 09/023,715
;  PRIOR FILING DATE: 1998-02-13
;  PRIOR APPLICATION NUMBER: 08/819,866
;  PRIOR FILING DATE: 1997-03-14
;  NUMBER OF SEQ ID NOS: 3
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 19040
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
;   OTHER INFORMATION: referred to as "Mandy"
US-09-343-485A-3

  Query Match             60.4%;  Score 694.8;  DB 4;  Length 19040;
  Best Local Similarity   99.7%;  Pred. No. 1e-170;
  Matches  696;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 TGGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 64
              | || ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10140 TTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC 10199

Qy         65 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10200 TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC 10259

Qy        125 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10260 GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGT 10319

Qy        185 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10320 TCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGC 10379

Qy        245 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 304
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10380 AGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGA 10439

Qy        305 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10440 ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA 10499

Qy        365 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10500 CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCC 10559

Qy        425 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 484
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10560 GGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 10619

Qy        485 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 544
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10620 GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGC 10679

Qy        545 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 604
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10680 CTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGA 10739

Qy        605 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 664
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      10740 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC 10799

Qy        665 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 702
              |||||||||||||||||||||||||||||||||||||||
Db      10800 ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 10837

RESULT 14
```

```
PCT-US95-03866-11
; Sequence 11, Application PC/TUS9503866
;  GENERAL INFORMATION:
;     APPLICANT:  CytoMed, Inc. (all states except US)
;     APPLICANT:  Nocka, Karl (US only)
;     APPLICANT:  Lobell, Robert B (US only)
;     TITLE OF INVENTION:  STABILIZED DIMER OF KIT LIGAND AND
;     TITLE OF INVENTION:  FLT-3/FLK-2 LIGAND
;     NUMBER OF SEQUENCES:  36
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Fish & Neave
;       STREET:  1251 Avenue of the Americas
;       CITY:  New York
;       STATE:  New York
;       COUNTRY:  United States of America
;       ZIP:  10020
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/US95/03866
;       FILING DATE:
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/220,379
;       FILING DATE:  28-MAR-1994
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Haley Jr, James F
;       REGISTRATION NUMBER:  27,794
;       REFERENCE/DOCKET NUMBER:  CytoMed/2
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  212-596-9000
;       TELEFAX:  212-596-9090
;  INFORMATION FOR SEQ ID NO:  11:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1272 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  double
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA
;     HYPOTHETICAL:  NO
;     ANTI-SENSE:  NO
;     FEATURE:
;       NAME/KEY:  mat_peptide
;       LOCATION:  76..1272
;       OTHER INFORMATION:  /product= "human KL-Ig fusion
;       OTHER INFORMATION:  protein"
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  1..1272
PCT-US95-03866-11

  Query Match             60.4%;  Score 694.6;  DB 5;  Length 1272;
  Best Local Similarity   99.4%;  Pred. No. 4.3e-171;
  Matches  697;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          2 ATATGGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAAC 61
              ||   || ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        572 ATCCCGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAAC 631

Qy         62 TCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCT 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        632 TCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCT 691

Qy        122 CCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCA 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        692 CCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCA 751

Qy        182 AGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGG 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        752 AGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGG 811
```

```
Qy        242 AGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGC 301
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        812 AGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGC 871

Qy        302 TGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGA 361
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        872 TGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGA 931

Qy        362 AAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCAT 421
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        932 AAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCAT 991

Qy        422 CCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATC 481
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        992 CCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATC 1051

Qy        482 CCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCA 541
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1052 CCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCA 1111

Qy        542 CGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACA 601
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1112 CGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACA 1171

Qy        602 AGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACA 661
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1172 AGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACA 1231

Qy        662 ACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 702
              |||||||||||||||||||||||||||||||||||||||||
Db       1232 ACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 1272
```

```
RESULT 15
PCT-US95-03866-13
; Sequence 13, Application PC/TUS9503866
;  GENERAL INFORMATION:
;    APPLICANT:  CytoMed, Inc. (all states except US)
;    APPLICANT:  Nocka, Karl (US only)
;    APPLICANT:  Lobell, Robert B (US only)
;    TITLE OF INVENTION:  STABILIZED DIMER OF KIT LIGAND AND
;    TITLE OF INVENTION:  FLT-3/FLK-2 LIGAND
;    NUMBER OF SEQUENCES:  36
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Neave
;      STREET:  1251 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  United States of America
;      ZIP:  10020
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/03866
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/220,379
;      FILING DATE:  28-MAR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Haley Jr, James F
;      REGISTRATION NUMBER:  27,794
;      REFERENCE/DOCKET NUMBER:  CytoMed/2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-596-9000
;      TELEFAX:  212-596-9090
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1272 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FEATURE:
;      NAME/KEY:  mat_peptide
;      LOCATION:  76..1272
;      OTHER INFORMATION:  /product= "human KL-Ig fusion
;      OTHER INFORMATION:  protein"
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..1272
PCT-US95-03866-13

  Query Match             60.4%;  Score 694.6;  DB 5;  Length 1272;
  Best Local Similarity   99.4%;  Pred. No. 4.3e-171;
  Matches  697;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          2 ATATGGAACCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAAC 61
              ||  || ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        572 ATCCCGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAAC 631

Qy         62 TCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCT 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        632 TCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCT 691

Qy        122 CCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCA 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        692 CCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCA 751

Qy        182 AGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGG 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        752 AGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGG 811

Qy        242 AGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGC 301
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        812 AGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGC 871

Qy        302 TGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGA 361
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        872 TGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGA 931

Qy        362 AAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCAT 421
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        932 AAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCAT 991

Qy        422 CCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATC 481
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        992 CCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATC 1051

Qy        482 CCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCA 541
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1052 CCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCA 1111

Qy        542 CGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACA 601
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1112 CGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACA 1171

Qy        602 AGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACA 661
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1172 AGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACA 1231

Qy        662 ACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 702
              |||||||||||||||||||||||||||||||||||||||||
Db       1232 ACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 1272


Search completed: October 17, 2004, 17:00:19
Job time : 107.054 secs
```

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 17, 2004, 15:34:57 ; Search time 4411.65 Seconds
(without alignments)
11298.387 Million cell updates/sec

Title: US-10-679-999-8
Perfect score: 1150
Sequence: 1 GTATACCTTGGGTTTAGAAC.....AGGCCCAACAATTACCTAGG 1150

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1150	100.0	1150	6	BD056518	BD056518 OB fusion
2	1134	98.6	1150	6	BD056520	BD056520 OB fusion
3	1117.8	97.2	1135	6	BD056522	BD056522 OB fusion
4	1105	96.1	1135	6	BD056524	BD056524 OB fusion
5	676.2	58.8	1142	6	I27618	I27618 Sequence 9
6	674.4	58.6	861	6	BD263010	BD263010 Dimeric t
7	673	58.5	684	6	BD263000	BD263000 Dimeric t
8	440.8	38.3	454	6	BD004077	BD004077 Methods o
9	440.8	38.3	454	6	BD056516	BD056516 OB fusion
10	378.4	32.9	491	6	BD004075	BD004075 Methods o
11	378.4	32.9	491	6	BD056514	BD056514 OB fusion
12	371.2	32.3	1528	6	BD105735	BD105735 A method
13	371.2	32.3	1528	6	BD105743	BD105743 Immunoglo
14	60	5.2	2287	6	AR029004	AR029004 Sequence
15	60	5.2	2287	6	AR037308	AR037308 Sequence
16	60	5.2	2287	6	I90051	I90051 Sequence 1
17	60	5.2	2287	6	AR392155	AR392155 Sequence
18	60	5.2	2287	6	BD000539	BD000539 Antibody
c 19	54.6	4.7	232373	2	AC134805	AC134805 Rattus no
c 20	52.8	4.6	234964	2	AC094679	AC094679 Rattus no
21	51.6	4.5	178323	2	AC126315	AC126315 Rattus no
c 22	51	4.4	125020	9	AF429315	AF429315 Homo sapi
23	50.8	4.4	908	8	AB029092	AB029092 Cucumis s
24	50.8	4.4	1110	8	AB029147	AB029147 Cucumis s
25	49.8	4.3	125020	9	AF429315	AF429315 Homo sapi
26	49.8	4.3	243553	2	AC096320	AC096320 Rattus no
27	49.4	4.3	178372	2	BX569797	BX569797 Danio rer
c 28	49.4	4.3	181047	5	AC139110	AC139110 Danio rer
29	49.4	4.3	191401	5	BX470130	BX470130 Zebrafish
30	49.2	4.3	158134	5	AL953878	AL953878 Zebrafish
c 31	49.2	4.3	174423	2	AC141189	AC141189 Rattus no
c 32	48	4.2	294769	2	AC098907	AC098907 Rattus no
33	47.8	4.2	2000	6	AX655393	AX655393 Sequence
34	47.8	4.2	266056	2	AC094507	AC094507 Rattus no
c 35	47.6	4.1	255447	2	AC096032	AC096032 Rattus no
c 36	47.6	4.1	261604	2	AC119819	AC119819 Mus muscu
37	47.4	4.1	171286	3	AC008226	AC008226 Drosophil
38	47.4	4.1	301397	3	AE003672	AE003672 Drosophil
c 39	47	4.1	2000	6	AX655393	AX655393 Sequence
c 40	47	4.1	175351	2	AC117900	AC117900 Rattus no
41	47	4.1	242516	2	AC106523	AC106523 Rattus no
c 42	47	4.1	247341	2	AC099178	AC099178 Rattus no
43	46.8	4.1	125026	10	AC091616	AC091616 Rattus no
c 44	46.8	4.1	241327	2	AC127126	AC127126 Rattus no
c 45	46.8	4.1	251075	2	AC132995	AC132995 Rattus no

ALIGNMENTS

RESULT 1
BD056518
LOCUS BD056518 1150 bp DNA linear PAT 27-AUG-2002
DEFINITION OB fusion protein compositions and methods.
ACCESSION BD056518
VERSION BD056518.1 GI:22602124
KEYWORDS JP 2001512417-A/6.
SOURCE Aequorea victoria
ORGANISM Aequorea victoria
Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
Aequoreidae; Aequorea.
REFERENCE 1 (bases 1 to 1150)
AUTHORS Mann,M.B. and Hecht,R.I.
TITLE OB fusion protein compositions and methods
JOURNAL Patent: JP 2001512417-A 6 21-AUG-2001;

```
            AMGEN INC
COMMENT     PN   JP 2001512417-A/6
            PD   21-AUG-2001
            PF   11-DEC-1997 JP 1998528896
            PR   20-DEC-1996 US    08/770973
            PI   MICHAEL BENJAMIN MANN,RANDY IRA HECHT
            PC   C07K14/575,A61K38/00,A61P3/04,A61P3/06,A61P3/10,A61P9/10, PC
            A61P43/00,
            PC   C12N15/09,C12N15/00,A61K37/02
            CC   Strandedness: Double;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers.
FEATURES        Location/Qualifiers
     source     1. .1150
                /organism="Aequorea victoria"
                /mol_type="genomic DNA"
                /db_xref="taxon:6100"
ORIGIN

  Query Match           100.0%;  Score 1150;  DB 6;  Length 1150;
  Best Local Similarity  100.0%;  Pred. No. 1.6e-266;
  Matches 1150;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTATACCTTGGGTTTAGAACACTGTTTTGAGTGTGTACGGGTGGCACGGGTCGTGGACTT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GTATACCTTGGGTTTAGAACACTGTTTTGAGTGTGTACGGGTGGCACGGGTCGTGGACTT 60

Qy         61 GAGGACCCCCCTGGCAGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GAGGACCCCCCTGGCAGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAG 120

Qy        121 AGGGCCTGGGGACTCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AGGGCCTGGGGACTCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAG 180

Qy        181 TTCAAGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TTCAAGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTC 240

Qy        241 CTCGTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTCGTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACC 300

Qy        301 GACTTACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GACTTACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTC 360

Qy        361 TTTTGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TTTTGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGT 420

Qy        421 AGGGCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AGGGCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATA 480

Qy        481 GGGTCGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGGTCGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGG 540

Qy        541 TGCGGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TGCGGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTG 600

Qy        601 TTCTCGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TTCTCGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTG 660

Qy        661 TTGGTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCATTTCATGGCTAGGTCTTTCAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TTGGTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCATTTCATGGCTAGGTCTTTCAA 720

Qy        721 GTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATGCGCATAGTTGCTGTAGTCAGTG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATGCGCATAGTTGCTGTAGTCAGTG 780

Qy        781 TGGGTCAGCCACTCGAGATTTGTCTTTCAATGTCCGGACCTGAAGTAGGGCCCAGACGTG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TGGGTCAGCCACTCGAGATTTGTCTTTCAATGTCCGGACCTGAAGTAGGGCCCAGACGTG 840

Qy        841 GGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCGACATATGGTCGTCTAGAATTGG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCGACATATGGTCGTCTAGAATTGG 900

Qy        901 AGGTACGGCAGGGCATTGCAATAGGTCTAGAGATTGCTGGAGCTCTTGGAAGCGCTGGAC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 AGGTACGGCAGGGCATTGCAATAGGTCTAGAGATTGCTGGAGCTCTTGGAAGCGCTGGAC 960

Qy        961 GACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGGTACCCGAAGTCCAGAACTCTGA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGGTACCCGAAGTCCAGAACTCTGA 1020

Qy       1021 GACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCAATGTCGTGGCTTCAACAACGAGAC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCAATGTCGTGGCTTCAACAACGAGAC 1080

Qy       1081 AGGGCAGACGTCCCAAGGGAAGTCCTGTACGAAACCGTCGACCTGGACAGAGGCCCAACA 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 AGGGCAGACGTCCCAAGGGAAGTCCTGTACGAAACCGTCGACCTGGACAGAGGCCCAACA 1140

Qy       1141 ATTACCTAGG 1150
              ||||||||||
Db       1141 ATTACCTAGG 1150


RESULT 2
BD056520
LOCUS       BD056520               1150 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  OB fusion protein compositions and methods.
ACCESSION   BD056520
VERSION     BD056520.1  GI:22602126
KEYWORDS    JP 2001512417-A/8.
SOURCE      Aequorea victoria
  ORGANISM  Aequorea victoria
            Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
            Aequoreidae; Aequorea.
REFERENCE   1  (bases 1 to 1150)
  AUTHORS   Mann,M.B. and Hecht,R.I.
  TITLE     OB fusion protein compositions and methods
  JOURNAL   Patent: JP 2001512417-A 8 21-AUG-2001;
            AMGEN INC
COMMENT     PN   JP 2001512417-A/8
            PD   21-AUG-2001
            PF   11-DEC-1997 JP 1998528896
            PR   20-DEC-1996 US    08/770973
            PI   MICHAEL BENJAMIN MANN,RANDY IRA HECHT
            PC   C07K14/575,A61K38/00,A61P3/04,A61P3/06,A61P3/10,A61P9/10, PC
            A61P43/00,
            PC   C12N15/09,C12N15/00,A61K37/02
            CC   Strandedness: Double;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers.
FEATURES        Location/Qualifiers
     source     1. .1150
                /organism="Aequorea victoria"
                /mol_type="genomic DNA"
                /db_xref="taxon:6100"
ORIGIN

  Query Match           98.6%;  Score 1134;  DB 6;  Length 1150;
  Best Local Similarity  99.1%;  Pred. No. 1.2e-262;
  Matches 1140;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          1 GTATACCTTGGGTTTAGAACACTGTTTTGAGTGTGTACGGGTGGCACGGGTCGTGGACTT 60
              |||||||||||  ||||||  |||||||||||||||||||  ||||| ||  |||||| ||  |||
Db          1 GTATACCTTGGTTTTAGACGACTGTTTTGAGTGTGTACAGGTGGAACAGGTCGAGGCCTT 60
```

```
Qy        61 GAGGACCCCCCTGGCAGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAG 120
Db        61 GAGGACCCCCCAGGAAGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAG 120

Qy       121 AGGGCCTGGGGACTCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAG 180
Db       121 AGGGCCTGGGGACTCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAG 180

Qy       181 TTCAAGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTC 240
Db       181 TTCAAGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTC 240

Qy       241 CTCGTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACC 300
Db       241 CTCGTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACC 300

Qy       301 GACTTACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTC 360
Db       301 GACTTACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTC 360

Qy       361 TTTTGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGT 420
Db       361 TTTTGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGT 420

Qy       421 AGGGCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATA 480
Db       421 AGGGCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATA 480

Qy       481 GGGTCGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGG 540
Db       481 GGGTCGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGG 540

Qy       541 TGCGGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTG 600
Db       541 TGCGGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTG 600

Qy       601 TTCTCGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTG 660
Db       601 TTCTCGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTG 660

Qy       661 TTGGTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCATTTCATGGCTAGGTCTTTCAA 720
Db       661 TTGGTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCATTTCATGGCTAGGTCTTTCAA 720

Qy       721 GTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATGCGCATAGTTGCTGTAGTCAGTG 780
Db       721 GTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATGCGCATAGTTGCTGTAGTCAGTG 780

Qy       781 TGGGTCAGCCACTCGAGATTTGTCTTTCAATGTCCGGACCTGAAGTAGGGCCCAGACGTG 840
Db       781 TGGGTCAGCCACTCGAGATTTGTCTTTCAATGTCCGGACCTGAAGTAGGGCCCAGACGTG 840

Qy       841 GGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCGACATATGGTCGTCTAGAATTGG 900
Db       841 GGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCGACATATGGTCGTCTAGAATTGG 900

Qy       901 AGGTACGGCAGGGCATTGCAATAGGTCTAGAGATTGCTGGAGCTCTTGGAAGCGCTGGAC 960
Db       901 AGGTACGGCAGGGCATTGCAATAGGTCTAGAGATTGCTGGAGCTCTTGGAAGCGCTGGAC 960

Qy       961 GACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGGTACCCGAAGTCCAGAACTCTGA 1020
Db       961 GACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGGTACCCGAAGTCCAGAACTCTGA 1020

Qy      1021 GACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCAATGTCGTGGCTTCAACAACGAGAC 1080
Db      1021 GACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCAATGTCGTGGCTTCAACAACGAGAC 1080

Qy      1081 AGGGCAGACGTCCCAAGGGAAGTCCTGTACGAAACCGTCGACCTGGACAGAGGCCCAACA 1140
Db      1081 AGGGCAGACGTCCCAAGGGAAGTCCTGTACGAAACCGTCGACCTGGACAGAGGCCCAACA 1140

Qy      1141 ATTACCTAGG 1150
Db      1141 ATTACCTAGG 1150
```

```
RESULT 3
BD056522
LOCUS       BD056522                1135 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  OB fusion protein compositions and methods.
ACCESSION   BD056522
VERSION     BD056522.1  GI:22602128
KEYWORDS    JP 2001512417-A/10.
SOURCE      Aequorea victoria
  ORGANISM  Aequorea victoria
            Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
            Aequoreidae; Aequorea.
REFERENCE   1  (bases 1 to 1135)
  AUTHORS   Mann,M.B. and Hecht,R.I.
  TITLE     OB fusion protein compositions and methods
  JOURNAL   Patent: JP 2001512417-A 10 21-AUG-2001;
            AMGEN INC
COMMENT     PN   JP 2001512417-A/10
            PD   21-AUG-2001
            PF   11-DEC-1997 JP 1998528896
            PR   20-DEC-1996 US    08/770973
            PI   MICHAEL BENJAMIN MANN,RANDY IRA HECHT
            PC   C07K14/575,A61K38/00,A61P3/04,A61P3/06,A61P3/10,A61P9/10, PC
            A61P43/00,
            PC   C12N15/09,C12N15/00,A61K37/02
            CC   Strandedness: Double;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers.
FEATURES                Location/Qualifiers
     source             1. .1135
                        /organism="Aequorea victoria"
                        /mol_type="genomic DNA"
                        /db_xref="taxon:6100"
ORIGIN

  Query Match             97.2%;  Score 1117.8;  DB 6;  Length 1135;
  Best Local Similarity   99.4%;  Pred. No. 9.5e-259;
  Matches 1122;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy         22 CTGTTTTGAGTGTGTACGGGTGGCACGGGTCGTGGACTTGAGGACCCCCCTGGCAGTCAG 81
Db          7 CTGTTTTGAGTGTGTACAGGTGGAACAGGTCGAGGCCTTGAGGACCCCCCAGGAAGTCAG 66

Qy         82 AAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGT 141
Db         67 AAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGT 126

Qy        142 ACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTG 201
Db        127 ACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTG 186

Qy        202 CCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATG 261
Db        187 CCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATG 246

Qy        262 GCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATGTTC 321
Db        247 GCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATGTTC 306

Qy        322 ACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTT 381
Db        307 ACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTT 366

Qy        382 CCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTC 441
Db        367 CCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTC 426

Qy        442 TTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTC 501
Db        427 TTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTC 486
```

```
Qy       502 ACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGG 561
Db       487 ACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGG 546

Qy       562 CTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCC 621
Db       547 CTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCC 606

Qy       622 TTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCG 681
Db       607 TTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCG 666

Qy       682 GAGAGGGACAGAGGCCCATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAAT 741
Db       667 GAGAGGGACAGAGGCCCATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAAT 726

Qy       742 TAATTTTGCTAGCAATGCGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTT 801
Db       727 TAATTTTGCTAGCAATGCGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTT 786

Qy       802 GTCTTTCAATGTCCGGACCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTT 861
Db       787 GTCTTTCAATGTCCGGACCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTT 846

Qy       862 TACCTGGTCTGGGACCGACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAA 921
Db       847 TACCTGGTCTGGGACCGACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAA 906

Qy       922 TAGGTCTAGAGATTGCTGGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGG 981
Db       907 TAGGTCTAGAGATTGCTGGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGG 966

Qy       982 TTTAGGACGGTGGACGGTACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAG 1041
Db       967 TTTAGGACGGTGGACGGTACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAG 1026

Qy      1042 GACCTTCGTAGGCCAATGTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAA 1101
Db      1027 GACCTTCGTAGGCCAATGTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAA 1086

Qy      1102 GTCCTGTACGAAACCGTCGACCTGGACAGAGGCCCAACAATTACCTAGG 1150
Db      1087 GTCCTGTACGAAACCGTCGACCTGGACAGAGGCCCAACAATTACCTAGG 1135
```

RESULT 4
BD056524

LOCUS	BD056524 1135 bp DNA linear PAT 27-AUG-2002
DEFINITION	OB fusion protein compositions and methods.
ACCESSION	BD056524
VERSION	BD056524.1 GI:22602130
KEYWORDS	JP 2001512417-A/12.
SOURCE	Aequorea victoria
ORGANISM	Aequorea victoria Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae; Aequoreidae; Aequorea.
REFERENCE	1 (bases 1 to 1135)
AUTHORS	Mann,M.B. and Hecht,R.I.
TITLE	OB fusion protein compositions and methods
JOURNAL	Patent: JP 2001512417-A 12 21-AUG-2001; AMGEN INC
COMMENT	PN JP 2001512417-A/12 PD 21-AUG-2001 PF 11-DEC-1997 JP 1998528896 PR 20-DEC-1996 US 08/770973 PI MICHAEL BENJAMIN MANN,RANDY IRA HECHT PC C07K14/575,A61K38/00,A61P3/04,A61P3/06,A61P3/10,A61P9/10, PC A61P43/00, PC C12N15/09,C12N15/00,A61K37/02 CC Strandedness: Double; CC Topology: Linear; FH Key Location/Qualifiers.

FEATURES	Location/Qualifiers
source	1. .1135 /organism="Aequorea victoria" /mol_type="genomic DNA" /db_xref="taxon:6100"

ORIGIN

Query Match 96.1%; Score 1105; DB 6; Length 1135;
Best Local Similarity 98.7%; Pred. No. 1.2e-255;
Matches 1114; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

```
Qy        22 CTGTTTTGAGTGTGTACGGGTGGCACGGGTCGTGGACTTGAGGACCCCCCTGGCAGTCAG 81
Db         7 CTGTTTTGAGTGTGTACGGGTGGCACGGGTCGAGGCCTTGAGCTTCCACCAGGCAGTCAG 66

Qy        82 AAGGAGAAGGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGT 141
Db        67 AAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGT 126

Qy       142 ACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTG 201
Db       127 ACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTG 186

Qy       202 CCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATG 261
Db       187 CCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATG 246

Qy       262 GCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATGTTC 321
Db       247 GCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTTCGAATGCGT 306

Qy       322 ACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTT 381
Db       307 ACGCGCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTT 366

Qy       382 CCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTC 441
Db       367 CCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTC 426

Qy       442 TTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTC 501
Db       427 TTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTC 486

Qy       502 ACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGG 561
Db       487 ACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGG 546

Qy       562 CTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCC 621
Db       547 CTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCC 606

Qy       622 TTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCG 681
Db       607 TTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCG 666

Qy       682 GAGAGGGACAGAGGCCCATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAAT 741
Db       667 GAGAGGGACAGAGGCCCATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAAT 726

Qy       742 TAATTTTGCTAGCAATGCGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTT 801
Db       727 TAATTTTGCTAGCAATGCGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTT 786

Qy       802 GTCTTTCAATGTCCGGACCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTT 861
Db       787 GTCTTTCAATGTCCGGACCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTT 846

Qy       862 TACCTGGTCTGGGACCGACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAA 921
Db       847 TACCTGGTCTGGGACCGACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAA 906

Qy       922 TAGGTCTAGAGATTGCTGGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGG 981
```

```
Db        907 TAGGTCTAGAGATTGCTGGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGG 966

Qy        982 TTTAGGACGGTGGACGGTACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAG 1041
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        967 TTTAGGACGGTGGACGGTACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAG 1026

Qy       1042 GACCTTCGTAGGCCAATGTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAA 1101
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1027 GACCTTCGTAGGCCAATGTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAA 1086

Qy       1102 GTCCTGTACGAAACCGTCGACCTGGACAGAGGCCCAACAATTACCTAGG 1150
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db       1087 GTCCTGTACGAAACCGTCGACCTGGACAGAGGCCCAACAATTACCTAGG 1135


RESULT 5
I27618
LOCUS       I27618                  1142 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 9 from patent US 5565335.
ACCESSION   I27618
VERSION     I27618.1  GI:1818394
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1142)
  AUTHORS   Capon,D.J. and Gregory,T.J.
  TITLE     Adhesion variants
  JOURNAL   Patent: US 5565335-A 9 15-OCT-1996;
FEATURES             Location/Qualifiers
     source          1. .1142
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match           58.8%;  Score 676.2;  DB 6;  Length 1142;
  Best Local Similarity   98.6%;  Pred. No. 2.9e-152;
  Matches  695;  Conservative    0;  Mismatches    3;  Indels    7;  Gaps    1;

Qy          5 ACCTTGGGTTTAGAACACTGTTTTGAGTGTGTACGGGTGGCACGGGTCGTGGACTTGAGG 64
              | || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        423 AACTCGGGTTTAGAACACTGTTTTGAGTGTGTACGGGTGGCACGGGTCGTGGACTTGAGG 482

Qy         65 ACCCCCCTGGCAGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGG 124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        483 ACCCCCCTGGCAGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGG 542

Qy        125 CCTGGGGACTCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCA 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        543 CCTGGGGACTCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCA 602

Qy        185 AGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCG 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        603 AGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCG 662

Qy        245 TCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACT 304
              |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db        663 TCATGTTGTCGTGCATGGCCCACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACT 722

Qy        305 TACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTT 364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        723 TACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTT 782

Qy        365 GGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGG 424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        783 GGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGG 842

Qy        425 CCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGT 484
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        843 CCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGT 902

Qy        485 CGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCG 544
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        903 CGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCG 962

Qy        545 GAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCT 604
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        963 GAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCT 1022

Qy        605 CGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGC-------ACTACGTACTCCGAGAC 657
              |||||||||||||||||||||||||||||||||||||       |||||||||||||||||
Db       1023 CGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTACGTACTCCGAGAC 1082

Qy        658 GTGTTGGTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCATTT 702
              |||||||||||||||||||||||||||||||||||||||||||||
Db       1083 GTGTTGGTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCATTT 1127


RESULT 6
BD263010
LOCUS       BD263010                861 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Dimeric thrombopoietin peptide mimetics binding to MP1 receptor and
            having thrombopoietic activity.
ACCESSION   BD263010
VERSION     BD263010.1  GI:33072778
KEYWORDS    JP 2002536960-A/12.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 861)
  AUTHORS   Liu,C.F., Feige,U. and Cheetham,J.
  TITLE     Dimeric thrombopoietin peptide mimetics binding to MP1 receptor and
            having thrombopoietic activity
  JOURNAL   Patent: JP 2002536960-A 12 05-NOV-2002;
            AMGEN INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002536960-A/12
            PD   05-NOV-2002
            PF   22-OCT-1999 JP 2000578340
            PR   23-OCT-1998 US    60/105348
            PI   CHUAN FA LIU,ULRICH FEIGE,JANET CHEETHAM
            PC   C12N15/09,A61K38/00,A61P7/00,C07K14/52,C07K19/00,C12N1/15, PC
             C12N1/19,
            PC   C12N1/21,C12N5/10,C12P21/02,C12N15/00,C12N5/00,A61K37/02 CC
            Description of Artificial Sequence: oligonucleotide FH   Key
                Location/Qualifiers
            FT   source          1. .861
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .861
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
ORIGIN

  Query Match           58.6%;  Score 674.4;  DB 6;  Length 861;
  Best Local Similarity   97.7%;  Pred. No. 7.9e-152;
  Matches  684;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          4 TACCTTGGGTTTAGAACACTGTTTTGAGTGTGTACGGGTGGCACGGGTCGTGGACTTGAG 63
              | |||      || |   |||||||||||||||| ||||| || ||||| || ||||||
Db         24 TTCCTCCTTATTGTATACCTGTTTTGAGTGTGTACAGGTGGAACAGGTCGAGGCCTTGAG 83

Qy         64 GACCCCCCTGGCAGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGG 123
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         84 GACCCCCCTGGCAGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGG 143

Qy        124 GCCTGGGGACTCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTC 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        144 GCCTGGGGACTCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTC 203

Qy        184 AAGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTC 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        204 AAGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTC 263

Qy        244 GTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGAC 303
```

```
Db        264 GTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGAC 323

Qy        304 TTACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTT 363

Db        324 TTACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTT 383

Qy        364 TGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGG 423

Db        384 TGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGG 443

Qy        424 GCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGG 483

Db        444 GCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGG 503

Qy        484 TCGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGC 543

Db        504 TCGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGC 563

Qy        544 GGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTC 603

Db        564 GGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTC 623

Qy        604 TCGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTG 663

Db        624 TCGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTG 683

Qy        664 GTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCATTTC 703

Db        684 GTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCATTTC 723
```

RESULT 7
BD263000
LOCUS BD263000 684 bp DNA linear PAT 17-JUL-2003
DEFINITION Dimeric thrombopoietin peptide mimetics binding to MP1 receptor and having thrombopoietic activity.
ACCESSION BD263000
VERSION BD263000.1 GI:33072768
KEYWORDS JP 2002536960-A/2.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 684)
AUTHORS Liu,C.F., Feige,U. and Cheetham,J.
TITLE Dimeric thrombopoietin peptide mimetics binding to MP1 receptor and having thrombopoietic activity
JOURNAL Patent: JP 2002536960-A 2 05-NOV-2002;
AMGEN INC
COMMENT OS Artificial Sequence
PN JP 2002536960-A/2
PD 05-NOV-2002
PF 22-OCT-1999 JP 2000578340
PR 23-OCT-1998 US 60/105348
PI CHUAN FA LIU,ULRICH FEIGE,JANET CHEETHAM
PC C12N15/09,A61K38/00,A61P7/00,C07K14/52,C07K19/00,C12N1/15, PC C12N1/19,
PC C12N1/21,C12N5/10,C12P21/02,C12N15/00,C12N5/00,A61K37/02 CC
Description of Artificial Sequence: oligonucleotide FH Key Location/Qualifiers
FT source 1. .684
FT /organism='Artificial Sequence'.
FEATURES Location/Qualifiers
source 1. .684
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN

Query Match 58.5%; Score 673; DB 6; Length 684;
Best Local Similarity 99.3%; Pred. No. 1.7e-151;
Matches 676; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

```
Qy         22 CTGTTTTGAGTGTGTACGGGTGGCACGGGTCGTGGACTTGAGGACCCCCCTGGCAGTCAG 81

Db          4 CTGTTTTGAGTGTGTACAGGTGGAACAGGTCGAGGCCTTGAGGACCCCCCTGGCAGTCAG 63

Qy         82 AAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGT 141

Db         64 AAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGT 123

Qy        142 ACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTG 201

Db        124 ACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTG 183

Qy        202 CCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATG 261

Db        184 CCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATG 243

Qy        262 GCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATGTTC 321

Db        244 GCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATGTTC 303

Qy        322 ACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTT 381

Db        304 ACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTT 363

Qy        382 CCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTC 441

Db        364 CCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTC 423

Qy        442 TTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTC 501

Db        424 TTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTC 483

Qy        502 ACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGG 561

Db        484 ACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGG 543

Qy        562 CTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCC 621

Db        544 CTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCC 603

Qy        622 TTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCG 681

Db        604 TTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCG 663

Qy        682 GAGAGGGACAGAGGCCCATTT 702

Db        664 GAGAGGGACAGAGGCCCATTT 684
```

RESULT 8
BD004077
LOCUS BD004077 454 bp DNA linear PAT 31-JAN-2002
DEFINITION Methods of increasing sensitivity of an individual to OB protein by up-regulating OB protein receptor.
ACCESSION BD004077
VERSION BD004077.1 GI:18632038
KEYWORDS JP 2001501177-A/4.
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 454)
AUTHORS Pelleymounter,M.A.
TITLE Methods of increasing sensitivity of an individual to OB protein by up-regulating OB protein receptor
JOURNAL Patent: JP 2001501177-A 4 30-JAN-2001;
AMGEN INC
COMMENT OS Unidentified
PN JP 2001501177-A/4
PD 30-JAN-2001
PF 26-AUG-1997 JP 1998511882
PR 30-AUG-1996 US 08/705981
PI MARY ANN PELLEYMOUNTER
PC A61K38/00,A61K31/425,A61P1/16,A61P3/04,A61P3/06,A61P3/10, PC

```
            A61P9/10,
            PC   A61K37/02
            CC   Strandedness: Single;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers
            FT   source          1. .454
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .454
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
ORIGIN

  Query Match             38.3%;  Score 440.8;  DB 6;  Length 454;
  Best Local Similarity   98.5%;  Pred. No. 1.7e-95;
  Matches  445;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy        699 ATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATG 758
              ||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 ATACCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATG 62

Qy        759 CGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTTGTCTTTCAATGTCCGGA 818
              ||||||||||||||||||||||||||||||||||||||||||||||    ||||||||||
Db         63 CGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTTGTCGCACAATGTCCGGA 122

Qy        819 CCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCG 878
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 CCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCG 182

Qy        879 ACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAATAGGTCTAGAGATTGCT 938
              |||||||||||||||||||||||||||||||||||||||||| | ||||||||||||||
Db        183 ACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAAGAAGTCTAGAGATTGCT 242

Qy        939 GGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGG 998
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        243 GGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGG 302

Qy        999 TACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCAAT 1058
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        303 TACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCAAT 362

Qy       1059 GTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAAGTCCTGTACGAAACCGT 1118
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        363 GTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAAGTCCTGTACGAAACCGT 422

Qy       1119 CGACCTGGACAGAGGCCCAACAATTACCTAGG 1150
              ||||||||||||||||||||||||||||||
Db        423 CGACCTGGACAGAGGCCCAACAATTACCTAGG 454


RESULT 9
BD056516
LOCUS       BD056516                454 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  OB fusion protein compositions and methods.
ACCESSION   BD056516
VERSION     BD056516.1  GI:22602122
KEYWORDS    JP 2001512417-A/4.
SOURCE      Aequorea victoria
  ORGANISM  Aequorea victoria
            Bukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
            Aequoreidae; Aequorea.
REFERENCE   1  (bases 1 to 454)
  AUTHORS   Mann,M.B. and Hecht,R.I.
  TITLE     OB fusion protein compositions and methods
  JOURNAL   Patent: JP 2001512417-A 4 21-AUG-2001;
            AMGEN INC
COMMENT     PN   JP 2001512417-A/4
            PD   21-AUG-2001
            PF   11-DEC-1997 JP 1998528896
            PR   20-DEC-1996 US    08/770973
            PI   MICHAEL BENJAMIN MANN,RANDY IRA HECHT
            PC   C07K14/575,A61K38/00,A61P3/04,A61P3/06,A61P3/10,A61P9/10, PC
```

```
            A61P43/00,
            PC   C12N15/09,C12N15/00,A61K37/02
            CC   Strandedness: Double;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
     source          1. .454
                     /organism="Aequorea victoria"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:6100"
ORIGIN

  Query Match             38.3%;  Score 440.8;  DB 6;  Length 454;
  Best Local Similarity   98.5%;  Pred. No. 1.7e-95;
  Matches  445;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy        699 ATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATG 758
              ||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 ATACCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATG 62

Qy        759 CGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTTGTCTTTCAATGTCCGGA 818
              ||||||||||||||||||||||||||||||||||||||||||||||    ||||||||||
Db         63 CGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTTGTCGCACAATGTCCGGA 122

Qy        819 CCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCG 878
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 CCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCG 182

Qy        879 ACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAATAGGTCTAGAGATTGCT 938
              |||||||||||||||||||||||||||||||||||||||||| | ||||||||||||||
Db        183 ACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAAGAAGTCTAGAGATTGCT 242

Qy        939 GGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGG 998
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        243 GGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGG 302

Qy        999 TACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCAAT 1058
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        303 TACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCAAT 362

Qy       1059 GTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAAGTCCTGTACGAAACCGT 1118
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        363 GTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAAGTCCTGTACGAAACCGT 422

Qy       1119 CGACCTGGACAGAGGCCCAACAATTACCTAGG 1150
              ||||||||||||||||||||||||||||||
Db        423 CGACCTGGACAGAGGCCCAACAATTACCTAGG 454


RESULT 10
BD004075
LOCUS       BD004075                491 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Methods of increasing sensitivity of an individual to OB protein by
            up-regulating OB protein receptor.
ACCESSION   BD004075
VERSION     BD004075.1  GI:18632036
KEYWORDS    JP 2001501177-A/2.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 491)
  AUTHORS   Pelleymounter,M.A.
  TITLE     Methods of increasing sensitivity of an individual to OB protein by
            up-regulating OB protein receptor
  JOURNAL   Patent: JP 2001501177-A 2 30-JAN-2001;
            AMGEN INC
COMMENT     OS   Unidentified
            PN   JP 2001501177-A/2
            PD   30-JAN-2001
            PF   26-AUG-1997 JP 1998511882
            PR   30-AUG-1996 US    08/705981
            PI   MARY ANN PELLEYMOUNTER
            PC   A61K38/00,A61K31/425,A61P1/16,A61P3/04,A61P3/06,A61P3/10, PC
```

```
            A61P9/10,
            PC   A61K37/02
            CC   Strandedness: Single;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers
            FT   source          1. .491
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .491
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
ORIGIN

  Query Match             32.9%;  Score 378.4;  DB 6;  Length 491;
  Best Local Similarity   89.8%;  Pred. No. 1.9e-80;
  Matches  406;  Conservative    0;  Mismatches   46;  Indels    0;  Gaps    0;

Qy        699 ATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATG 758
              ||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         40 ATACCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATG 99

Qy        759 CGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTTGTCTTTCAATGTCCGGA 818
              ||||||||||||||||||||||||||||||||||    | ||||||||   ||||| || ||
Db        100 CGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCAGAGGCGATTTGTCGCACAATGGCCAGA 159

Qy        819 CCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCG 878
              |||||||||||||||||||||||||||||| | ||||||||||||||||||||||||||
Db        160 CCTGAAGTAGGGCCCAGACGTGGGCTAGGATTCGAACAGGTTTTACCTGGTCTGGGACCG 219

Qy        879 ACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAATAGGTCTAGAGATTGCT 938
              |||||||||||||  | |||||||| ||||||||   |||||| | |||||| |||||||
Db        220 ACATATGGTCGTCCACAATTGGAGGGACGGCAGGGTCTTGCAAGAAGTCTAGCGATTGCT 279

Qy        939 GGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGG 998
              |||||||||||||||||||||||||||||| |||||||||||||||||||||||   ||||||
Db        280 GGAGCTCTTGGAAGCGCTGGACGACGTGGACGACCGTAAGAGGTTTAGGACGAGGGACGG 339

Qy        999 TACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCAAT 1058
                | | |||||||||  |||   | |||  || ||||  ||||||||||||||||||   ||
Db        340 CGTCTGGAGTCCAGAAGTCTTTGGCCTTAGGGACCTGCCCCAGGACCTTCGTAGGGACAT 399

Qy       1059 GTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAAGTCCTGTACGAAACCGT 1118
              |||||||||||||||||||||||||||||||||||||||||||||||||||  |||  |||
Db        400 GTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAAGTCCTGTAGGAAGTCGT 459

Qy       1119 CGACCTGGACAGAGGCCCAACAATTACCTAGG 1150
              |||||||  |||||||  ||||||||||||
Db        460 CGACCTGCAAAGAGGCCTTACAATTACCTAGG 491


RESULT 11
BD056514
LOCUS       BD056514                491 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  OB fusion protein compositions and methods.
ACCESSION   BD056514
VERSION     BD056514.1  GI:22602120
KEYWORDS    JP 2001512417-A/2.
SOURCE      Aequorea victoria
  ORGANISM  Aequorea victoria
            Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Leptomedusae;
            Aequoreidae; Aequorea.
REFERENCE   1  (bases 1 to 491)
  AUTHORS   Mann,M.B. and Hecht,R.I.
  TITLE     OB fusion protein compositions and methods
  JOURNAL   Patent: JP 2001512417-A 2 21-AUG-2001;
            AMGEN INC
COMMENT     PN   JP 2001512417-A/2
            PD   21-AUG-2001
            PF   11-DEC-1997 JP 1998528896
            PR   20-DEC-1996 US    08/770973
            PI   MICHAEL BENJAMIN MANN,RANDY IRA HECHT
            PC   C07K14/575,A61K38/00,A61P3/04,A61P3/06,A61P3/10,A61P9/10, PC
            A61P43/00,
            PC   C12N15/09,C12N15/00,A61K37/02
            CC   Strandedness: Double;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
     source          1. .491
                     /organism="Aequorea victoria"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:6100"
ORIGIN

  Query Match             32.9%;  Score 378.4;  DB 6;  Length 491;
  Best Local Similarity   89.8%;  Pred. No. 1.9e-80;
  Matches  406;  Conservative    0;  Mismatches   46;  Indels    0;  Gaps    0;

Qy        699 ATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATG 758
              ||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         40 ATACCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATG 99

Qy        759 CGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTTGTCTTTCAATGTCCGGA 818
              ||||||||||||||||||||||||||||||||||    | ||||||||   ||||| || ||
Db        100 CGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCAGAGGCGATTTGTCGCACAATGGCCAGA 159

Qy        819 CCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCG 878
              |||||||||||||||||||||||||||||| | ||||||||||||||||||||||||||
Db        160 CCTGAAGTAGGGCCCAGACGTGGGCTAGGATTCGAACAGGTTTTACCTGGTCTGGGACCG 219

Qy        879 ACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAATAGGTCTAGAGATTGCT 938
              |||||||||||||  | |||||||| ||||||||   |||||| | |||||| |||||||
Db        220 ACATATGGTCGTCCACAATTGGAGGGACGGCAGGGTCTTGCAAGAAGTCTAGCGATTGCT 279

Qy        939 GGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGG 998
              |||||||||||||||||||||||||||||| |||||||||||||||||||||||   ||||||
Db        280 GGAGCTCTTGGAAGCGCTGGACGACGTGGACGACCGTAAGAGGTTTAGGACGAGGGACGG 339

Qy        999 TACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCAAT 1058
                | | |||||||||  |||   | |||  || ||||  ||||||||||||||||||   ||
Db        340 CGTCTGGAGTCCAGAAGTCTTTGGCCTTAGGGACCTGCCCCAGGACCTTCGTAGGGACAT 399

Qy       1059 GTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAAGTCCTGTACGAAACCGT 1118
              |||||||||||||||||||||||||||||||||||||||||||||||||||  |||  |||
Db        400 GTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAAGTCCTGTAGGAAGTCGT 459

Qy       1119 CGACCTGGACAGAGGCCCAACAATTACCTAGG 1150
              |||||||  |||||||  ||||||||||||
Db        460 CGACCTGCAAAGAGGCCTTACAATTACCTAGG 491


RESULT 12
BD105735
LOCUS       BD105735                1528 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  A method for preparing a recombinant immunoglobulin.
ACCESSION   BD105735
VERSION     BD105735.1  GI:22651309
KEYWORDS    JP 2001346591-A/7.
SOURCE      Mus sp.
  ORGANISM  Mus sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 1528)
  AUTHORS   Cabilly,S., Heyneker,H.L., Holmes,W.E., Riggs,A.D. and Wetzel,R.B.
  TITLE     A method for preparing a recombinant immunoglobulin
  JOURNAL   Patent: JP 2001346591-A 7 18-DEC-2001;
            GENENTECH INC,CITY OF HOPE
COMMENT     OS   Mus sp. (mouse)
            PN   JP 2001346591-A/7
            PD   18-DEC-2001
            PF   03-APR-2001 JP 2001104856
            PR   08-APR-1983 US       483457
            PI   SHMUEL CABILLY,HERBERT L HEYNEKER,WILLIAM E HOLMES,ARTHUR D
            PI   RIGGS,
            PI   RONALD B WETZEL
```

```
            PC   C12N15/09,C07K16/00,C07K19/00,C12N1/21,C12P21/02//G01N33/531,
            PC   (C12N1/21,C12R1:19),C12N15/00
            CC   A method for preparing a recombinant immunoglobulin FH   Key
                      Location/Qualifiers
            FT   source          1. .1528
            FT                   /organism='Mus sp. (mouse)'.
FEATURES             Location/Qualifiers
     source          1. .1528
                     /organism="Mus sp."
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10095"
ORIGIN

  Query Match             32.3%;  Score 371.2;  DB 6;  Length 1528;
  Best Local Similarity   73.3%;  Pred. No. 1e-78;
  Matches  475;  Conservative    0;  Mismatches  173;  Indels    0;  Gaps    0;

Qy          60 TGAGGACCCCCCTGGCAGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTA 119
               | ||| |  | | | || |||||| |||||||||||||| ||||||||     ||||  ||
Db         785 TCAGGGTCTTCATAGTAGACAGAAGTAGAAGGGGGGTTTCGGGTTCCTACACGAGTGGTA 844

Qy         120 GAGGGCCTGGGGACTCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCA 179
                 | | ||| ||| ||||||| || || ||||| ||| | ||| | || || || |||||
Db         845 ATGAGACTGAGGATTCCAGTGCACACAACACCATCTGTAGTCGTTCCTACTAGGGCTCCA 904

Qy         180 GTTCAAGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCT 239
               | |||||| |||||  || || |  |||||||||||| |  ||  ||||  | || |||||
Db         905 GGTCAAGTCGACCAAACATCTACTACACCTCCACGTGTGTCGAGTCTGCGTTGGGGCCCT 964

Qy         240 CCTCGTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGAC 299
               |||||||| |||||||| | |||    ||||| |  ||  || || ||||||||||||||
Db         965 CCTCGTCAAGTTGTCGTGAAAGGCGAGTCAGTCACTTGAAGGGTAGTACGTGGTCCTGAC 1024

Qy         300 CGACTTACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCT 359
               ||| ||||||||||||| ||| |||| ||||  ||   |||  |||| ||||||||||||
Db        1025 CGAGTTACCGTTCCTCAAGTTTACGTCCCAGTTGTCACGTCGAAAGGGACGGGGGTAGCT 1084

Qy         360 CTTTTGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGG 419
               ||||||||||||||| |||||||    ||     |||||||||||||| | || ||
Db        1085 CTTTTGGTAGAGGTTTTGGTTTCCGTCTGGCTTCCGAGGTGTCCACATGTGGTAAGGTGG 1144

Qy         420 TAGGGCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGAT 479
                  ||  |||  || || ||||| |  | ||||| |||||||| || | | || |||||
Db        1145 AGGGTTCCTCGTCTACCGGTTCCTATTTCAGTCAGACTGGACGTACTATTGTCTGAAGAA 1204

Qy         480 AGGGTCGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTG 539
                  ||  |||||  | |||||||||| || | |||||||||||  | | | ||||||||||
Db        1205 GGGACTTCTGTAATGACACCTCACCGTCACCTTACCCGTCGGTCGCCTCTTGATGTTCTT 1264

Qy         540 GTGCGGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCT 599
               ||| |  ||| |  || || |  | ||||| | |||| ||||||||||||||  ||| |
Db        1265 GTGAGTCGGGTAGTACTTGTGCTTACCGAGAATGAAGCAGATGTCGTTCGAGTTACACGT 1324

Qy         600 GTTCTCGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGT 659
               |||||||  ||| ||   || ||     ||| | ||||| ||| | |||||||  |||||
Db        1325 CTTCTCGTTGACCCTCCGTCCTTTATGAAAGTGGACGAGACACAATGTACTCCCGGACGT 1384

Qy         660 GTTGGTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCATTTCATGG 707
               ||||||| | ||  |||||||||||||||  ||||| ||||||  | |
Db        1385 GTTGGTGGTATGACTCTTCTCGGAGAGGGTGAGAGGACCATTTACTAG 1432


RESULT 13
BD105743
LOCUS       BD105743                1528 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Immunoglobulin DNA-containing expression vector and recombinant
            host cells.
ACCESSION   BD105743
VERSION     BD105743.1  GI:22651317
KEYWORDS    JP 2001346592-A/7.
SOURCE      Mus sp.
  ORGANISM  Mus sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 1528)
  AUTHORS   Cabilly,S., Heyneker,H.L., Holmes,W.E., Riggs,A.D. and Wetzel,R.B.
  TITLE     Immunoglobulin DNA-containing expression vector and recombinant
            host cells
  JOURNAL   Patent: JP 2001346592-A 7 18-DEC-2001;
            GENENTECH INC,CITY OF HOPE
COMMENT     OS   Mus sp. (mouse)
            PN   JP 2001346592-A/7
            PD   18-DEC-2001
            PF   03-APR-2001 JP 2001104857
            PR   08-APR-1983 US       483457
            PI   SHMUEL CABILLY,HERBERT L HEYNEKER,WILLIAM E HOLMES,ARTHUR D
            PI   RIGGS,
            PI   RONALD B WETZEL
            PC   C12N15/09,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N15/00,C12N5/
            PC   00
            CC   Immunoglobulin DNA-containing expression vector and  CC
                 recombinant host cells
            FH   Key             Location/Qualifiers
            FT   source          1. .1528
            FT                   /organism='Mus sp. (mouse)'.
FEATURES             Location/Qualifiers
     source          1. .1528
                     /organism="Mus sp."
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10095"
ORIGIN

  Query Match             32.3%;  Score 371.2;  DB 6;  Length 1528;
  Best Local Similarity   73.3%;  Pred. No. 1e-78;
  Matches  475;  Conservative    0;  Mismatches  173;  Indels    0;  Gaps    0;

Qy          60 TGAGGACCCCCCTGGCAGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTA 119
               | ||| |  | | | || |||||| |||||||||||||| ||||||||     ||||  ||
Db         785 TCAGGGTCTTCATAGTAGACAGAAGTAGAAGGGGGGTTTCGGGTTCCTACACGAGTGGTA 844

Qy         120 GAGGGCCTGGGGACTCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCA 179
                 | | ||| ||| ||||||| || || ||||| ||| | ||| | || || || |||||
Db         845 ATGAGACTGAGGATTCCAGTGCACACAACACCATCTGTAGTCGTTCCTACTAGGGCTCCA 904

Qy         180 GTTCAAGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCT 239
               | |||||| |||||  || || |  |||||||||||| |  ||  ||||  | || |||||
Db         905 GGTCAAGTCGACCAAACATCTACTACACCTCCACGTGTGTCGAGTCTGCGTTGGGGCCCT 964

Qy         240 CCTCGTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGAC 299
               |||||||| |||||||| | |||    ||||| |  ||  || || ||||||||||||||
Db         965 CCTCGTCAAGTTGTCGTGAAAGGCGAGTCAGTCACTTGAAGGGTAGTACGTGGTCCTGAC 1024

Qy         300 CGACTTACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCT 359
               ||| ||||||||||||| ||| |||| ||||  ||   |||  |||| ||||||||||||
Db        1025 CGAGTTACCGTTCCTCAAGTTTACGTCCCAGTTGTCACGTCGAAAGGGACGGGGGTAGCT 1084

Qy         360 CTTTTGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGG 419
               ||||||||||||||| |||||||    ||     |||||||||||||| | || ||
Db        1085 CTTTTGGTAGAGGTTTTGGTTTCCGTCTGGCTTCCGAGGTGTCCACATGTGGTAAGGTGG 1144

Qy         420 TAGGGCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGAT 479
                  ||  |||  || || ||||| |  | ||||| |||||||| || | | || |||||
Db        1145 AGGGTTCCTCGTCTACCGGTTCCTATTTCAGTCAGACTGGACGTACTATTGTCTGAAGAA 1204

Qy         480 AGGGTCGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTG 539
                  ||  |||||  | |||||||||| || | |||||||||||  | | | ||||||||||
Db        1205 GGGACTTCTGTAATGACACCTCACCGTCACCTTACCCGTCGGTCGCCTCTTGATGTTCTT 1264

Qy         540 GTGCGGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCT 599
               ||| |  ||| |  || || |  | ||||| | |||| ||||||||||||||  ||| |
Db        1265 GTGAGTCGGGTAGTACTTGTGCTTACCGAGAATGAAGCAGATGTCGTTCGAGTTACACGT 1324

Qy         600 GTTCTCGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGT 659
               |||||||  ||| ||   || ||     ||| | ||||| ||| | |||||||  |||||
Db        1325 CTTCTCGTTGACCCTCCGTCCTTTATGAAAGTGGACGAGACACAATGTACTCCCGGACGT 1384
```

```
Qy        660 GTTGGTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCATTTCATGG 707
              ||||||| | ||  |||||||||||||||  ||||| ||||||  | |
Db       1385 GTTGGTGGTATGACTCTTCTCGGAGAGGGTGAGAGGACCATTTACTAG 1432
```

RESULT 14
AR029004
LOCUS AR029004 2287 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 1 from patent US 5858983.
ACCESSION AR029004
VERSION AR029004.1 GI:5940977
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 2287)
AUTHORS Seed,B. and Walz,G.
TITLE Inhibition of cell adhesion protein-carbohydrate interactions
JOURNAL Patent: US 5858983-A 1 12-JAN-1999;
FEATURES Location/Qualifiers
source 1. .2287
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN

Query Match 5.2%; Score 60; DB 6; Length 2287;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy         89 AGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGCACC 148
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 AGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGCACC 1620
```

RESULT 15
AR037308
LOCUS AR037308 2287 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 1 from patent US 5801044.
ACCESSION AR037308
VERSION AR037308.1 GI:5955164
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 2287)
AUTHORS Seed,B. and Walz,G.
TITLE Nucleic acid encoding an antibody that inhibits cell adhesion protein-carbohydrate interactions
JOURNAL Patent: US 5801044-A 1 01-SEP-1998;
FEATURES Location/Qualifiers
source 1. .2287
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN

Query Match 5.2%; Score 60; DB 6; Length 2287;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy         89 AGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGCACC 148
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 AGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGCACC 1620
```

Search completed: October 18, 2004, 01:19:44
Job time : 4416.65 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 17, 2004, 15:27:13 ; Search time 4046.52 Seconds
(without alignments)
10355.995 Million cell updates/sec

Title: US-10-679-999-8
Perfect score: 1150
Sequence: 1 GTATACCTTGGGTTTAGAAC.....AGGCCCAACAATTACCTAGG 1150

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	50	4.3	714	6	CD781337	EST652698
c	2	48.8	4.2	527	1	AV962678	AV962678 AV962678
c	3	48.2	4.2	610	5	BW035294	BW035294 BW035294
c	4	47.6	4.1	619	5	BW251013	BW251013 BW251013
c	5	47	4.1	546	5	BW249566	BW249566 BW249566
c	6	47	4.1	660	5	BW193819	BW193819 BW193819
c	7	45.8	4.0	602	5	BW192111	BW192111 BW192111
c	8	45.8	4.0	617	5	BW314712	BW314712 BW314712
	9	43.6	3.8	1039	6	CA128348	CA128348 SCJLLR200
c	10	43.6	3.8	1933	3	AY325173	AY325173 Rattus no
c	11	43.2	3.8	486	1	AI869699	AI869699 wm02f07.x
c	12	43.2	3.8	658	5	BW265514	BW265514 BW265514
c	13	43.2	3.8	663	5	BW259047	BW259047 BW259047
	14	43.2	3.8	910	9	CNS006ON	AL065629 Drosophil
c	15	43	3.7	1203	7	CK206445	CK206445 FGAS01803
c	16	42.8	3.7	509	2	BF593096	BF593096 7o56e02.x
c	17	42.8	3.7	552	6	CA686322	CA686322 wlm96.pk0
c	18	42.8	3.7	587	5	BP504875	BP504875 BP504875
c	19	42.6	3.7	642	6	CA012935	CA012935 HT06O08r
c	20	42.6	3.7	649	6	CD907542	CD907542 G468.107E
c	21	42.6	3.7	673	6	CA014102	CA014102 HT10G06r
c	22	42.6	3.7	725	6	CD910343	CD910343 G550.001A
c	23	42.6	3.7	763	6	CD906072	CD906072 G468.103N
c	24	42.6	3.7	838	4	BI948448	BI948448 HVSMEl000
c	25	42.2	3.7	512	1	AI289506	AI289506 qw28e11.x
c	26	42.2	3.7	586	1	AI687271	AI687271 tp94e04.x
c	27	42.2	3.7	659	6	CA014547	CA014547 HT11K11r
	28	42	3.7	645	9	CNS012I3	AL101589 Drosophil
	29	41.8	3.6	343	1	AA330793	AA330793 EST34531
	30	41.8	3.6	1101	9	CNS00LXJ	AL078875 Drosophil
	31	41.6	3.6	337	6	CB047414	CB047414 NISC_gg02
	32	41.6	3.6	340	1	AA302570	AA302570 EST15740
c	33	41.6	3.6	408	6	CA720412	CA720412 wkm2n.pk0
c	34	41.6	3.6	414	4	BJ248630	BJ248630 BJ248630
c	35	41.6	3.6	439	2	BE488609	BE488609 WHE1051_G
c	36	41.6	3.6	442	6	CA719617	CA719617 wkm2n.pk0
c	37	41.6	3.6	443	1	AI582641	AI582641 tn47h04.x
c	38	41.6	3.6	443	6	CA656554	CA656554 wlm0.pk00
c	39	41.6	3.6	447	6	CA687517	CA687517 wlm96.pk0
c	40	41.6	3.6	448	6	CA692819	CA692819 wlm96.pk0
c	41	41.6	3.6	451	1	AI083954	AI083954 oz53b09.x
c	42	41.6	3.6	451	2	AW276084	AW276084 xq45c08.x
c	43	41.6	3.6	455	2	AW590575	AW590575 hg46c10.x
c	44	41.6	3.6	458	2	AW088852	AW088852 xd31e06.x
c	45	41.6	3.6	463	2	BF056551	BF056551 7k06g10.x

ALIGNMENTS

RESULT 1
CD781337
LOCUS CD781337 714 bp mRNA linear EST 01-JUL-2004
DEFINITION EST652698 RAA Rhipicephalus appendiculatus cDNA clone RAAAT27 5' end, mRNA sequence.
ACCESSION CD781337
VERSION CD781337.1 GI:49537010
KEYWORDS EST.
SOURCE Rhipicephalus appendiculatus
ORGANISM Rhipicephalus appendiculatus
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari; Parasitiformes; Ixodida; Ixodidae; Rhipicephalus.
REFERENCE 1 (bases 1 to 714)
AUTHORS Nene,V., Lee,Y., Skilton,R., Mwaura,S., Quackenbush,J., Gardner,M. and Bishop,R.
TITLE An index of genes transcribed in the salivary glands of Rhipicephalus appendiculatus
JOURNAL Unpublished (2003)
COMMENT Other_ESTs: EST652697
Contact: Vishvanath Nene
Parasite Genomics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-610-5968
Fax: 301-838-0208
Email: nene@tigr.org
Seq primer: M13 reverse.
FEATURES Location/Qualifiers
source 1. .714
/organism="Rhipicephalus appendiculatus"
/mol_type="mRNA"
/strain="Muguga"
/db_xref="taxon:34631"
/clone="RAAAT27"
/dev_stage="Adult"
/lab_host="E. coli strain DH10B-TonA"
/clone_lib="RAA"
/note="Organ: Salivary glands; Vector: pCMVSport6.0.ccdb; Salivary glands were dissected on day four after initiation of feeding. Total RNA was prepared using acid guanidium thiocyanate-phenol-chloroform extraction. The cDNA library was custom prepared by Invitrogen Corporation. Briefly, first strand cDNA was primed using oligo(dT) containing a NotI site. Size fractionated double stranded cDNA was ligated to EcoRV-NotI cleaved vector and electroporated into E.coli. Library RAA was made from uninfected ticks."

```
ORIGIN

  Query Match             4.3%;  Score 50;  DB 6;  Length 714;
  Best Local Similarity   55.1%;  Pred. No. 0.016;
  Matches   98;  Conservative    0;  Mismatches   80;  Indels    0;  Gaps    0;

Qy        447 CCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCACCCT 506
              | ||||   |  |||   |||         | |||| ||  |||  |  | || ||| |||
Db        253 CAAGTCCATCACGACACTCCAAGGCGAAGACATAGTGTTCCTGGCGACGGACATCAACCT 312

Qy        507 CTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGGCTGCC 566
                |      |||||| |    || |||||   | ||||   |||||| || | | ||||
Db        313 GCCCGGCGCCGTCGACTGGGTGATGATGCAGTCGTGCTTTGGGCACCACTTCATGCTGGT 372

Qy        567 GAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCCTTG 624
              | | |||||  |   |  || |||  | ||||     |  |   |||||||  |  |||
Db        373 GCTGGAGAAGCAAGAGAAGTACGACGGCCACCAACAGTTCTTTGCCGTCGTGCAGTTG 430


RESULT 2
AV962678/c
LOCUS       AV962678                527 bp    mRNA    linear   EST 14-MAR-2002
DEFINITION  AV962678 Nori Satoh unpublished cDNA library, larva Ciona
            intestinalis cDNA clone cilv05e12 5', mRNA sequence.
ACCESSION   AV962678
VERSION     AV962678.1  GI:19450977
KEYWORDS    EST.
SOURCE      Ciona intestinalis
  ORGANISM  Ciona intestinalis
            Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
            Phlebobranchia; Cionidae; Ciona.
REFERENCE   1  (bases 1 to 527)
  AUTHORS   Satoh,N., Satou,Y., Kohara,Y. and Shin-i,T.
  TITLE     Expressed genes in Ciona intestinalis
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Nori Satoh
            Department of Zoology
            Kyoto University
            Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
            Tel: 81-75-753-4081
            Fax: 81-75-705-1113
            Email: satoh@ascidian.zool.kyoto-u.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .527
                     /organism="Ciona intestinalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:7719"
                     /clone="cilv05e12"
                     /tissue_type="whole animal"
                     /dev_stage="larva"
                     /clone_lib="Nori Satoh unpublished cDNA library, larva"
ORIGIN

  Query Match             4.2%;  Score 48.8;  DB 1;  Length 527;
  Best Local Similarity   45.8%;  Pred. No. 0.033;
  Matches  167;  Conservative    0;  Mismatches  198;  Indels    0;  Gaps    0;

Qy        242 TCGTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCG 301
              | ||  || |||  |  ||    |  ||  ||| || |  |    || |  ||
Db        476 TGGTGGTGATGTGTTNTGTGTTGTTCTTGTATTAGGCGTTGTTGTTGTTGTTGATGTATT 417

Qy        302 ACTTACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCT 361
              | |   ||| ||  ||||   |||   |  |||||| | |  ||  | |  || | ||
Db        416 TCGTGTTGTTGCTGCTGTTGTTGTTGTTGCTGTTGTTCCTGTTGGTGCTGTTGTTGTTCC 357

Qy        362 TTTGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTA 421
              | | || |   |  | | ||  |   ||     |  | ||| ||    |
Db        356 TGTTGTTGTTCCTGTTGGTGCCGTTGTTGTTCCTGTTGTTGTTCCTGTTGGTGCCGTTGT 297

Qy        422 GGGCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAG 481
              |  |||  | |   ||| ||| ||| || |   ||  |   |||  || |||
Db        296 TGTTCCTGTTGGTGCTGTTGTTGTTCCTGTTGTTGGTGATGCTGTTGTTGTTGATGATGC 237

Qy        482 GGTCGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGT 541
              || | ||| |  |   |    ||  |||     |    | ||| || |||| | ||
Db        236 TGTTGTTGTTGGTGATGTTGTTGTTCCTGTTGGTGCTGTTGTTGTTGGTGTTGTTGTTGT 177

Qy        542 GCGGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGT 601
              |   ||     ||  |||| |  |  |  |  ||||| ||| | |   |    ||
Db        176 TGGTGTTGCTGTTGTTGCCGCTGCTGTTGTTGTTGATGATGTTGTTGGTGCTTCTGTAGT 117

Qy        602 TCTCG 606
              |  ||
Db        116 TGCCG 112


RESULT 3
BW035294/c
LOCUS       BW035294                610 bp    mRNA    linear   EST 13-OCT-2002
DEFINITION  BW035294 Nori Satoh unpublished cDNA library, blood cells Ciona
            intestinalis cDNA clone cibd028f16 5', mRNA sequence.
ACCESSION   BW035294
VERSION     BW035294.1  GI:23951246
KEYWORDS    EST.
SOURCE      Ciona intestinalis
  ORGANISM  Ciona intestinalis
            Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
            Phlebobranchia; Cionidae; Ciona.
REFERENCE   1  (bases 1 to 610)
  AUTHORS   Satou,Y., Satake,M., Azumi,K., Nonaka,M., Shin-i,T., Kohara,Y. and
            Satoh,N.
  TITLE     Expressed genes in Ciona intestinalis (2002)
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Nori Satoh
            Department of Zoology
            Kyoto University
            Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
            Tel: 81-75-753-4081
            Fax: 81-75-705-1113
            Email: satoh@ascidian.zool.kyoto-u.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .610
                     /organism="Ciona intestinalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:7719"
                     /clone="cibd028f16"
                     /tissue_type="blood cells"
                     /clone_lib="Nori Satoh unpublished cDNA library, blood
                     cells"
ORIGIN

  Query Match             4.2%;  Score 48.2;  DB 5;  Length 610;
  Best Local Similarity   45.8%;  Pred. No. 0.049;
  Matches  167;  Conservative    0;  Mismatches  198;  Indels    0;  Gaps    0;

Qy        242 TCGTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCG 301
              | ||  || |||  |  ||    |  ||  ||| || |  |    || |  ||
Db        475 TGGTGGTGATGTGTTTTGTGTTGTTCTTGTATTAGGCGTTGTTGTTGTTGTTGATGTATT 416

Qy        302 ACTTACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCT 361
              | |   ||| ||  ||||   |||   |  |||||| | |  ||  | |  || | ||
Db        415 TCGTGTTGTTGCTGCTGTTGTTGTTGTTGCTGTTGTTCCTGTTGGTGCTGTTGTTGTTCC 356

Qy        362 TTTGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTA 421
              | | || |   |  | | ||  |   ||     |  | ||| ||    |
Db        355 TGTTGTTGTTCCTGTTGGTGCCGTTGTTGTTCCTGTTGTTGTTCCTGTTGGTGCCGTTGT 296

Qy        422 GGGCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAG 481
              |  |||  | |   ||| ||| ||| || |   ||  |   |||  || |||
Db        295 TGTTCCTGTTGGTGCTGTTGTTGTTCCTGTTGTTGGTGATGCTGTTGTTGTTGATGATGC 236

Qy        482 GGTCGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGT 541
              || | ||| |  |   |    ||  |||     |    | ||| || |||| | ||
Db        235 TGTTGTTGTTGGTGATGTTGTTGTTCCTGTTGGTGCTGTTGTTGTTGGTGTTGTTGTTGT 176

Qy        542 GCGGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGT 601
```

```
Db        175 TGGTGTTGCTGTTGTTGCCGCTGCTGTTGTTGTTGATGATGTTGTTGGTGCTTCTGTAGT 116

Qy        602 TCTCG 606
              | ||
Db        115 TGCCG 111


RESULT 4
BW251013/c
LOCUS       BW251013                619 bp    mRNA    linear   EST 09-NOV-2002
DEFINITION  BW251013 Nori Satoh unpublished cDNA library, tailbud embryo Ciona
            intestinalis cDNA clone citb088l19 5', mRNA sequence.
ACCESSION   BW251013
VERSION     BW251013.1  GI:24830931
KEYWORDS    EST.
SOURCE      Ciona intestinalis
  ORGANISM  Ciona intestinalis
            Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
            Phlebobranchia; Cionidae; Ciona.
REFERENCE   1  (bases 1 to 619)
  AUTHORS   Satou,Y., Shin-i,T., Kohara,Y. and Satoh,N.
  TITLE     Expressed genes in Ciona intestinalis (2002c)
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Nori Satoh
            Department of Zoology
            Kyoto University
            Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
            Tel: 81-75-753-4081
            Fax: 81-75-705-1113
            Email: satoh@ascidian.zool.kyoto-u.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .619
                     /organism="Ciona intestinalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:7719"
                     /clone="citb088l19"
                     /tissue_type="whole animal"
                     /dev_stage="tailbud embryo"
                     /clone_lib="Nori Satoh unpublished cDNA library, tailbud
                     embryo"
ORIGIN

  Query Match             4.1%;  Score 47.6;  DB 5;  Length 619;
  Best Local Similarity   46.0%;  Pred. No. 0.073;
  Matches  161;  Conservative    0;  Mismatches  189;  Indels    0;  Gaps    0;

Qy        242 TCGTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCG 301
              | ||  || |||  |   ||     |  ||   ||| || |  |    || |  ||
Db        506 TGGTGGTGATGTGTTTTGTGTTGTTCTTGTATTAGGCGTTGTTGTTGTTGATGTATT 447

Qy        302 ACTTACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCT 361
              | |   ||| ||  ||||   |||    |  ||||| | |  ||  | |  || | ||
Db        446 TCGTGTTGTTGCTGCTGTTGTTGTTGTTGCTGTTGTTCCTGTTGGTGCTGTTGTTGTTCC 387

Qy        362 TTTGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTA 421
              | | || |    |  | | ||  |    ||     |  | ||| ||     |
Db        386 TGTTGTTGTTCCTGTTGGTGCCGTTGTTGTTCCTGTTGTTGTTCCTGTTGGTGCCGTTGT 327

Qy        422 GGGCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAG 481
              |  |||  | |    ||| ||| ||| || |     || |     |||   || |||
Db        326 TGTTCCTGTTGGTGCTGTTGTTGTTCCTGTTGTTGGTGATGCTGTTGTTGTTGATGATGC 267

Qy        482 GGTCGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGT 541
              || | ||| | |    |     || |||     |     | ||| || |||| | ||
Db        266 TGTTGTTGTTGGTGATGTTGTTGTTCCTGTTGGTGCTGTTGTTGTTGGTGTTGTTGTTGT 207

Qy        542 GCGGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAG 591
              |   ||      ||  ||||| | | |  | ||||| ||| | |
Db        206 TGGTGTTGCTGTTGTTGCCGCTGCTGTTGTTGTTGATGATGTTGTTGGTG 157


RESULT 5
```

```
BW249566/c
LOCUS       BW249566                546 bp    mRNA    linear   EST 09-NOV-2002
DEFINITION  BW249566 Nori Satoh unpublished cDNA library, tailbud embryo Ciona
            intestinalis cDNA clone citb082d19 5', mRNA sequence.
ACCESSION   BW249566
VERSION     BW249566.1  GI:24829484
KEYWORDS    EST.
SOURCE      Ciona intestinalis
  ORGANISM  Ciona intestinalis
            Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
            Phlebobranchia; Cionidae; Ciona.
REFERENCE   1  (bases 1 to 546)
  AUTHORS   Satou,Y., Shin-i,T., Kohara,Y. and Satoh,N.
  TITLE     Expressed genes in Ciona intestinalis (2002c)
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Nori Satoh
            Department of Zoology
            Kyoto University
            Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
            Tel: 81-75-753-4081
            Fax: 81-75-705-1113
            Email: satoh@ascidian.zool.kyoto-u.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .546
                     /organism="Ciona intestinalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:7719"
                     /clone="citb082d19"
                     /tissue_type="whole animal"
                     /dev_stage="tailbud embryo"
                     /clone_lib="Nori Satoh unpublished cDNA library, tailbud
                     embryo"
ORIGIN

  Query Match             4.1%;  Score 47;  DB 5;  Length 546;
  Best Local Similarity   45.5%;  Pred. No. 0.1;
  Matches  167;  Conservative    0;  Mismatches  200;  Indels    0;  Gaps    0;

Qy        242 TCGTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCG 301
              | ||  || |||  |   ||     |  ||   ||| || |  |    || |  ||
Db        512 TGGTGGTGATGTGTTTTGTGTTGTTCTTGTATTAGGCGTTGTTGTTGTTGATGTATT 453

Qy        302 ACTTACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCT 361
              | |   ||| ||  ||||   |||    |  ||||| | |  ||  | |  || | ||
Db        452 TCGTGTTGTTGCTGCTGTTGTTGTTGTTGCTGTTGTTCCTGTTGGTGCTGTTGTTGTTCC 393

Qy        362 TTTGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTA 421
              | | || |    |  | | ||  |    ||     |  | ||| ||     |
Db        392 TGTTGTTGTTCCTGTTGGTGCCGTTGTTGTTCCTGTTGTTGTTCCTGTTGGTGCCGTTGT 333

Qy        422 GGGCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAG 481
              |  |||  | |    ||| ||| ||| || |     || |     |||   || |||
Db        332 TGTTCCTGTTGGTGCTGTTGTTGTTCCTGTTGTTGGTGATGCTGTTGTTGTTGATGATGC 273

Qy        482 GGTCGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGT 541
              || | ||| | |    |     || |||     |     | ||| || |||| | ||
Db        272 TGTTGTTGTTGGTGATGTTGTTGTTCCTGTTGGTGCTGTTGTTGTTGTTGGTGTTGTTGT 213

Qy        542 GCGGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGT 601
              | |       ||  || || | |  | |  |||| |||  |  ||  ||||
Db        212 TGTTGGTGTTGCTGTTGTTGCCGCTGCTGTTGTTGTTGATGATGTTGTTGGTGCTTCTGT 153

Qy        602 TCTCGTC 608
              | | |
Db        152 AGTTGCC 146


RESULT 6
BW193819/c
LOCUS       BW193819                660 bp    mRNA    linear   EST 05-NOV-2002
DEFINITION  BW193819 Nori Satoh unpublished cDNA library, cleaving embryo Ciona
            intestinalis cDNA clone cicl101p23 5', mRNA sequence.
ACCESSION   BW193819
```

```
VERSION     BW193819.1  GI:24608221
KEYWORDS    EST.
SOURCE      Ciona intestinalis
  ORGANISM  Ciona intestinalis
            Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
            Phlebobranchia; Cionidae; Ciona.
REFERENCE   1  (bases 1 to 660)
  AUTHORS   Satou,Y., Shin-i,T., Kohara,Y. and Satoh,N.
  TITLE     Expressed genes in Ciona intestinalis (2002c)
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Nori Satoh
            Department of Zoology
            Kyoto University
            Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
            Tel: 81-75-753-4081
            Fax: 81-75-705-1113
            Email: satoh@ascidian.zool.kyoto-u.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .660
                     /organism="Ciona intestinalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:7719"
                     /clone="cicl101p23"
                     /tissue_type="whole body"
                     /dev_stage="cleaving embryo"
                     /clone_lib="Nori Satoh unpublished cDNA library, cleaving
                     embryo"
ORIGIN

  Query Match             4.1%;  Score 47;  DB 5;  Length 660;
  Best Local Similarity   45.5%;  Pred. No. 0.11;
  Matches  167;  Conservative    0;  Mismatches  200;  Indels    0;  Gaps    0;

Qy        242 TCGTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCG 301
              | ||  || ||| |   ||      |  ||   ||| || | |    || | ||
Db        489 TGGTGGTGATGTGTTTTGTGTTGTTCTTGTATTAGGCGTTGTTGTTGTTGTTGATGTATT 430

Qy        302 ACTTACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCT 361
               | |   ||| ||  |||| |||   |  |||||| | |  ||  | |  || | ||
Db        429 TCGTGTTGTTGCTGCTGTTGTTGTTGTTGCTGTTGTTCCTGTTGGTGCTGTTGTTGTTCC 370

Qy        362 TTTGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTA 421
              | | || |    |   | | ||  |   |   ||      |   | ||| ||    |
Db        369 TGTTGTTGTTCCTGTTGGTGCCGTTGTTGTTCCTGTTGTTGTTCCTGTTGGTGCCGTTGT 310

Qy        422 GGGCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAG 481
                |  |||  | |    ||| ||| ||  ||      || |      |||   || |||
Db        309 TGTTCCTGTTGGTGCTGTTGTTGTTCCTGTTGTTGGTGATGCTGTTGTTGTTGATGATGC 250

Qy        482 GGTCGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGT 541
              || | ||| |  |   |    ||  |||      |    | |||||| |||| | ||
Db        249 TGTTGTTGTTGGTGATGTTGTTGTTCCTGTTGGTGCTGTTGTTGTTGTTGGTGTTGTTGT 190

Qy        542 GCGGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGT 601
                | |        ||  || || | |  |  |  | ||||  |||   |  ||  ||||
Db        189 TGTTGGTGTTGCTGTTGTTGCCGCTGCTGTTGTTGTTGATGATGTTGTTGGTGCTTCTGT 130

Qy        602 TCTCGTC 608
                | | |
Db        129 AGTTGCC 123


RESULT 7
BW192111/c
LOCUS       BW192111                602 bp    mRNA    linear   EST 05-NOV-2002
DEFINITION  BW192111 Nori Satoh unpublished cDNA library, young adult Ciona
            intestinalis cDNA clone ciad095m14 5', mRNA sequence.
ACCESSION   BW192111
VERSION     BW192111.1  GI:24606513
KEYWORDS    EST.
SOURCE      Ciona intestinalis
  ORGANISM  Ciona intestinalis
            Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
            Phlebobranchia; Cionidae; Ciona.
REFERENCE   1  (bases 1 to 602)
  AUTHORS   Satou,Y., Shin-i,T., Kohara,Y. and Satoh,N.
  TITLE     Expressed genes in Ciona intestinalis (2002c)
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Nori Satoh
            Department of Zoology
            Kyoto University
            Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
            Tel: 81-75-753-4081
            Fax: 81-75-705-1113
            Email: satoh@ascidian.zool.kyoto-u.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .602
                     /organism="Ciona intestinalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:7719"
                     /clone="ciad095m14"
                     /tissue_type="whole animal"
                     /dev_stage="young adult"
                     /clone_lib="Nori Satoh unpublished cDNA library, young
                     adult"
ORIGIN

  Query Match             4.0%;  Score 45.8;  DB 5;  Length 602;
  Best Local Similarity   45.8%;  Pred. No. 0.23;
  Matches  158;  Conservative    0;  Mismatches  187;  Indels    0;  Gaps    0;

Qy        248 TGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTAC 307
              || ||| ||   ||   |   ||  | |  |  || |    || |||||      || |
Db        444 TGCTGTTGTTGTTGTTGCTGTTGTTCCTGTTGGTGCTGTTGTTGTTCCTGTTGTTGTTCC 385

Qy        308 CGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGT 367
               |||  |   |||   ||||| |  |||||| | |  ||  | |  || | || | | ||
Db        384 TGTTGGTGCCGTTGTTGTTCCTGTTGTTGTTCCTGTTGGTGCCGTTGTTGTTCCTGTTGT 325

Qy        368 AGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCC 427
              |    |  | | ||  |   | | ||    || |   ||| |  |  |    ||
Db        324 TGTTCCTGTTGGTGCCGTTGTTGTCCCTGTTGGTGCTGTTGTTGTTCCTGTTGTTGGTGA 265

Qy        428 TACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGC 487
              | ||  | ||| ||| |  |  |  | |  ||   |||   |   |  |  ||
Db        264 TGCTGTTGTTGTTGTTGATGATGCTGTTGTTGTTGGTGATGTTGTTGTTCCTGTTGGTGC 205

Qy        488 TGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAG 547
              ||| |  |    |   || | |||  |  |    | ||||||  || | | ||  |
Db        204 TGTTGTTGTTGGTGTTGCTGTTGTTGGCGCTGCTGTTGTTGTTGTTGATGTTGTTGGTGC 145

Qy        548 GGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGT 592
                |   |  ||  |||  ||     |  || |||  || |   ||
Db        144 TTCTGTAGTTGCCGCTGTTGATATTGGCGGTGATTGCGCTTTTGT 100


RESULT 8
BW314712/c
LOCUS       BW314712                617 bp    mRNA    linear   EST 11-NOV-2002
DEFINITION  BW314712 Nori Satoh unpublished cDNA library, heart Ciona
            intestinalis cDNA clone ciht039h07 5', mRNA sequence.
ACCESSION   BW314712
VERSION     BW314712.1  GI:24895396
KEYWORDS    EST.
SOURCE      Ciona intestinalis
  ORGANISM  Ciona intestinalis
            Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
            Phlebobranchia; Cionidae; Ciona.
REFERENCE   1  (bases 1 to 617)
  AUTHORS   Satou,Y., Shin-i,T., Kohara,Y. and Satoh,N.
  TITLE     Expressed genes in Ciona intestinalis (2002c)
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Nori Satoh
            Department of Zoology
            Kyoto University
            Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
```

Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satoh@ascidian.zool.kyoto-u.ac.jp.

FEATURES Location/Qualifiers
source 1. .617
/organism="Ciona intestinalis"
/mol_type="mRNA"
/db_xref="taxon:7719"
/clone="ciht039h07"
/tissue_type="heart"
/clone_lib="Nori Satoh unpublished cDNA library, heart"

ORIGIN

Query Match 4.0%; Score 45.8; DB 5; Length 617;
Best Local Similarity 43.2%; Pred. No. 0.23;
Matches 212; Conservative 0; Mismatches 279; Indels 0; Gaps 0;

```
Qy      102 GTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGCACCACCACCTGCACTC 161
Db      602 GTTGCTGTTTCTGTGTTCGGTGTATTNTGTGTTGTTGTTGTTGTGNTAGTTGCTGCTGCT 543

Qy      162 GGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGCACCTCCACGTATTACG 221
Db      542 GCTGTTGTTGTTGCTGTAGTTGGTGGTGATGTGTTTTGTGTTGTTCTTGTATTAGGCGTT 483

Qy      222 GTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTG 281
Db      482 GTTGTTGATGTATTTCGTGTTGTTGCTGCTGTTGTTGTTGTTGCTGTTGTTCCTGTTGGT 423

Qy      282 GCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCG 341
Db      422 GCTGTTGTTGTTCCTGTTGTTGTTCCTGTTGGTGCCGTTGTTGTTCCTGTTGTTGTTCCT 363

Qy      342 GGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGT 401
Db      362 GTTGGTGCCGTTGTTGTTCCTGTTGTTGTTCCTGTTGGTGCCGTTGTTGTCCCTGTTGGT 303

Qy      402 CCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGAC 461
Db      302 GCTGTTGTTGTTCCTGTTGTTGGTGATGCTGTTGTTGTTGTTGATGATGCTGTTGTTGTT 243

Qy      462 GGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGG 521
Db      242 GGTGATGTTGTTGTTCCTGTTGGTGCTGTTGTTGTTGGTGTTGCTGTTGTTGGCGCTGCT 183

Qy      522 CCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGAT 581
Db      182 GTTGTTGTTGTTGATGTTGTTGGTGCTTCTGTAGTTGCCGCTGTTGATATTGGCGGTGAT 123

Qy      582 GTCGTTCGAGT 592
Db      122 TGCGCTTTTGT 112
```

RESULT 9
CA128348
LOCUS CA128348 1039 bp mRNA linear EST 24-SEP-2003
DEFINITION SCJLLR2006A05.g LR2 Saccharum officinarum cDNA clone SCJLLR2006A05 5', mRNA sequence.
ACCESSION CA128348
VERSION CA128348.1 GI:35009126
KEYWORDS EST.
SOURCE Saccharum officinarum
ORGANISM Saccharum officinarum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum complex.
REFERENCE 1 (bases 1 to 1039)
AUTHORS Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.
TITLE The libraries that made SUCEST
JOURNAL Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
COMMENT Contact: Arruda P

Centro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
Email: parruda@unicamp.br
Clone distribution: clone distribution information can be found through the Brazilian Clone Collection Center (BCCC) at http://www.bcccenter.fcav.unesp.br
Plate: 006 row: A column: 05
Seq primer: T7 Promoter Primer.

FEATURES Location/Qualifiers
source 1. .1039
/organism="Saccharum officinarum"
/mol_type="mRNA"
/db_xref="taxon:4547"
/clone="SCJLLR2006A05"
/lab_host="DH10B"
/clone_lib="LR2"
/note="Organ: Leaf roll from field grown adult plants (small insert library); Vector: pSport1; Site_1: SalI; Site_2: NotI; An unidirectional cDNA library generated from [Leaf roll from field grown adult plants (small insert library)]. cDNA was prepared from polyA+ mRNA using SuperScript Plasmid System Kit (Invitrogen). The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 Kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at http://sucest.lad.ic.unicamp.br/public"

ORIGIN

Query Match 3.8%; Score 43.6; DB 6; Length 1039;
Best Local Similarity 45.6%; Pred. No. 1;
Matches 154; Conservative 0; Mismatches 184; Indels 0; Gaps 0;

```
Qy      442 TTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTC 501
Db      303 TCGGTGGAGACGTACAAGATCTACATCTTCAAGGTGCTGAAGCAGGTGCACCCGGACATC 362

Qy      502 ACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGG 561
Db      363 TGCATCTCGTCCAAGGCCATGTCCATCATGAACTTCTTCATCAACGACATCTTCCATAAG 422

Qy      562 CTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCC 621
Db      423 CTGGCGGCGGAGGCGGCCAAACTGGCGCGCTACAACAAGAAGCCCACCATCACGTGCCGC 482

Qy      622 TTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCG 681
Db      483 GAGATCCAGACTTTCGTCCGCCTCGTCCTCCCCGGCGAGCTCGCCAAGCACGCCTTCTTC 542

Qy      682 GAGAGGGACAGAGGCCCATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAAT 741
Db      543 GAGGTGCACCAAGGCCGTTACCAAGTTCACCAGCTCCTATGCGAGCGATGGGACCTGCCT 602

Qy      742 TAATTTTGCTAGCAATGCGCATAGTTGCTGTAGTCAGT 779
Db      603 TAGTTTCGTTCATGAAGTACTAGTGTGTTGTCGTGTGT 640
```

RESULT 10
AY325173/c
LOCUS AY325173 1933 bp mRNA linear HTC 26-JUL-2003
DEFINITION Rattus norvegicus Aa2-050 mRNA, complete cds.
ACCESSION AY325173
VERSION AY325173.1 GI:33086523
KEYWORDS HTC.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

```
REFERENCE   1  (bases 1 to 1933)
  AUTHORS   Xu,C.S., Li,W.Q., Li,Y.C., Yang,K.J., Yan,H.M., Chang,C.F.,
            Zhao,L.F., Ma,H., Wang,L., Wang,S.F., Han,H.P., Wang,G.P.,
            Chai,L.Q., Yuan,J.Y., Shi,J.B., Rahman,S., Wang,Q.N. and Zhang,J.B.
  TITLE     Liver regeneration after PH
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1933)
  AUTHORS   Xu,C.S., Li,W.Q., Li,Y.C., Yang,K.J., Yan,H.M., Chang,C.F.,
            Zhao,L.F., Ma,H., Wang,L., Wang,S.F., Han,H.P., Wang,G.P.,
            Chai,L.Q., Yuan,J.Y., Shi,J.B., Rahman,S., Wang,Q.N. and Zhang,J.B.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-JUN-2003) Henan Bioengineering Key Lab, Henan Normal
            University, NO. 148 Jianshe Road, Xinxiang City, Henan 453002, P.R.
            China
FEATURES             Location/Qualifiers
     source          1. .1933
                     /organism="Rattus norvegicus"
                     /mol_type="mRNA"
                     /db_xref="taxon:10116"
     CDS             41. .1927
                     /note="liver regeneration-related protein LRRG146"
                     /codon_start=1
                     /product="Aa2-050"
                     /protein_id="AAP92574.1"
                     /db_xref="GI:33086524"
                     /translation="MAAGLDQGGPARCAGAGPGPPLLLRDSILAFVLQMTGSNEFKLN
                     QPPEDGISSVKFSPNTSQFLLVSSWDTSVRLYDVPANSMRLKYQHTGAVLDCAFYVEN
                     LVGTHDAPIRCVEYCPEVNVMVTGSWDQTVKLWDPRTPCNAGTFSQPEKGYVLSSIEG
                     RVAVEYLDPSPEVQKKKYAFKCHRLKENNIEQIYPVNAISLSQYPQHICHSNDGTTLA
                     IASSYMYEMDDTEHPEDGIFIRQVTDAETKPKSSRKSSVNICGLSQDGHRLAASSWRL
                     AVPGLWSSRIPVLTIPPSADTAKRQAPLDIATNCYSKFPDVHTAVTLVASMHKSRTGV
                     ITLLVFVTTYLMRSTIKEESLLLLVVKGGKVHHGGEGKSGSPKSQKHFLLALQFFIWH
                     NSNSNNNNNSNNNNSNNNNSNNNNNSNNSSSNNSNSNNSNSNNSSSNSTSNNSNSNNS
                     NSNNSNNNNNNSNNSNSNNSNSNSNNSNNKNSNNNSNNNNSNSNSNNSNNSSNNSSSS
                     NNSNSNNNSNNSNNSNNSSSSNNSNNKNNSNNNNSNNNNNSNSSSSNNNSNSNN
                     NSNSSSSNNNSSSNNNSNNNSNNNSNSNNHHHHPGNLAAAPLICIGIFLLLQALKGLN
                     DTML"
ORIGIN

  Query Match             3.8%;  Score 43.6;  DB 3;  Length 1933;
  Best Local Similarity   42.2%;  Pred. No. 1.2;
  Matches  247;  Conservative    0;  Mismatches  339;  Indels    0;  Gaps    0;

Qy        200 TGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCA 259
              ||| |   ||      | || | ||| |  ||         |  |   |  || | | ||
Db       1820 TGCTGTTGCTGTTGTTGTTGCTGTTGTTGTTGCTGTTGTTGTTGCTGCTGCTATTGTTGT 1761

Qy        260 TGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATGT 319
              ||   | | |  |  | || | |    || | |||      || | | | ||  |||
Db       1760 TGCTGCTGCTGCTGTTGCTGTTGTTGTTGCTGTTGCTGTTGTTGTTGCTGCTGCTGCTGT 1701

Qy        320 TCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGT 379
              |  |||   |  |||||| | |  |     |  | | |||| || |  | |   ||
Db       1700 TGCTGTTGTTGTTGTTGTTGCTGTTGTTGTTGTTGCTGTTGTTTTTGTTGTTGCTGTTGT 1641

Qy        380 TTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGT 439
              | |   |   |     |   | |  ||| |      |      |   | ||   | ||
Db       1640 TGCTGCTGCTGCTATTGTTGCTGCTGTTGTTGCTGTTGTTGCTGTTGTTGCTGTTGTTGT 1581

Qy        440 TCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACC 499
              |  || | | ||  |     |  |   |  ||   | | |   || ||||| |  ||
Db       1580 TGCTGTTGCTGTTGTTGCTGCTGCTGCTATTGTTGCTGCTGTTGTTGCTGTTGTTGCTGT 1521

Qy        500 TCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGA 559
              |     |   |||      |    || |||||| || | |  |    |  ||      ||
Db       1520 TGCTGTTGCTGTTGTTGTTGTTGCTGTTGTTGTTGCTGTTTTTGTTATTGCTGTTGTTGC 1461

Qy        560 GGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCC 619
              | ||| |  |  |  |  | ||| | |   || ||   |||| | ||      |  |
Db       1460 TGTTGCTGTTGCTGTTGTTGCTGTTGCTGTTGTTGCTGTTGTTGTTGTTGTTGTTGCTGT 1401

Qy        620 CCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTCT 679
                |||| |  |     |  ||  |  | |       ||| || || ||    | || |
```

```
Db       1400 TGTTGCTGTTGCTGTTGTTGCTGTTGCTGTTGTTGCTGGTGCTGTTGCTGCTGCTGTTGT 1341

Qy        680 CGGAGAGGGACAGAGGCCCATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGA 739
              |  |  |          |  || |     | | |  | |   |  |||||| ||| | |
Db       1340 TGCTGTTGCTGTTGTTGCTGTTGCTGTTGTTGCTGCTGCTGTTGTTGCTGTTGTTGTTGT 1281

Qy        740 ATTAATTTTGCTAGCAATGCGCATAGTTGCTGTAGTCAGTGTGGGT 785
              |   | | | |   |    || |||| ||| |    ||| | |
Db       1280 TGTTGCTGTTGTTGTTGTTGCTATTGTTGTTGTTGCTGTTGTTGTT 1235


RESULT 11
AI869699/c
LOCUS       AI869699                486 bp    mRNA    linear   EST 07-MAR-2000
DEFINITION  wm02f07.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2433253 3'
            similar to gb:J05016 PROTEIN DISULFIDE ISOMERASE-RELATED PROTEIN
            PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION   AI869699
VERSION     AI869699.1  GI:5543667
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 486)
  AUTHORS   NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute / National Institute of Neurological
            Disorders and Stroke, Brain Tumor Genome Anatomy Project
            (CGAP/BTGAP), Tumor Gene Index
  JOURNAL   Unpublished (1998)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
            Ph.D.
            cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
            Bonaldo, Ph.D.
            cDNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Insert Length: 751   Std Error: 0.00
            Seq primer: -40UP from Gibco
            High quality sequence stop: 282.
FEATURES             Location/Qualifiers
     source          1. .486
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2433253"
                     /tissue_type="anaplastic oligodendroglioma"
                     /lab_host="DH10B"
                     /clone_lib="NCI_CGAP_Brn25"
                     /note="Organ: brain; Vector: pT7T3D-Pac (Pharmacia) with a
                     modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                     strand cDNA was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCATAGGTTTTTTTTTTTTTTTTTTTTT
                     T 3']; double-stranded cDNA was ligated to Eco RI
                     adaptors (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of the modified pT7T3 vector.
                     Library is normalized, and was constructed by Bento
                     Soares and M.Fatima Bonaldo."
ORIGIN

  Query Match             3.8%;  Score 43.2;  DB 1;  Length 486;
  Best Local Similarity   54.4%;  Pred. No. 1.2;
  Matches   87;  Conservative    0;  Mismatches   73;  Indels    0;  Gaps    0;

Qy        929 AGAGATTGCTGGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGA 988
              | |||   |||||||  |||    | |    || |  || | |  ||   |  ||||
Db        430 ACAGAGATCTGGAGCATTTGAGCAAGTTTATAGAAGAACATGCCACAAAACTGAGCAGGA 371

Qy        989 CGGTGGACGGTACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTC 1048
```

```
Db        370 CCAAGGAAGAGCTTTGAAGGCCTGAGGTCTGCGAAAGGTGGGAGGAGGCAGACGCCCTGC 311

Qy       1049 GTAGGCCAATGTCGTGGCTTCAACAACGAGACAGGGCAGA 1088
              || | ||| |||| ||| || ||  |||| | ||  ||
Db        310 GTGGCCCATGGTCGGGGCGTCCACGCCGAGGCCGGCAACA 271
```

RESULT 12
BW265514/c

```
LOCUS       BW265514                658 bp    mRNA    linear   EST 09-NOV-2002
DEFINITION  BW265514 Nori Satoh unpublished cDNA library, gastrula and neurula
            Ciona intestinalis cDNA clone cign040o10 5', mRNA sequence.
ACCESSION   BW265514
VERSION     BW265514.1  GI:24845432
KEYWORDS    EST.
SOURCE      Ciona intestinalis
  ORGANISM  Ciona intestinalis
            Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
            Phlebobranchia; Cionidae; Ciona.
REFERENCE   1  (bases 1 to 658)
  AUTHORS   Satou,Y., Shin-i,T., Kohara,Y. and Satoh,N.
  TITLE     Expressed genes in Ciona intestinalis (2002c)
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Nori Satoh
            Department of Zoology
            Kyoto University
            Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
            Tel: 81-75-753-4081
            Fax: 81-75-705-1113
            Email: satoh@ascidian.zool.kyoto-u.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .658
                     /organism="Ciona intestinalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:7719"
                     /clone="cign040o10"
                     /tissue_type="whole body"
                     /dev_stage="gastrula and neurula"
                     /clone_lib="Nori Satoh unpublished cDNA library, gastrula
                     and neurula"
ORIGIN
```

```
  Query Match             3.8%;  Score 43.2;  DB 5;  Length 658;
  Best Local Similarity   44.1%;  Pred. No. 1.2;
  Matches  180;  Conservative    0;  Mismatches  228;  Indels    0;  Gaps    0;

Qy        180 GTTCAAGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCT 239
              |||   ||||     |   |||| ||  ||     | || | ||  |   | |
Db        566 GTTGTTGTTGTTGTAGTTGCTGCTGCTGCTGTTGTTGTTGCTGTAGTTGGTGGTGATGTG 507

Qy        240 CCTCGTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGAC 299
              | ||  |||| | ||    |||       || |  | |  | |   ||||  |  ||
Db        506 TTTTGTGTTGTTCTTGTATTAGGCGTTGTTGTTGTTGTTGATGTATTTCGTGTTGTTGCT 447

Qy        300 CGACTTACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCT 359
              || | |||  |  ||||   ||||| |  |||||| | |  ||  | |  || | |
Db        446 GTTGTTCCTGTTGGTGCTGTTGTTGTTCCTGTTGTTGTTCCTGTTGGTGCCGTTGTTGTT 387

Qy        360 CTTTTGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGG 419
              | | | |  | |||  ||| |   |   |  ||    || |  ||| |  | |
Db        386 CCTGTTGGTGCCGTTGTTGTTCCTGTTGTTGTTCCTGTTGGTGCCGTTGTTGTTCCTGTT 327

Qy        420 TAGGGCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGAT 479
              |    |  |   | ||| ||||   |  |  | | |     | |   |  | |
Db        326 GGTGCTGTTGTTGTTCCTGTTGTTGGTGATGCTGTTGTTGTTGATGATGCTGTTGTTGTT 267

Qy        480 AGGGTCGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTG 539
              | |  | ||| |   |   |   || | |||    ||    | |||||| |||| |
Db        266 GGTGATGTTGTTGTTCCTGTTGGTGCTGTTGTTGTTGGTGTTGTTGTTGTTGTTGTT 207

Qy        540 GTGCGGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTT 587
              |       |      | |  ||||  |  |  || |  | ||| | |
```

```
Db        206 GGTGTTGCTGTTGTTGCCGCTGCTGTTGTTGTTGATGATGTTGTTGGT 159
```

RESULT 13
BW259047/c

```
LOCUS       BW259047                663 bp    mRNA    linear   EST 09-NOV-2002
DEFINITION  BW259047 Nori Satoh unpublished cDNA library, gastrula and neurula
            Ciona intestinalis cDNA clone cign001j16 5', mRNA sequence.
ACCESSION   BW259047
VERSION     BW259047.1  GI:24838965
KEYWORDS    EST.
SOURCE      Ciona intestinalis
  ORGANISM  Ciona intestinalis
            Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
            Phlebobranchia; Cionidae; Ciona.
REFERENCE   1  (bases 1 to 663)
  AUTHORS   Satou,Y., Shin-i,T., Kohara,Y. and Satoh,N.
  TITLE     Expressed genes in Ciona intestinalis (2002c)
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Nori Satoh
            Department of Zoology
            Kyoto University
            Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
            Tel: 81-75-753-4081
            Fax: 81-75-705-1113
            Email: satoh@ascidian.zool.kyoto-u.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .663
                     /organism="Ciona intestinalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:7719"
                     /clone="cign001j16"
                     /tissue_type="whole body"
                     /dev_stage="gastrula and neurula"
                     /clone_lib="Nori Satoh unpublished cDNA library, gastrula
                     and neurula"
ORIGIN
```

```
  Query Match             3.8%;  Score 43.2;  DB 5;  Length 663;
  Best Local Similarity   44.1%;  Pred. No. 1.2;
  Matches  180;  Conservative    0;  Mismatches  228;  Indels    0;  Gaps    0;

Qy        180 GTTCAAGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCT 239
              |||   ||||     |   |||| ||  ||     | || | ||  |   | |
Db        566 GTTGTTGTTGTTGTAGTTGCTGCTGCTGCTGTTGTTGTTGCTGTAGTTGGTGGTGATGTG 507

Qy        240 CCTCGTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGAC 299
              | ||  |||| | ||    |||       || |  | |  | |   ||||  |  ||
Db        506 TTTTGTGTTGTTCTTGTATTAGGCGTTGTTGTTGTTGTTGATGTATTTCGTGTTGTTGCT 447

Qy        300 CGACTTACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCT 359
              || | |||  |  ||||   ||||| |  |||||| | |  ||  | |  || | |
Db        446 GTTGTTCCTGTTGGTGCTGTTGTTGTTCCTGTTGTTGTTCCTGTTGGTGCCGTTGTTGTT 387

Qy        360 CTTTTGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGG 419
              | | | |  | |||  ||| |   |   |  ||    || |  ||| |  | |
Db        386 CCTGTTGGTGCCGTTGTTGTTCCTGTTGTTGTTCCTGTTGGTGCCGTTGTTGTTCCTGTT 327

Qy        420 TAGGGCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGAT 479
              |    |  |   | ||| ||||   |  |  | | |     | |   |  | |
Db        326 GGTGCTGTTGTTGTTCCTGTTGTTGGTGATGCTGTTGTTGTTGATGATGCTGTTGTTGTT 267

Qy        480 AGGGTCGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTG 539
              | |  | ||| |   |   |   || | |||    ||    | |||||| |||| |
Db        266 GGTGATGTTGTTGTTCCTGTTGGTGCTGTTGTTGTTGGTGTTGTTGTTGTTGTTGTT 207

Qy        540 GTGCGGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTT 587
              |       |      | |  ||||  |  |  || |  | ||| | |
Db        206 GGTGTTGCTGTTGTTGCCGCTGCTGTTGTTGTTGATGATGTTGTTGGT 159
```

RESULT 14
CNS006ON

```
LOCUS       CNS006ON                910 bp    DNA     linear   GSS 03-JUN-1999
DEFINITION  Drosophila melanogaster genome survey sequence T7 end of BAC #
            BACR14J21 of RPCI-98 library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL065629
VERSION     AL065629.1  GI:4944698
KEYWORDS    GSS.
SOURCE      Drosophila melanogaster (fruit fly)
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 910)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the Berkeley Drosophila Genome Project (BDGP).
            The BDGP is constructing a physical map of the Drosophila
            melanogaster genome using these BACs. For further information
            please see  http://www.fruitfly.org The BDGP Drosophila
            melanogaster BAC library was prepared by Kazutoyo Osoegawa and
            Aaron Mammoser in Pieter de Jong's laboratory in the Department of
            Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
            NY. The library is named RPCI-98 and was constructed by partial
            EcoRI digestion of Drosophila DNA provided by the BDGP from the
            isogenic strain y2; cn bw sp, the same strain used for the BDGP's
            P1 and EST libraries. A more detailed description of the library
            and how to order individual BAC clones, the entire library, or
            filters for hybridization from the BACPAC Resource Center can be
            found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES             Location/Qualifiers
     source          1. .910
                     /organism="Drosophila melanogaster"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:7227"
                     /clone="BACR14J21"
                     /clone_lib="RPCI-98"
                     /note="end : T7"
ORIGIN

  Query Match             3.8%;  Score 43.2;  DB 9;  Length 910;
  Best Local Similarity   19.2%;  Pred. No. 1.3;
  Matches   81;  Conservative  159;  Mismatches  180;  Indels    2;  Gaps    1;

Qy        330 GAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTTCCCGTCGG 389
              | ||: |  : ||| ||| :|||||  | | |:|: |  : ||     |:   :::: |
Db        468 GGGGKGGGGKGGGGGGGGGHGGGGGSGGGTDTKTWTGGKSTGGGGGGGSSGGSSSKGGGC 527

Qy        390 GGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTCTTGGTCCA 449
              |:  :  || |:      : ||| :::| :  :::::  :  : ::| : :   | |: :
Db        528 GSGSYGGGGGGYGGTGSGSGGGGSSSSGCSSSSSSSSSSSSCGSSSBGCBSSCGCGSCSY 587

Qy        450 GTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCACCCTCTC 509
              : ::  :||:   | :: :   ::     | :::|:||    : ::: :| : : : :|
Db        588 SSSSTGSTGSCGCGSSSSSSSSSSCSSTSTSSSSTSGCGYSSSGSBSSSCSSTBTSSSTT 647

Qy        510 GTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGGCTGCCGAG 569
              :|:  : :|:: ::|:|  ||: |:|::: ::|::: : :: ::  : : ::: :::  :
Db        648 BTBTKBTSTYSTSYTST--TTSTTSTBSBTSYGSBBKSTSSTSSSTSSSTSSSSSSSTSS 705

Qy        570 GAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCCTTGCAGAA 629
                  : : :::::||:   |: : ::|  |:: ::   : :    : : :| : :
Db        706 CTSTKBYSTSTBSYSBTTBTBTTSTSTBBTTSTBYTBBTTBYTKSTTSMTSTYTTBBSTS 765

Qy        630 GAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCGGAGAGGGA 689
              : :|  : :::  |  :| :|  :  : :: : |:    |: ::::: :|: :   : :
Db        766 KBSTBTSTBKSTGTKTBTSBTTSCTSSSSSBSTSYSYSTSCBSSBSBSSTSYSBCTSTST 825

Qy        690 CAGAGGCCCATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTG 749
              : : :::::    :   ::| ::|:||    :| |: :||:::: |  :  ||  || |
```

```
Db        826 STSSBBSSBSSSSSCGTSBTSSSTSTTSTCTSTTCKTSTGBSSYGTGTSTYTTBTTTATT 885

Qy        750 CT 751
              :|
Db        886 ST 887


RESULT 15
CK206445/c
LOCUS       CK206445                1203 bp    mRNA    linear   EST 08-DEC-2003
DEFINITION  FGAS018038 Triticum aestivum FGAS: Library 5 GATE 7 Triticum
            aestivum cDNA, mRNA sequence.
ACCESSION   CK206445
VERSION     CK206445.1  GI:39568835
KEYWORDS    EST.
SOURCE      Triticum aestivum (bread wheat)
  ORGANISM  Triticum aestivum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Pooideae; Triticeae; Triticum.
REFERENCE   1  (bases 1 to 1203)
  AUTHORS   Allard,F., Crosby,W.L., Danyluk,J., Eudes,F., Frick,M., Gaudet,D.,
            Genswein,B., Graf,R., Gulick,P., Hrycan,L.D., Laroche,A.,
            Links,M.G., McCarthy,E.L., Monroy,A., Muzak,I., Nilson,D.,
            Penniket,C., Roach,J.L. and Sarhan,F.
  TITLE     Functional Genomics of Abiotic Stress In Wheat and Canola Crops
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Wm L Crosby
            Bioinformatics
            University of Saskatchewan, Department of Computer Science
            1C101 Engineering Building, 57 Campus Drive, Saskatoon,
            Saskatchewan, S7N 5A9, Canada
            Tel: 306 966 1769
            Fax: 306 966 2033
            Email: fgas_ests@cs.usask.ca
            This sequence is the direct result of the Base calling software
            Phred (default parameters). It is the raw base calls. To aid in the
            identification of the high quality insert the software Lucy
            (default parameters) has been run on this sequence. Lucy identified
            the region [1,533].
            Plate: L5B007  row: H  column: 02.
FEATURES             Location/Qualifiers
     source          1. .1203
                     /organism="Triticum aestivum"
                     /mol_type="mRNA"
                     /db_xref="taxon:4565"
                     /clone_lib="Triticum aestivum FGAS: Library 5 GATE 7"
                     /note="Vector: pCMV.SPORT6; Crown and developmental stages
                     of spike formation in wheat cultivar Norstar. 4 mRNA
                     populations were combined before constructing the library.
                     The first mRNA population is from 1cm crown sections after
                     30 days of cold acclimation. The second is from 1cm crown
                     sections after 11 days of deacclimation (before
                     deacclimation plants were fully vernalized for 49 days).
                     The third is from different developmental stages of spike
                     formation (5 to 50mm) that still have not emerged from the
                     leaf (dissection required). The last is from different
                     developmental stages of spike and seed formation after
                     having emerged from the leaf (visible). First strand
                     synthesis in this library was done in the presence of
                     methylated dCTP thereby protecting from internal cleavage
                     with NotI."
ORIGIN

  Query Match             3.7%;  Score 43;  DB 7;  Length 1203;
  Best Local Similarity   48.6%;  Pred. No. 1.6;
  Matches  118;  Conservative    0;  Mismatches  125;  Indels    0;  Gaps    0;

Qy        417 GGGTAGGGCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAA 476
              |||||| | | ||| |||          || ||||  || | || | |  ||||  ||| |
Db        315 GGGTAGAGGCGTACGCGATCACCCAGAGGCCCAGCGGGGCGGGCCTGTTCAGTGGCCGCA 256

Qy        477 GATAGGGTCGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTT 536
```

```
Db        255 GGTGCAGTTGGTGCAGGTGCAGCTGGCGCCGCACTTGCACTTGCCGTCGTTCTCCGCGGC 196

Qy        537 CTGGTGCGGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCA 596

Db        195 CTCCTGCACCTCGAAGTGGCTCTTCTCGGTGTCGACCATGACGATGCCGTAGCCGTCGCC 136

Qy        597 CCTGTTCTCGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGA 656

Db        135 CTTCTTCACGCACCCCCTCTTGTCGGCGCAGTCGCAGTTGCCGCACTTCTCACCCATGGC 76

Qy        657 CGT 659

Db         75 GGT 73
```

Search completed: October 18, 2004, 03:14:31
Job time : 4052.64 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 17, 2004, 15:27:12 ; Search time 596.39 Seconds
(without alignments)
10122.301 Million cell updates/sec

Title: US-10-679-999-8
Perfect score: 1150
Sequence: 1 GTATACCTTGGGTTTAGAAC.....AGGCCCAACAATTACCTAGG 1150

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_23Sep04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	694.8	60.4	993	12	ADM68910	Adm68910 Human IgG
	2	680.6	59.2	780	12	ADM17710	Adm17710 Fc N-term
	3	674.4	58.6	777	12	ADM17770	Adm17770 Fc C-term
	4	622.4	54.1	7033	12	ADJ65025	Adj65025 Plasmid p
	5	63.2	5.5	2572	6	AAD24594	Aad24594 Human ery
	6	60	5.2	2287	10	ADH54467	Adh54467 Human imm
	7	53.6	4.7	138	8	AAL51057	Aal51057 Cyclic si
	8	47.8	4.2	2000	8	ADA71938	Ada71938 Rice gene
	9	47.4	4.1	1464	4	ABL25527	Abl25527 Drosophil
c	10	47.4	4.1	4526	4	ABL25526	Abl25526 Drosophil
c	11	47	4.1	2000	8	ADA71938	Ada71938 Rice gene
	12	43.6	3.8	1161	11	ABD09099	Abd09099 Pseudomon
	13	43.6	3.8	1200	4	AAS51550	Aas51550 Pseudomon
	14	43.6	3.8	1200	8	ACA19541	Aca19541 Prokaryot
c	15	43.6	3.8	1287	11	ABD09256	Abd09256 Pseudomon
	16	43.6	3.8	1359	11	ABD09020	Abd09020 Pseudomon
	17	43	3.7	8874	12	ADJ65028	Adj65028 Plasmid p
	18	42.4	3.7	52	2	AAQ29203	Aaq29203 3' heavy
	19	42.4	3.7	52	2	AAQ29205	Aaq29205 3' heavy
c	20	41.8	3.6	1182	10	ADC16621	Adc16621 Secondary
c	21	41.8	3.6	3489	3	AAA30290	Aaa30290 Kaposi's
c	22	41.8	3.6	3489	4	AAF82901	Aaf82901 Nucleotid
c	23	41.8	3.6	3489	6	ABA93487	Aba93487 Kaposi's
c	24	41.8	3.6	3489	12	ADJ65095	Adj65095 HHV8 DNA
	25	41.8	3.6	32207	2	AAV73805	Aav73805 KSHV LUR
c	26	41.8	3.6	135638	10	ABX34289	Abx34289 S. atrool
	27	41.8	3.6	137507	2	AAV19941	Aav19941 KSHV long
	28	41.8	3.6	137508	12	ADN12162	Adn12162 Human her
	29	41.6	3.6	2171	3	AAF16286	Aaf16286 Human pro
	30	41.6	3.6	2172	6	ABQ54963	Abq54963 Human ova
	31	41.6	3.6	2300	6	AAS62246	Aas62246 cDNA sequ
	32	41.6	3.6	2300	6	ABK34737	Abk34737 Human cDN
c	33	41.2	3.6	1236	6	AAD44410	Aad44410 Human hun
c	34	41	3.6	2892	5	AAS66583	Aas66583 DNA encod
	35	40.6	3.5	268	2	AAT20112	Aat20112 Human gen
c	36	40.4	3.5	486	4	AAF75507	Aaf75507 Polygluta
c	37	40.4	3.5	1057	2	AAQ03405	Aaq03405 Streptomy
c	38	40.4	3.5	3042	4	ABL28445	Abl28445 Drosophil
	39	40.4	3.5	5215	4	ABL28444	Abl28444 Drosophil
	40	40.2	3.5	926	6	ABZ11846	Abz11846 Human pol
c	41	40.2	3.5	1404	12	ADJ76031	Adj76031 Marker ge
	42	40.2	3.5	1423	12	ADM44364	Adm44364 Novel hum
c	43	40	3.5	543	2	AAQ23092	Aaq23092 Antigen t
	44	40	3.5	2930	12	ADO19793	Ado19793 Human PRO
	45	39.8	3.5	774	12	ADO44398	Ado44398 Z. mays F

ALIGNMENTS

RESULT 1
ADM68910
ID ADM68910 standard; DNA; 993 BP.
XX
AC ADM68910;
XX
DT 03-JUN-2004 (first entry)
XX
DE Human IgG1 heavy chain DNA non-coding strand.
XX
KW Human; batch reformatting vector; ligand screening; phagemid;
KW phage display vector; pBRV; pRRV; internal ribosome entry site; IRES;
KW rapid reformatting vector; IgG1; immunoglobulin; heavy chain; ss.
XX
OS Homo sapiens.
XX
PN US2003224408-A1.
XX
PD 04-DEC-2003.
XX
PF 07-MAR-2003; 2003US-00383902.
XX
PR 07-MAR-2002; 2002US-0362403P.
XX
PA (DYAX-) DYAX CORP.
XX
PI Hoogenboom HRJM, Mullberg J, Ladner RC;
XX
DR WPI; 2004-119700/12.
XX
PT Screening ligands, by providing initial nucleic acid cassettes, modifying
PT cassette in single reaction mixture, introducing modified cassette into
PT mammalian cell, expressing modified cassette in transfected cells.
XX
PS Disclosure; SEQ ID NO 5; 63pp; English.
XX
CC The invention relates to screening ligands, by providing several initial
CC nucleic acid cassettes, modifying each nucleic acid cassette in single
CC reaction mixture so that it is functional in a second expression system,
CC introducing each modified nucleic acid cassette into a mammalian cell to
CC produce a mixture of transfected cells, and expressing each modified
CC nucleic acid cassette in transfected cells. Also included are screening
CC nucleic acids (involving providing a number of first different nucleic
CC acids, each encoding a hetero oligomeric candidate ligand, selecting a

CC subset of a number of first different nucleic acids by contacting
CC candidate ligands encoded by the members of a number of first different
CC nucleic acids to a target, reformatting each nucleic acid of the subset
CC for mammalian cell expression, such that each nucleic acid encodes a
CC hetero-oligomeric protein that includes a first functional domain of one
CC subunit of the candidate ligand, a second functional domain of another
CC subunit of the candidate ligand and an effector domain not encoded by the
CC nucleic acids of a number of first different nucleic acids, introducing
CC members of the subset into a mammalian cell to form several expression
CC cells that can produce the protein that includes the functional domain
CC and the effector domain, and screening the expression cells to identify
CC cells that produce at least a threshold amount of a ligand-effector
CC domain fusion protein) and evaluating display library members (involving
CC providing several display library members, determining an assessment for
CC each library member with respect to a property, storing information about
CC the assessments of the library members in a computer database, filtering
CC the information to identify a subset of the library members, and
CC reformatting each member of the subset for expression in a mammalian cell
CC by a method that comprises disposing nucleic acid for each member of the
CC selected subset into a single container). The method is useful for
CC screening ligands. Bacterial and mammalian expression vectors
CC (reformatting vectors) were prepared that support the transfer
CC individually or en masse of Fab heavy and light chain genes from a
CC bacterial expression vector to a mammalian expression vector. Typically,
CC the display vector was a phagemid or phage display vector, which mediate
CC the expression of the Fab on the surface of the bacteriophage M13 or fd.
CC The Fab-encoding segment was transferred from the bacterial display
CC vector to the eukaryotic vector, e.g., pBRV or pRRV by restricting the
CC vector with ApaL1 and BstE2. This fragment was subcloned into ApaL1/BstE2
CC sites of pBRV (batch reformatting vector) or pRRV (rapid reformatting
CC vector). This vector contained a CMV eukaryotic promoter in place of the
CC first bacterial leader sequence. The VH-CH1 sequence was no longer fused
CC to gene III but was fused in-frame to a sequence encoding an
CC immunoglobulin Fc region, e.g., including Hinge-CH2-CH3. Two intervening
CC segments which were inserted between heavy and light chain coding
CC sequences were IrES between the EcoRI and XhaI site for internal ribosome
CC entry and translation of the second coding region. The present sequence
CC is the non-coding strand of a DNA used in the constructs of the method of
CC the invention.
XX
SQ Sequence 993 BP; 161 A; 257 C; 340 G; 235 T; 0 U; 0 Other;

Query Match 60.4%; Score 694.8; DB 12; Length 993;
Best Local Similarity 99.7%; Pred. No. 2.5e-187;
Matches 696; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy        5 ACCTTGGGTTTAGAACACTGTTTTGAGTGTGTACGGGTGGCACGGGTCGTGGACTTGAGG 64
            | || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      293 AACTCGGGTTTAGAACACTGTTTTGAGTGTGTACGGGTGGCACGGGTCGTGGACTTGAGG 352

Qy       65 ACCCCCCTGGCAGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGG 124
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      353 ACCCCCCTGGCAGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGG 412

Qy      125 CCTGGGGACTCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCA 184
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      413 CCTGGGGACTCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCA 472

Qy      185 AGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCG 244
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      473 AGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCG 532

Qy      245 TCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACT 304
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      533 TCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACT 592

Qy      305 TACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTT 364
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      593 TACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTT 652

Qy      365 GGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGG 424
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      653 GGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGG 712
```

```
Qy      425 CCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGT 484
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      713 CCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGT 772

Qy      485 CGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCG 544
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      773 CGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCG 832

Qy      545 GAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCT 604
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      833 GAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCT 892

Qy      605 CGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGG 664
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      893 CGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGG 952

Qy      665 TGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCATTT 702
            |||||||||||||||||||||||||||||||||||||||
Db      953 TGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCATTT 990
```

RESULT 2
ADM17710
ID ADM17710 standard; DNA; 780 BP.
XX
AC ADM17710;
XX
DT 17-JUN-2004 (first entry)
XX
DE Fc N-terminal vector related oligonucleotide SEQ ID NO:62.
XX
KW nerve growth factor modulator; NGF modulator; analgesic; NGF inhibitor;
KW nerve growth factor inhibitor; neurologic pain; diabetic neuropathy;
KW post-herpetic neuralgia; inflammatory pain; migraine; asthma;
KW hyperactive bladder; psoriasis; cancer; acute pain; dental pain;
KW surgical pain; pain; causalgia; demyelinating disease;
KW trigeminal neuralgia; chronic alcoholism; stroke; thalamic pain syndrome;
KW diabetes; acquired immuno deficiency syndrome; AIDS; headache;
KW inflammation; arthritis; rheumatic disease; lupus; osteoarthritis;
KW inflammatory bowel disorder; inflammatory eye disorder; sunburn;
KW carditis; dermatitis; myositis; neuritis; collagen vascular disease;
KW chronic inflammatory condition; neuropathic pain; genitourinary; wound;
KW burn; allergic skin reaction; pruritus; vitiligo;
KW gastrointestinal disorder; colitis; gastric ulceration; duodenal ulcer;
KW ss.
XX
OS Synthetic.
XX
PN WO2004026329-A1.
XX
PD 01-APR-2004.
XX
PF 19-SEP-2003; 2003WO-US029866.
XX
PR 19-SEP-2002; 2002US-0412524P.
PR 18-SEP-2003; 2003US-00666480.
XX
PA (AMGE-) AMGEN INC.
XX
PI Boone TC, Wild KD, Sitney KC, Min H, Kimmel B;
XX
DR WPI; 2004-283150/26.
XX
PT Novel peptide capable of modulating nerve growth factor activity, useful
PT for treating disease or disorder e.g., acute pain, dental pain, cancer,
PT migraine and collagen vascular disease.
XX
PS Example 2; SEQ ID NO 62; 267pp; English.
XX
CC The present invention describes a peptide (I) that is capable of
CC modulating nerve growth factor (NGF) activity. Also described: (1)
CC modified peptide (II) comprising (I) and a vehicle, where the modified

```
CC   peptide is capable of modulating NGF activity; (2) dimer or multimer of
CC   (I); (3) modified peptide (III), its multimers or its salt, where the
CC   peptide is capable of modulating NGF activity; (4) polynucleotide (IV)
CC   encoding (I), (II) or (III); (5) expression vector (V) comprising (IV);
CC   (6) host cell (VI) comprising (V); (7) a composition (VII) of matter and
CC   a vehicle, where the composition of matter is capable of modulating NGF
CC   activity; and (8) pharmaceutical composition comprising (I), (II) or
CC   (III) and a diluent or carrier. (I) has analgesic activity, and can be
CC   used as an inhibitor of NGF. (I) is useful for treating or preventing a
CC   disease or disorder associated with NGF activity by administering (I) to
CC   human or animal. The disease or disorder chosen from neurologic pain,
CC   painful diabetic neuropathy, post-herpetic neuralgia, inflammatory pain,
CC   migraine, asthma, hyperactive bladder, psoriasis, cancer, acute pain,
CC   dental pain, pain from trauma, surgical pain, pain resulting from
CC   amputation or abscess, causalgia, demyelinating diseases, trigeminal
CC   neuralgia, chronic alcoholism, stroke, thalamic pain syndrome, diabetes,
CC   acquired immuno deficiency syndrome (AIDS), toxins and chemotherapy,
CC   general headache, cluster headache, mixed-vascular and non-vascular
CC   syndromes, tension headache, general inflammation, arthritis, rheumatic
CC   diseases, lupus, osteoarthritis, inflammatory bowel disorders,
CC   inflammatory eye disorders, inflammatory or unstable bladder disorders,
CC   skin complaints with inflammatory components, sunburn, carditis,
CC   dermatitis, myositis, neuritis, collagen vascular diseases, chronic
CC   inflammatory conditions, inflammatory pain associated hyperalgesia and
CC   allodynia, neuropathic pain and associated hyperalgesia and allodynia,
CC   diabetic neuropathy pain, sympathetically maintained pain,
CC   deafferentation syndromes, epithelial tissue damage or dysfunction,
CC   herpes simplex, post-herpetic neuralgia, disturbances of visceral
CC   motility at respiratory, genitourinary, gastrointestinal or vascular
CC   regions, wounds, burns, allergic skin reactions, pruritus, vitiligo,
CC   general gastrointestinal disorders, colitis, gastric ulceration, duodenal
CC   ulcers, vasomotor or allergic rhinitis, or bronchial disorders. (I) is
CC   also useful for modulating pain or promoting analgesia by administering
CC   (I) to human or animal. (I) is also useful in the manufacture of
CC   medicament for the treatment of disease or disorder. The present sequence
CC   is used in the exemplification of the present invention.
XX
SQ   Sequence 780 BP; 132 A; 208 C; 237 G; 203 T; 0 U; 0 Other;

  Query Match           59.2%;  Score 680.6;  DB 12;  Length 780;
  Best Local Similarity  98.7%;  Pred. No. 2.5e-183;
  Matches  686;  Conservative    0;  Mismatches    9;  Indels    0;  Gaps    0;

Qy         18 AACACTGTTTTGAGTGTGTACGGGTGGCACGGGTCGTGGACTTGAGGACCCCCCTGGCAG 77
              | | |||||||||||||||| ||||| ||||||||||||||||||||||||||||||||
Db         86 ACCCCTGTTTTGAGTGTGTACAGGTGGAACGGGTCGTGGACTTGAGGACCCCCCTGGCAG 145

Qy         78 TCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCA 137
              ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        146 TCAAAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCA 205

Qy        138 GTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCA 197
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        206 GTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCA 265

Qy        198 CCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTG 257
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        266 CCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTG 325

Qy        258 CATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCAT 317
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        326 CATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCAT 385

Qy        318 GTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCG 377
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        386 GTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCG 445

Qy        378 GTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTG 437
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        446 GTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTG 505

Qy        438 GTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCA 497
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        506 GTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCA 565

Qy        498 CCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCT 557
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        566 CCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCT 625

Qy        558 GAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGT 617
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        626 GAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGT 685

Qy        618 CCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTT 677
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        686 CCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTT 745

Qy        678 CTCGGAGAGGGACAGAGGCCCATTTCATGGCTAGG 712
              |||||||||||||||||||||||||   |  |||||
Db        746 CTCGGAGAGGGACAGAGGCCCATTTATTACCTAGG 780


RESULT 3
ADM17770
ID   ADM17770 standard; DNA; 777 BP.
XX
AC   ADM17770;
XX
DT   17-JUN-2004  (first entry)
XX
DE   Fc C-terminal vector related oligonucleotide SEQ ID NO:122.
XX
KW   nerve growth factor modulator; NGF modulator; analgesic; NGF inhibitor;
KW   nerve growth factor inhibitor; neurologic pain; diabetic neuropathy;
KW   post-herpetic neuralgia; inflammatory pain; migraine; asthma;
KW   hyperactive bladder; psoriasis; cancer; acute pain; dental pain;
KW   surgical pain; pain; causalgia; demyelinating disease;
KW   trigeminal neuralgia; chronic alcoholism; stroke; thalamic pain syndrome;
KW   diabetes; acquired immuno deficiency syndrome; AIDS; headache;
KW   inflammation; arthritis; rheumatic disease; lupus; osteoarthritis;
KW   inflammatory bowel disorder; inflammatory eye disorder; sunburn;
KW   carditis; dermatitis; myositis; neuritis; collagen vascular disease;
KW   chronic inflammatory condition; neuropathic pain; genitourinary; wound;
KW   burn; allergic skin reaction; pruritus; vitiligo;
KW   gastrointestinal disorder; colitis; gastric ulceration; duodenal ulcer;
KW   ss.
XX
OS   Synthetic.
XX
PN   WO2004026329-A1.
XX
PD   01-APR-2004.
XX
PF   19-SEP-2003; 2003WO-US029866.
XX
PR   19-SEP-2002; 2002US-0412524P.
PR   18-SEP-2003; 2003US-00666480.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Boone TC,  Wild KD,  Sitney KC,  Min H,  Kimmel B;
XX
DR   WPI; 2004-283150/26.
XX
PT   Novel peptide capable of modulating nerve growth factor activity, useful
PT   for treating disease or disorder e.g., acute pain, dental pain, cancer,
PT   migraine and collagen vascular disease.
XX
PS   Example 2; SEQ ID NO 122; 267pp; English.
XX
CC   The present invention describes a peptide (I) that is capable of
CC   modulating nerve growth factor (NGF) activity. Also described: (1)
CC   modified peptide (II) comprising (I) and a vehicle, where the modified
CC   peptide is capable of modulating NGF activity; (2) dimer or multimer of
CC   (I); (3) modified peptide (III), its multimers or its salt, where the
CC   peptide is capable of modulating NGF activity; (4) polynucleotide (IV)
```

CC encoding (I), (II) or (III); (5) expression vector (V) comprising (IV);
CC (6) host cell (VI) comprising (V); (7) a composition (VII) of matter and
CC a vehicle, where the composition of matter is capable of modulating NGF
CC activity; and (8) pharmaceutical composition comprising (I), (II) or
CC (III) and a diluent or carrier. (I) has analgesic activity, and can be
CC used as an inhibitor of NGF. (I) is useful for treating or preventing a
CC disease or disorder associated with NGF activity by administering (I) to
CC human or animal. The disease or disorder chosen from neurologic pain,
CC painful diabetic neuropathy, post-herpetic neuralgia, inflammatory pain,
CC migraine, asthma, hyperactive bladder, psoriasis, cancer, acute pain,
CC dental pain, pain from trauma, surgical pain, pain resulting from
CC amputation or abscess, causalgia, demyelinating diseases, trigeminal
CC neuralgia, chronic alcoholism, stroke, thalamic pain syndrome, diabetes,
CC acquired immuno deficiency syndrome (AIDS), toxins and chemotherapy,
CC general headache, cluster headache, mixed-vascular and non-vascular
CC syndromes, tension headache, general inflammation, arthritis, rheumatic
CC diseases, lupus, osteoarthritis, inflammatory bowel disorders,
CC inflammatory eye disorders, inflammatory or unstable bladder disorders,
CC skin complaints with inflammatory components, sunburn, carditis,
CC dermatitis, myositis, neuritis, collagen vascular diseases, chronic
CC inflammatory conditions, inflammatory pain associated hyperalgesia and
CC allodynia, neuropathic pain and associated hyperalgesia and allodynia,
CC diabetic neuropathy pain, sympathetically maintained pain,
CC deafferentation syndromes, epithelial tissue damage or dysfunction,
CC herpes simplex, post-herpetic neuralgia, disturbances of visceral
CC motility at respiratory, genitourinary, gastrointestinal or vascular
CC regions, wounds, burns, allergic skin reactions, pruritus, vitiligo,
CC general gastrointestinal disorders, colitis, gastric ulceration, duodenal
CC ulcers, vasomotor or allergic rhinitis, or bronchial disorders. (I) is
CC also useful for modulating pain or promoting analgesia by administering
CC (I) to human or animal. (I) is also useful in the manufacture of
CC medicament for the treatment of disease or disorder. The present sequence
CC is used in the exemplification of the present invention.
XX
SQ Sequence 777 BP; 133 A; 206 C; 236 G; 202 T; 0 U; 0 Other;

Query Match 58.6%; Score 674.4; DB 12; Length 777;
Best Local Similarity 97.7%; Pred. No. 1.4e-181;
Matches 684; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

```
Qy          4 TACCTTGGGTTTAGAACACTGTTTTGAGTGTGTACGGGTGGCACGGGTCGTGGACTTGAG 63
              |  |||   ||  |   |||||||||||||||| ||||| || ||||| || ||||||
Db         24 TTCCTCCTTATTGTATACCTGTTTTGAGTGTGTACAGGTGGAACAGGTCGAGGCCTTGAG 83

Qy         64 GACCCCCCTGGCAGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGG 123
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         84 GACCCCCCTGGCAGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGG 143

Qy        124 GCCTGGGGACTCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTC 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        144 GCCTGGGGACTCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTC 203

Qy        184 AAGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTC 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        204 AAGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTC 263

Qy        244 GTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGAC 303
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        264 GTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGAC 323

Qy        304 TTACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTT 363
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        324 TTACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTT 383

Qy        364 TGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGG 423
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        384 TGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGG 443

Qy        424 GCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGG 483
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        444 GCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGG 503

Qy        484 TCGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGC 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        504 TCGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGC 563

Qy        544 GGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTC 603
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        564 GGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTC 623

Qy        604 TCGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTG 663
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        624 TCGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTG 683

Qy        664 GTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCATTTC 703
              |||||||||||||||||||||||||||||||||||||||
Db        684 GTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCATTTC 723
```

RESULT 4
ADJ65025
ID ADJ65025 standard; DNA; 7033 BP.
XX
AC ADJ65025;
XX
DT 06-MAY-2004 (first entry)
XX
DE Plasmid pD17-H39E3-2.h4a complemetary strand DNA sequence SEQ ID NO:4.
XX
KW humanised antibody; human 4-1BB; human 4-1BB ligand; cancer; cytostatic;
KW gene therapy; antibody; plasmid; pD17-H39E3-2.h4a; gene; ds.
XX
OS Synthetic.
XX
PN WO2004010947-A2.
XX
PD 05-FEB-2004.
XX
PF 30-JUL-2003; 2003WO-US023735.
XX
PR 30-JUL-2002; 2002US-0399646P.
XX
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
XX
PI Jure-Kunkel M, Ganguly S, Abraham R, Hollenbaugh DL, Rillema J;
PI Thorne B, Shuford WW, Mittler RS;
XX
DR WPI; 2004-143726/14.
XX
PT New humanized antibody that binds to human 4-1BB and allows binding of
PT human 4-1BB to a human 4-1BB ligand, useful for preparing a composition
PT for treating cancer.
XX
PS Example; SEQ ID NO 4; 78pp; English.
XX
CC The present invention describes a humanised antibody (I) that binds to
CC human 4-1BB and allows binding of human 4-1BB to a human 4-1BB ligand.
CC Also described: (1) a pharmaceutical composition comprising the antibody
CC (I) and a carrier; (2) treating cancer in a subject; and (3) an isolated
CC polynucleotide comprising nucleotides 693-2072 of the 7033-base pairs
CC (bp) sequence (SEQ ID NO: 3, ADJ65024) or nucleotides 633-1034 or 1409-
CC 1726 of the 8874-bp sequence (SEQ ID NO: 6, ADJ65027). (I) has cytostatic
CC activity, and can be used in gene therapy. The humanised antibody (I) can
CC be used for preparing a composition for treating cancer. The present
CC sequence represents the complementary strand of the plasmid pD17-H39E3-
CC 2.h4a nucleotide sequence, which is used in an example from the present
CC invention.
XX
SQ Sequence 7033 BP; 1789 A; 1687 C; 1766 G; 1791 T; 0 U; 0 Other;

Query Match 54.1%; Score 622.4; DB 12; Length 7033;
Best Local Similarity 94.7%; Pred. No. 2.4e-166;
Matches 644; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

```
Qy         30 AGTGTGTACGGGTGGCACGGGTCGTGGACTTGAGGACCCCCCTGGCAGTCAGAAGGAGAA 89
              ||   | |||||||| ||||||||||||||  |||||||||||||| |||||||||||| ||
```

```
Db       1400 AGGTGGAACGGGTGGAACGGGTCGTGGACTCAAGGACCCCCCTGGTAGTCAGAAGGACAA 1459

Qy         90 GGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGCACCA 149
              |||||||||||||||||||| |||||||||||||||||||||||||||||| ||||||||
Db       1460 GGGGGGTTTTGGGTTCCTGTGAGAGTACTAGAGGGCCTGGGGACTCCAGTGCACGCACCA 1519

Qy        150 CCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGCACCT 209
              |||||||||||||||| |||||||| |||||| |||||||||||||||||| ||||||||
Db       1520 CCACCTGCACTCGGTCCTTCTGGGGCTCCAGGTCAAGTTGACCATGCACCTACCGCACCT 1579

Qy        210 CCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATGGCACACCA 269
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db       1580 CCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCAAGTTGTCGTGCATGGCACACCA 1639

Qy        270 GTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATGTTCACGTTCCA 329
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db       1640 GTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTGCCGTTCCTCATGTTCACGTTCCA 1699

Qy        330 GAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTTCCCGTCGG 389
              |||||||||||  ||||||   || ||||||||||||||||||||||||||||||||||||
Db       1700 GAGGTTGTTTCCGGAGGGCAGGAGGTAGCTCTTTTGGTAGAGGTTTCGGTTTCCCGTCGG 1759

Qy        390 GGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTCTTGGTCCA 449
              ||||||  |||||||||||||||||||||||||||  |||  |||  ||||||||||||||
Db       1760 GGCTCTCGGTGTCCACATGTGGGACGGGGGTAGGGTCCTCCTCTACTGGTTCTTGGTCCA 1819

Qy        450 GTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCACCCTCTC 509
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db       1820 GTCGGACTGGACGGACCAGTTTCCGAAGATGGGGTCGCTGTAGCGGCACCTCACCCTCTC 1879

Qy        510 GTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGGCTGCCGAG 569
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1880 GTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGGCTGCCGAG 1939

Qy        570 GAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCCTTGCAGAA 629
              |||||||||||||||| ||| ||||||||||||||||||||||| ||||||| |||||
Db       1940 GAAGAAGGAGATGTCGTCCGATTGGCACCTGTTCTCGTCCACCGTCCTCCCCTTACAGAA 1999

Qy        630 GAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCGGAGAGGGA 689
              |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db       2000 GAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGTGTCTTCTCGGAGAGGGA 2059

Qy        690 CAGAGGCCCATTTCATGGCT 709
              ||||| |||||||  | | |
Db       2060 CAGAGACCCATTTACTAGAT 2079


RESULT 5
AAD24594
ID   AAD24594 standard; DNA; 2572 BP.
XX
AC   AAD24594;
XX
DT   09-APR-2002  (first entry)
XX
DE   Human erythropoietin (Epo) related DNA.
XX
KW   Human; erythropoietin; Epo; haematocrit; anaemia; kidney function;
KW   cancer; myelosuppressive therapy; anti-viral drug; ds.
XX
OS   Homo sapiens.
XX
PN   WO200181405-A2.
XX
PD   01-NOV-2001.
XX
PF   19-APR-2001; 2001WO-US012836.
XX
PR   21-APR-2000; 2000US-00559001.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Egrie JC,  Elliott SG,  Browne JK,  Sitney KC;
XX
DR   WPI; 2002-034433/04.
XX
PT   Increasing and maintaining hematocrit in mammal suffering from anemia,
PT   comprising administering hyperglycosylated analog of erythropoietin less
PT   frequently and at lower molar amount of recombinant human erythropoietin.
XX
PS   Disclosure; Page 86-95; 95pp; English.
XX
CC   The invention relates to a method for increasing and maintaining
CC   haematocrit in a mammal. The method comprises administering a
CC   hyperglycosylated analogue of erythropoietin (Epo) in a pharmaceutical
CC   composition, less frequently than an equivalent molar amount of and at a
CC   lower molar amount than recombinant human Epo (rHuEpo) to obtain a
CC   comparable target haematocrit. Epo is a glycoprotein hormone necessary
CC   for the maturation of erythroid progenitor cells into erythrocytes. Human
CC   Epo analogue is useful for raising and maintaining haematocrit to a
CC   comparable target haematocrit in a mammal suffering from anaemia
CC   associated with a decline or loss of kidney function, myelosuppressive
CC   therapy comprising chemotherapeutic or anti-viral drugs or associated
CC   with excessive blood loss during surgical procedures, and in cancer
CC   condition. The present sequence is human Epo related DNA. Note: The
CC   present sequence is designated SEQ ID NO:26 in the sequence listing, but
CC   does not correspond to the sequence designated SEQ ID NO: 26 in the
CC   figure of the specification (AAE15348). The present sequence is not
CC   further referred to in the specification, and has been represented in a
CC   protein format in the sequence listing
XX
SQ   Sequence 2572 BP; 529 A; 757 C; 757 G; 529 T; 0 U; 0 Other;

  Query Match             5.5%;  Score 63.2;  DB 6;  Length 2572;
  Best Local Similarity   89.5%;  Pred. No. 3.7e-07;
  Matches   68;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy        431 TCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGT 490
              ||| |  |   | || ||||||||||||||||||||||||||||||||||||||||||||
Db       2085 TCGCCGTGGAGTGGGACCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGT 2144

Qy        491 AGCGGCACCTCACCCT 506
              ||||||||||||||||
Db       2145 AGCGGCACCTCACCCT 2160


RESULT 6
ADH54467
ID   ADH54467 standard; DNA; 2287 BP.
XX
AC   ADH54467;
XX
DT   25-MAR-2004  (first entry)
XX
DE   Human immunoglobulin IgG1gene.
XX
KW   Human; gene; ds; ELAM-1 protein; sialyl-Lex determinant; immune reaction;
KW   inflammation; sepsis; organ damage; leukocyte extravasation;
KW   adult respiratory distress syndrome; glomerular nephritis;
KW   rheumatoid arthritis; gene therapy; antibody-based therapy; heart attack;
KW   septic shock; septicaemia; rheumatoid arthritis; psoriasis;
KW   immunoglobulin; IgG1.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .2270
FT                   /*tag=  b
FT                   /product= "IgG1 protein"
FT                   /transl_except= (pos:1360. .1362, aa:Glu)
FT                   /transl_except= (pos:1363. .1365, aa:Pro)
FT                   /transl_except= (pos:1366. .1368, aa:Lys)
FT                   /transl_except= (pos:1369. .1371, aa:Ser)
FT                   /transl_except= (pos:1372. .1374, aa:Cys)
FT                   /transl_except= (pos:1375. .1377, aa:Asp)
FT                   /transl_except= (pos:1378. .1380, aa:Lys)
```

```
FT                   /transl_except= (pos:1381. .1383, aa:Thr)
FT                   /transl_except= (pos:1384. .1386, aa:His)
FT                   /transl_except= (pos:1387. .1389, aa:Thr)
FT                   /transl_except= (pos:1390. .1392, aa:Cys)
FT                   /transl_except= (pos:1396. .1398, aa:Pro)
FT                   /transl_except= (pos:1399. .1401, aa:Cys)
FT                   /transl_except= (pos:1560. .1562, aa:Phe)
FT                   /transl_except= (pos:1563. .1565, aa:Pro)
FT                   /transl_except= (pos:1566. .1568, aa:Pro)
FT                   /transl_except= (pos:1569. .1571, aa:Lys)
FT                   /transl_except= (pos:1572. .1574, aa:Pro)
FT                   /transl_except= (pos:1575. .1577, aa:Lys)
FT                   /transl_except= (pos:1578. .1580, aa:Asp)
FT                   /transl_except= (pos:1581. .1583, aa:Thr)
FT                   /transl_except= (pos:1584. .1586, aa:Lys)
FT                   /transl_except= (pos:1587. .1589, aa:Met)
FT                   /transl_except= (pos:1590. .1592, aa:Ile)
FT                   /transl_except= (pos:1593. .1595, aa:Ser)
FT                   /transl_except= (pos:1596. .1598, aa:Arg)
FT                   /transl_except= (pos:1599. .1601, aa:Thr)
FT                   /transl_except= (pos:1602. .1604, aa:Pro)
FT                   /transl_except= (pos:1605. .1607, aa:Glu)
FT                   /transl_except= (pos:1608. .1610, aa:Val)
FT                   /transl_except= (pos:1611. .1613, aa:Thr)
FT                   /transl_except= (pos:1614. .1616, aa:Cys)
FT                   /transl_except= (pos:1617. .1619, aa:Val)
FT                   /transl_except= (pos:1620. .1622, aa:Val)
FT   exon            1. .300
FT                   /*tag= a
FT   intron          301. .360
FT                   /*tag= c
FT   exon            361. .453
FT                   /*tag= d
FT   intron          454. .678
FT                   /*tag= e
FT   exon            679. .903
FT                   /*tag= f
FT   intron          904. .960
FT                   /*tag= g
FT   exon            961. .972
FT                   /*tag= h
FT   intron          973. .1359
FT                   /*tag= i
FT   exon            1360. .1404
FT                   /*tag= j
FT   intron          1405. .1523
FT                   /*tag= k
FT   exon            1524. .1853
FT                   /*tag= l
FT   intron          1854. .1949
FT                   /*tag= m
FT   exon            1950. .2270
FT                   /*tag= n
XX
PN   US6613746-B1.
XX
PD   02-SEP-2003.
XX
PF   07-JUN-1995;   95US-00472888.
XX
PR   23-NOV-1990;   90US-00618314.
XX
PA   (GEHO ) GEN HOSPITAL CORP.
XX
PI   Seed B,  Walz G;
XX
DR   WPI; 2003-895370/82.
DR   P-PSDB; ADH54473.
XX
PT   Inhibiting the binding of a cell bearing ELAM-1 protein to a cell bearing
PT   sialyl-Lex determinant, useful in treating inflammation, comprises
PT   contacting the ELAM-1 bearing cell with alpha 1-acid glycoprotein-
PT   antibody fusion protein.
XX
PS   Disclosure; SEQ ID NO 1; 40pp; English.
XX
CC   The invention relates to a method for inhibiting the binding of a cell
CC   bearing an ELAM-1 protein to a molecule or cell bearing a sialyl-Lex
CC   determinant. The method comprising contacting the ELAM-1 bearing cell
CC   with an alpha1 -acid glycoprotein (AGP)-antibody fusion protein bearing
CC   the sialyl-Lex determinant, where the inhibition of an ELAM-1-sialyl-Lex-
CC   based interaction treats an adverse immune reaction. The invention is
CC   useful in reducing inflammation in a human patient and protecting a
CC   mammal against any adverse immune reaction (including sepsis, organ
CC   damage attributable to inappropriate leukocyte extravasation, adult
CC   respiratory distress syndrome, glomerular nephritis or rheumatoid
CC   arthritis). The invention is useful in gene therapy. The method, as well
CC   as the AGP-antibody fusion protein, are useful in any antibody-based
CC   therapy, for e.g. to reduce inflammation or to treat heart attack, septic
CC   shock, septicaemia, rheumatoid arthritis or psoriasis. The present
CC   sequence is human immunoglobulin IgG1 gene.
XX
SQ   Sequence 2287 BP; 478 A; 739 C; 667 G; 403 T; 0 U; 0 Other;

  Query Match             5.2%;  Score 60;  DB 10;  Length 2287;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-06;
  Matches   60;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         89 AGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGCACC 148
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 AGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGCACC 1620


RESULT 7
AAL51057
ID   AAL51057 standard; DNA; 138 BP.
XX
AC   AAL51057;
XX
DT   20-FEB-2003  (first entry)
XX
DE   Cyclic single-strand anti-tumour antibody-related coding sequence #6.
XX
KW   Cyclic single-strand anti-tumour antibody; anti-tumour Fab; ds;
KW   anti-human Cd3 Fab; anti-human CD28 Fab; immunotherapy; tumour;
KW   ovarian cancer.
XX
OS   Unidentified.
XX
PN   WO200283738-A1.
XX
PD   24-OCT-2002.
XX
PF   10-APR-2002; 2002WO-CN000252.
XX
PR   11-APR-2001; 2001CN-00110554.
XX
PA   (GENE-) INST GENETICS CAS.
PA   (BEIJ-) BEIJING ABT GENETIC ENG TECHNOLOGY CO LT.
XX
PI   Huang H,  Cheng J,  Wang X,  Song L,  Zhang Z,  Lin Q,  Gu Y;
XX
DR   WPI; 2003-075525/07.
DR   P-PSDB; AAO16031.
XX
PT   Cyclic single-strand tri-specific antibody made from antitumor Fab,
PT   single-strand antibody and modified anti-human CD3 or CD28 Fab,
PT   applicable in early-stage diagnosis, and prevention or treatment of
PT   tumors e.g. ovarian cancer.
XX
PS   Disclosure; Fig 4A; 49pp; Chinese.
XX
CC   The invention comprises a cyclic single-strand anti-tumour antibody, the
CC   antibody of the invention is obtained by combining anti-tumour Fab and
CC   modified anti-human Cd3 or CD28 Fab. The antibody is useful in the
CC   immunotherapy of tumours - particularly ovarian cancer, including the
```

```
CC   sensitive early-stage diagnosis and post-operative eradication of
CC   disease. The present DNA sequence encodes a peptide which was used in the
CC   invention
XX
SQ   Sequence 138 BP; 35 A; 37 C; 39 G; 27 T; 0 U; 0 Other;

  Query Match             4.7%;  Score 53.6;  DB 8;  Length 138;
  Best Local Similarity   93.3%;  Pred. No. 5.7e-05;
  Matches   56;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        250 TTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCG 309
              ||||||||||||||| || || ||||||||||||||| |||||||||||||||||||||||
Db         61 TTGTCGTGCATGGCCCAACATTCGCAGGAGTGGCATGACGTGGTCCTGACCGACTTACCG 120


RESULT 8
ADA71938
ID   ADA71938 standard; DNA; 2000 BP.
XX
AC   ADA71938;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Rice gene, SEQ ID 5263.
XX
KW   Plant; bacterial infection; fungal infection; viral infection; rice;
KW   gene; ds.
XX
OS   Oryza sativa.
XX
PN   WO2003000898-A1.
XX
PD   03-JAN-2003.
XX
PF   22-JUN-2001; 2001WO-IB001105.
XX
PR   22-JUN-2001; 2001WO-IB001105.
XX
PA   (SYGN ) SYNGENTA PARTICIPATIONS AG.
XX
PI   Chang H,  Chen W,  Cooper B,  Glazebrook J,  Goff SA,  Hou Y;
PI   Katagiri F,  Quan S,  Tao Y,  Whitham S,  Xie Z,  Zhu T,  Zou G;
XX
DR   WPI; 2003-175290/17.
XX
PT   Identifying at least one gene involved in plant resistance or response to
PT   pathogenic infection for conferring resistance or tolerance to a plant to
PT   bacterial, fungal or viral infection by determining or detecting plant
PT   gene expression.
XX
PS   Claim 27; SEQ ID NO 5263; 899pp; English.
XX
CC   The present invention relates to a method (M1) for identifying genes
CC   involved in plant resistance or response to pathogenic infection. M1
CC   comprises identifying a gene whose expression is significantly altered in
CC   the incompatible interaction of plant gene expression relative to
CC   expression of the gene in an uninfected plant, in a mutant plant that
CC   does not express a gene associated with response to pathogenic infection,
CC   or in a corresponding incompatible or compatible interaction. (M1) is
CC   useful for conferring resistance to resistance or tolerance to a plant to
CC   bacterial, fungal or viral infection. The present sequence was used to
CC   illustrate the invention.
XX
SQ   Sequence 2000 BP; 336 A; 265 C; 284 G; 363 T; 0 U; 752 Other;

  Query Match             4.2%;  Score 47.8;  DB 8;  Length 2000;
  Best Local Similarity   9.8%;  Pred. No. 0.008;
  Matches   74;  Conservative  329;  Mismatches  351;  Indels    3;  Gaps    1;

Qy         10 GGGTTTAGAACACTGTTTTGAGTGTGTACGGGTGGCACGGGTCGTGGACTTGAGGACCCC 69
              ::::: |: |:  || :: : ::: : : :: ::: : :|:  :  :::  :: |::  |
Db         63 KSKWYSASSASGRTGSKWSSGSYSGKGMKKRYKRSKRWRGRGRRGMRRSRMRWMGRYRRC 122

Qy         70 CCTGGCAGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGG 129
              |::|| : :::|| :::: :  :  |: :  :::||::|: | :||:||: :::
Db        123 ARSGRMAGGSGRMMGGKSRMSYWMWCYARGCGSCKRKKSKGGSWGKTCRRGARGGSGWSS 182

Qy        130 GGACTCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTG 189
              | ::: : :  : | ::  :  : : ||: :: | ::: :::|:  ::|  |
Db        183 GAKYKSGSMSKRMWMSSCGRSGCGRRSAYSRYYGTSRKYGTYKKMTYYSASRCMRAYMTT 242

Qy        190 ACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATG 249
              :::  : : :  :: :::   ::::: :  :  ::   :::  |  : :::::::|
Db        243 SYSWACSSYTWCRSKRRSMMWKMMRKMRWSRSYGWYSWSYKMWMCTAYKKSYYSRWCYMY 302

Qy        250 TTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCG 309
              |  :   :: |  ::: :  :     :  |    ::  : | :: : :|::::  ::
Db        303 RGGGWRGATRYWGRGYMSRMAMMYKKMYWYRGYKGMKRGWWAGRMMMRSMCRWSKACYYM 362

Qy        310 TTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAG 369
              : :: :|:   : :: :  ::::: ::   ::: ::    :: :  :   : :  :  :
Db        363 RWRMWRMTRRRRWAKKSSRTSRRKKRKWCMRKRKYKRMRGYSRMRSCKRARWMKRCRSGR 422

Qy        370 AGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTA 429
              | :   |  | : ::  :    :    ::  :::   ::   ::   :|:  :
Db        423 AWKMGCRGCMTCRMKSYGMMRWKSWKRMASKYKWMSRMYRWRKKKCSRTTMWGKTRGGMM 482

Qy        430 CTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTG 489
              |:|:|  :: :  :::| ::  |:::  :: :  ::|::|  : |:: :  :   :
Db        483 GTMGRCRYKKRSGMKRKCRRRRWGRMYRMRWKRYYMSARYTMRYCARKKYSYSAARKARC 542

Qy        490 TAGCGGCACCTCACCCT---CTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGA 546
              : : :|:    :::  :   : ::  : : :::::|::: :  : |   :: :: | :
Db        543 WYRGKGYYWAGMWMKRYKRMYMYKMMWWYKRKYSKCSWYCKMSYYASCMKSARKAGAKMC 602

Qy        547 GGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCG 606
              ::: :: ::   ::: :    |::: :| : | : |  :     ::::: |:::::  ::
Db        603 KRSKMSAWSKSMRSSRKCRKCASKRSSAKRYAMMGGMTSGSRMSRWKSYTCYWRKWGSMK 662

Qy        607 TCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTG 666
              |  : ::::: : ::|:  : : : :|     :::     :  : |   :       ||
Db        663 STCTWMYYMSKYTYAKYGSYWRYRYRAWCMYMWRWYYYRYRSYMTYMAWYTSSTRMAMTG 722

Qy        667 ATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCATTTCATGGCTAGGTCTTTCAAGTCCTG 726
              ::  |  :  :::: : ::: : ::   :   |:|: :::::  :    ::    : :|
Db        723 MKYSGRYWTSWYKYCKCSWKYRSMWYYWSWWWAKTWKMWRRYATRMMWMWYRYSMKWYTW 782

Qy        727 CTGTGGTTTTGGAATTAATTTTGCTAGCAATGCGCAT 763
              || :| :::: :   :::: :::||  :: ::  ::|
Db        783 CTMWGYWWYWWRTYMKMRYMWYKCTKTYWYWSATYWT 819


RESULT 9
ABL25527
ID   ABL25527 standard; DNA; 1464 BP.
XX
AC   ABL25527;
XX
DT   26-MAR-2002  (first entry)
XX
DE   Drosophila melanogaster genomic polynucleotide SEQ ID NO 28054.
XX
KW   Drosophila; developmental biology; cell signalling; insecticide;
KW   pharmaceutical; gene; ds.
XX
OS   Drosophila melanogaster.
XX
PN   WO200171042-A2.
XX
PD   27-SEP-2001.
XX
PF   23-MAR-2001; 2001WO-US009231.
XX
PR   23-MAR-2000; 2000US-0191637P.
PR   11-JUL-2000; 2000US-00614150.
XX
```

PA (PEKE) PE CORP NY.
XX
PI Venter JC, Adams M, Li PWD, Myers EW;
XX
DR WPI; 2001-656860/75.
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signaling and cell-cell
PT interactions.
XX
PS Claim 1; SEQ ID NO 28054; 21pp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
CC ABB72072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1464 BP; 332 A; 427 C; 345 G; 360 T; 0 U; 0 Other;

Query Match 4.1%; Score 47.4; DB 4; Length 1464;
Best Local Similarity 51.2%; Pred. No. 0.0091;
Matches 111; Conservative 0; Mismatches 106; Indels 0; Gaps 0;

```
Qy        144 GCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCC 203
              | | | ||| ||||        ||   ||   |||||| ||  | ||  | ||   || |
Db        433 GTATCTCCAGCTGCTGCTCCGGCCAATGTTGCTCCAGCTCCTGCTGCTCCTGTTGCTCCG 492

Qy        204 GCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATGGC 263
              ||  | |||  |     | ||  ||  |        ||  ||   | |  ||| || | || |
Db        493 GCTGCCCCAGCTGCCCCTGTGGTGCCTGTCGCTCCAGCTGCCCCTTCTGTTGTTCCTGTC 552

Qy        264 ACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATGTTCAC 323
                | || |||||    || |  |  | |  | ||| ||   |   ||| | || || ||
Db        553 GCTCCTGTCGCCCCTGTAGTGGTTCATCCTGCTGCCCCCATACTCGTCCATCCTGCTCCA 612

Qy        324 GTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTC 360
              ||||||| ||  | | | |    | |   | | ||||
Db        613 GTTCCAGTGGCAGCTCCAGCTCCGGCCCCGATTGCTC 649
```

RESULT 10
ABL25526/c
ID ABL25526 standard; DNA; 4526 BP.
XX
AC ABL25526;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 28051.
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical; gene; ds.
XX
OS Drosophila melanogaster.
XX
PN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-US009231.
XX
PR 23-MAR-2000; 2000US-0191637P.
PR 11-JUL-2000; 2000US-00614150.
XX
PA (PEKE) PE CORP NY.
XX
PI Venter JC, Adams M, Li PWD, Myers EW;
XX
DR WPI; 2001-656860/75.
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signaling and cell-cell
PT interactions.
XX
PS Claim 1; SEQ ID NO 28051; 21pp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
CC ABB72072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 4526 BP; 1338 A; 912 C; 1011 G; 1265 T; 0 U; 0 Other;

Query Match 4.1%; Score 47.4; DB 4; Length 4526;
Best Local Similarity 51.2%; Pred. No. 0.015;
Matches 111; Conservative 0; Mismatches 106; Indels 0; Gaps 0;

```
Qy        144 GCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCC 203
              | | | ||| ||||        ||   ||   |||||| ||  | ||  | ||   || |
Db       2838 GTATCTCCAGCTGCTGCTCCGGCCAATGTTGCTCCAGCTCCTGCTGCTCCTGTTGCTCCG 2779

Qy        204 GCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATGGC 263
              ||  | |||  |     | ||  ||  |        ||  ||   | |  ||| || | || |
Db       2778 GCTGCCCCAGCTGCCCCTGTGGTGCCTGTCGCTCCAGCTGCCCCTTCTGTTGTTCCTGTC 2719

Qy        264 ACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATGTTCAC 323
                | || |||||    || |  |  | |  | ||| ||   |   ||| | || || ||
Db       2718 GCTCCTGTCGCCCCTGTAGTGGTTCATCCTGCTGCCCCCATACTCGTCCATCCTGCTCCA 2659

Qy        324 GTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTC 360
              ||||||| ||  | | | |    | |   | | ||||
Db       2658 GTTCCAGTGGCAGCTCCAGCTCCGGCCCCGATTGCTC 2622
```

RESULT 11
ADA71938/c
ID ADA71938 standard; DNA; 2000 BP.
XX
AC ADA71938;
XX
DT 20-NOV-2003 (first entry)
XX
DE Rice gene, SEQ ID 5263.
XX
KW Plant; bacterial infection; fungal infection; viral infection; rice;
KW gene; ds.
XX
OS Oryza sativa.
XX
PN WO2003000898-A1.
XX
PD 03-JAN-2003.
XX
PF 22-JUN-2001; 2001WO-IB001105.
XX
PR 22-JUN-2001; 2001WO-IB001105.
XX
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
XX
PI Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;
PI Katagiri F, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;
XX
DR WPI; 2003-175290/17.
XX

PT Identifying at least one gene involved in plant resistance or response to
PT pathogenic infection for conferring resistance or tolerance to a plant to
PT bacterial, fungal or viral infection by determining or detecting plant
PT gene expression.
XX
PS Claim 27; SEQ ID NO 5263; 899pp; English.
XX
CC The present invention relates to a method (M1) for identifying genes
CC involved in plant resistance or response to pathogenic infection. M1
CC comprises identifying a gene whose expression is significantly altered in
CC the incompatible interaction of plant gene expression relative to
CC expression of the gene in an uninfected plant, in a mutant plant that
CC does not express a gene associated with response to pathogenic infection,
CC or in a corresponding incompatible or compatible interaction. (M1) is
CC useful for conferring resistance to resistance or tolerance to a plant to
CC bacterial, fungal or viral infection. The present sequence was used to
CC illustrate the invention.
XX
SQ Sequence 2000 BP; 336 A; 265 C; 284 G; 363 T; 0 U; 752 Other;

Query Match 4.1%; Score 47; DB 8; Length 2000;
Best Local Similarity 8.9%; Pred. No. 0.014;
Matches 78; Conservative 392; Mismatches 397; Indels 8; Gaps 2;

Qy 193 ATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTG 252
Db 879 MTKWAWTWMTCMCMAKWYMATGWATWMWWRYTMYTYCYAMTCAKCKYKMAMTKWWTTWAC 820

Qy 253 TCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTC 312
Db 819 AWRATSWRWRAMAGMRWKRYKMKRAYWWRWWRCWKAGWARWMKSRYRWKWKKYATRYYWK 760

Qy 313 CTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTT--TGGTAGA 370
Db 759 MWAMTWWWSWRRWKSYRMWSGMGRMRWSAWRYCSRMKCAKTKYASSARWTKRAKRSYRYR 700

Qy 371 GGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTAC 430
Db 699 RRWYWKRKGWTYRYRYWRSCRMTRARMSKRRKWAGASMKSCWMYWRGARSMWYSKYSCSA 640

Qy 431 TCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGT 490
Db 639 KCCKKTRYMTSSYMSTGMYGMYSSYKSMSWTSKMSYMGKMTCTMYTSMKGSTRRSKMGRW 580

Qy 491 AGCGGC------ACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCG 544
Db 579 SGMSRMYMRWWKKMRKRKYMRYMKWKCTWRRCMCYRWGYTMYTTSRSRMMYTGRYKARYT 520

Qy 545 GAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCT 604
Db 519 SKRRYMWYKYRKYCWYYYYGMYMKCSYMMRYGYCKACKKCCYAMCWKAAYSGMMMYWYRK 460

Qy 605 CGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGG 664
Db 459 YSKWMRMSTKYMWSMWYKKCRSMKYGAKGCYGCKMWTYCSYGYMKWYTYMGSYKYSRCYK 400

Qy 665 TGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCATTTCATGGCTAGGTCTTTCAAGTCC 724
Db 399 YMRMYMYKGWMYMMYYSAYSSMMTWYYYYAKYWKYWYKRRGTMSWYGKSYKKKYCTWWCY 340

Qy 725 TGCTGTGGTTTTGGAATTAATTTTGCTAGCAATGCGCATAGTTGCTGTAGTCAGTGTGGG 784
Db 339 MKCMRCYRWRKMMRKKTKYSKRCYCWRYATCYWCCCYRKRGWYSRRSMMRTAGKWKMRSW 280

Qy 785 TCAGCCACTCGAGATTTGTCTTTCAATGTCCGGACCTGAAGTAGGGCCCAGACGTGGGCT 844
Db 279 SRWCRSYSWYKMYKKMWKKSYYMSYGWARSSGTWSRSAAKRTYKGYSTSRRAKMMRACRM 220

Qy 845 AGGACTGGAACAGGTTTTACCTGGTCTGGGACCGACATATGGTCGTCTAGAATTGGAGGT 904
Db 219 YSACRRYSRTSYYCGCSYCGSSKWKYMSKSCSMRMTCSSWCSCCYTCYYGAMCWSCCMSM 160

Qy 905 ACGGCAGGGCATTGCAATAGGTCTAGAGATTGCTGGAGCTCTTGGAAGCGCTGGACGACG 964

Db 159 MYMGSCGCYTRGWKWRSKYSMCCKKYCSCCTKYCSYTGYYRYCKWYKYSYYKCYYCYCYW 100

Qy 965 TGCACGACCGTAAGAGGTTTAGGACGGTGGACGGTACCCGAAGTCCAGAACTCTGAGACC 1024
Db 99 YMSYMRYMMKCMCSRSCSSWMSCAYCSTSSTSRWMSMYYAAKMGMCGSSGMYRMSKSCKM 40

Qy 1025 TGAGAGACCCGCCCCAGGACCTTCGTAGGCCAATG 1059
Db 39 YSKYSSCKYTGSKKCTKRKYYYCYWSSGYSMWCTS 5

RESULT 12
ABD09099
ID ABD09099 standard; DNA; 1161 BP.
XX
AC ABD09099;
XX
DT 29-JUL-2004 (first entry)
XX
DE Pseudomonas aeruginosa polynucleotide #7703.
XX
KW Bacterial infection; gene; ds; Pseudomonas aeruginosa infection;
KW antibacterial.
XX
OS Pseudomonas aeruginosa.
XX
PN US6551795-B1.
XX
PD 22-APR-2003.
XX
PF 18-FEB-1999; 99US-00252991.
XX
PR 18-FEB-1998; 98US-0074788P.
PR 27-JUL-1998; 98US-0094190P.
XX
PA (GENO-) GENOME THERAPEUTICS CORP.
XX
PI Rubenfield MJ, Nolling J, Deloughery C, Bush D;
XX
DR WPI; 2003-615309/58.
DR P-PSDB; ABO75528.
XX
PT Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,
PT useful as molecular targets for diagnostics, prophylaxis and treatment of
PT pathological conditions resulting from bacterial infection.
XX
PS Disclosure; SEQ ID NO 7703; 455pp; English.
XX
CC The invention relates to Pseudomonas aeruginosa polypeptides and the
CC polynucleotides encoding them. The sequences are useful in diagnosis and
CC therapy of pathological conditions, as molecular targets for diagnostics,
CC prophylaxis and treatment of pathological conditions resulting from a
CC bacterial infection, for evaluating a compound, such as a polypeptide,
CC for the ability to bind a P. aeruginosa nucleic acid, as components of
CC effective antibacterial targets, as targets for antibacterial drugs,
CC including anti-P. aeruginosa drugs, as templates for recombinant
CC production of P. aeruginosa-derived peptides or polypeptides, as target
CC components for diagnosis and/or treatment of P. aeruginosa-caused
CC infection, and in detection of P. aeruginosa sequences or other sequences
CC of Pseudomonas species using biochip technology. Sequences ABD01397-
CC ABD17967 represent P. aeruginosa polynucleotides of the invention. Note:
CC The sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format from USPTO at
CC seqdata.uspto.gov/sequence.html
XX
SQ Sequence 1161 BP; 156 A; 367 C; 390 G; 248 T; 0 U; 0 Other;

Query Match 3.8%; Score 43.6; DB 11; Length 1161;
Best Local Similarity 47.4%; Pred. No. 0.1;
Matches 130; Conservative 0; Mismatches 144; Indels 0; Gaps 0;

Qy 134 TCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCA 193

```
Db        332 TCCAGCCTTCGGAGATCGCCAAGGTCTGCGTGGTGATCTTCATGGCCGGCTACCTGATCC 391

Qy        194 TGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGT 253

Db        392 GCCGCCAGCAGGAGGTCCGGGAAAGCTGGATGGGCTTCTTCAAGCCCTTCGTGGTGTTGC 451

Qy        254 CGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCC 313

Db        452 TGCCGATGGCCGGCCTGCTGCTGCGCGAGCCGGACTTCGGCGCCACCGTGGTAATGATGG 511

Qy        314 TCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGT 373

Db        512 GCGCTGCCGCGGCCATGCTGTTCCTCGGCGGGGTGGGGCTGTTCCGCTTCGGCCTGATGG 571

Qy        374 TTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACAT 407

Db        572 TGCTGCTGGCGGTCGGCGCGGTGGTCCTGCTGAT 605
```

RESULT 13
AAS51550
ID AAS51550 standard; DNA; 1200 BP.
XX
AC AAS51550;
XX
DT 13-FEB-2002 (first entry)
XX
DE Pseudomonas aeruginosa DNA for cellular proliferation protein #135.
XX
KW Antisense; ds; prokaryotic cellular proliferation gene; antibiotic;
KW antibacterial; drug design.
XX
OS Pseudomonas aeruginosa.
XX
PN WO200170955-A2.
XX
PD 27-SEP-2001.
XX
PF 21-MAR-2001; 2001WO-US009180.
XX
PR 21-MAR-2000; 2000US-0191078P.
PR 23-MAY-2000; 2000US-0206848P.
PR 26-MAY-2000; 2000US-0207727P.
PR 23-OCT-2000; 2000US-0242578P.
PR 27-NOV-2000; 2000US-0253625P.
PR 22-DEC-2000; 2000US-0257931P.
PR 16-FEB-2001; 2001US-0269308P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
PI Yamamoto RT, Xu HH;
XX
DR WPI; 2001-611495/70.
DR P-PSDB; AAU33691.
XX
PT New polynucleotides for the identification and development of
PT antibiotics, comprise sequences of antisense nucleic acids.
XX
PS Claim 27; SEQ ID NO 4132; 511pp; English.
XX
CC The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the genes,
CC their use in the discovery of novel antibiotics, the essential genes
CC themselves and the encoded proteins. The prokaryotes used are Escherichia
CC coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,
CC Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also
CC useful for the identification of potential new targets for antibiotic
CC development. The antisense nucleic acids can also be used to identify
CC proteins used in proliferation, to express these proteins, and to obtain
CC antibodies capable of binding to the expressed proteins. The proteins can
CC be used to screen compounds in rational drug discovery programmes. The
CC antisense nucleic acid sequence is also useful to screen for homologous
CC nucleic acids which are required for cell proliferation in a wide variety
CC of organisms. The present sequence encodes an essential prokaryotic
CC cellular proliferation protein. Note: The sequence data for this patent
CC did not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1200 BP; 157 A; 384 C; 402 G; 257 T; 0 U; 0 Other;

```
  Query Match             3.8%;  Score 43.6;  DB 4;  Length 1200;
  Best Local Similarity   47.4%;  Pred. No. 0.1;
  Matches  130;  Conservative    0;  Mismatches  144;  Indels    0;  Gaps    0;

Qy        134 TCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCA 193

Db        371 TCCAGCCTTCGGAGATCGCCAAGGTCTGCGTGGTGATCTTCATGGCCGGCTACCTGATCC 430

Qy        194 TGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGT 253

Db        431 GCCGCCAGCAGGAGGTCCGGGAAAGCTGGATGGGCTTCTTCAAGCCCTTCGTGGTGTTGC 490

Qy        254 CGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCC 313

Db        491 TGCCGATGGCCGGCCTGCTGCTGCGCGAGCCGGACTTCGGCGCCACCGTGGTAATGATGG 550

Qy        314 TCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGT 373

Db        551 GCGCTGCCGCGGCCATGCTGTTCCTCGGCGGGGTGGGGCTGTTCCGCTTCGGCCTGATGG 610

Qy        374 TTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACAT 407

Db        611 TGCTGCTGGCGGTCGGCGCGGTGGTCCTGCTGAT 644
```

RESULT 14
ACA19541
ID ACA19541 standard; DNA; 1200 BP.
XX
AC ACA19541;
XX
DT 19-JUN-2003 (first entry)
XX
DE Prokaryotic essential gene #1198.
XX
KW Antisense; ds; prokaryotic essential gene; cell proliferation;
KW drug design; gene.
XX
OS Pseudomonas aeruginosa.
XX
PN WO200277183-A2.
XX
PD 03-OCT-2002.
XX
PF 21-MAR-2002; 2002WO-US009107.
XX
PR 21-MAR-2001; 2001US-00815242.
PR 06-SEP-2001; 2001US-00948993.
PR 25-OCT-2001; 2001US-0342923P.
PR 08-FEB-2002; 2002US-00072851.
PR 06-MAR-2002; 2002US-0362699P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX
DR WPI; 2003-029926/02.
DR P-PSDB; ABU15671.
XX
PT New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.

```
XX
PS   Claim 14; SEQ ID NO 7411; 1766pp; English.
XX
CC   The invention relates to an isolated nucleic acid comprising any one of
CC   the 6213 antisense sequences given in the specification where expression
CC   of the nucleic acid inhibits proliferation of a cell. Also included are:
CC   (1) a vector comprising a promoter operably linked to the nucleic acid
CC   encoding a polypeptide whose expression is inhibited by the antisense
CC   nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC   polypeptide or its fragment whose expression is inhibited by the
CC   antisense nucleic acid; (4) an antibody capable of specifically binding
CC   the polypeptide;(5) producing the polypeptide; (6) inhibiting cellular
CC   proliferation or the activity of a gene in an operon required for
CC   proliferation; (7) identifying a compound that influences the activity of
CC   the gene product or that has an activity against a biological pathway
CC   required for proliferation, or that inhibits cellular proliferation; (8)
CC   identifying a gene required for cellular proliferation or the biological
CC   pathway in which a proliferation-required gene or its gene product lies
CC   or a gene on which the test compound that inhibits proliferation of an
CC   organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC   compound's activity; (11) a culture comprising strains in which the gene
CC   product is overexpressed or underexpressed; (12) determining the extent
CC   to which each of the strains is present in a culture or collection of
CC   strains; or (13) identifying the target of a compound that inhibits the
CC   proliferation of an organism. The antisense nucleic acids are useful for
CC   identifying proteins or screening for homologous nucleic acids required
CC   for cellular proliferation to isolate candidate molecules for rational
CC   drug discovery programs, or for screening homologous nucleic acids
CC   required for proliferation in cells other than S. aureus, S. typhimurium,
CC   K. pneumoniae or P. aeruginosa. The present sequence is one of the target
CC   prokaryotic essential genes. Note: The sequence data for this patent did
CC   not form part of the printed specification, but was obtained in
CC   electronic format directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 1200 BP; 157 A; 384 C; 402 G; 257 T; 0 U; 0 Other;

  Query Match             3.8%;  Score 43.6;  DB 8;  Length 1200;
  Best Local Similarity   47.4%;  Pred. No. 0.1;
  Matches  130;  Conservative    0;  Mismatches  144;  Indels    0;  Gaps    0;

Qy        134 TCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCA 193
              ||||| | || |   | | | || ||| |  |      |       | | |||| |
Db        371 TCCAGCCTTCGGAGATCGCCAAGGTCTGCGTGGTGATCTTCATGGCCGGCTACCTGATCC 430

Qy        194 TGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGT 253
              | || || | |  ||| | |    || | | ||| |   | | |||| |||||
Db        431 GCCGCCAGCAGGAGGTCCGGGAAAGCTGGATGGGCTTCTTCAAGCCCTTCGTGGTGTTGC 490

Qy        254 CGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCC 313
              |   |||||   || |  || |     || |||| | | |   ||||  ||  | |
Db        491 TGCCGATGGCCGGCCTGCTGCTGCGCGAGCCGGACTTCGGCGCCACCGTGGTAATGATGG 550

Qy        314 TCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGT 373
              |     | ||  |  |  ||| |  | | ||  ||  ||  | |||  |   || |
Db        551 GCGCTGCCGCGGCCATGCTGTTCCTCGGCGGGGTGGGGCTGTTCCGCTTCGGCCTGATGG 610

Qy        374 TTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACAT 407
              | | | |  | ||||| ||  | |   | |  ||
Db        611 TGCTGCTGGCGGTCGGCGCGGTGGTCCTGCTGAT 644


RESULT 15
ABD09256/c
ID   ABD09256 standard; DNA; 1287 BP.
XX
AC   ABD09256;
XX
DT   29-JUL-2004  (first entry)
XX
DE   Pseudomonas aeruginosa polynucleotide #7860.
XX
KW   Bacterial infection; gene; ds; Pseudomonas aeruginosa infection;
KW   antibacterial.
XX
OS   Pseudomonas aeruginosa.
XX
PN   US6551795-B1.
XX
PD   22-APR-2003.
XX
PF   18-FEB-1999;   99US-00252991.
XX
PR   18-FEB-1998;   98US-0074788P.
PR   27-JUL-1998;   98US-0094190P.
XX
PA   (GENO-) GENOME THERAPEUTICS CORP.
XX
PI   Rubenfield MJ,  Nolling J,  Deloughery C,  Bush D;
XX
DR   WPI; 2003-615309/58.
DR   P-PSDB; ABO75685.
XX
PT   Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,
PT   useful as molecular targets for diagnostics, prophylaxis and treatment of
PT   pathological conditions resulting from bacterial infection.
XX
PS   Disclosure; SEQ ID NO 7860; 455pp; English.
XX
CC   The invention relates to Pseudomonas aeruginosa polypeptides and the
CC   polynucleotides encoding them. The sequences are useful in diagnosis and
CC   therapy of pathological conditions, as molecular targets for diagnostics,
CC   prophylaxis and treatment of pathological conditions resulting from a
CC   bacterial infection, for evaluating a compound, such as a polypeptide,
CC   for the ability to bind a P. aeruginosa nucleic acid, as components of
CC   effective antibacterial targets, as targets for antibacterial drugs,
CC   including anti-P. aeruginosa drugs, as templates for recombinant
CC   production of P. aeruginosa-derived peptides or polypeptides, as target
CC   components for diagnosis and/or treatment of P. aeruginosa-caused
CC   infection, and in detection of P. aeruginosa sequences or other sequences
CC   of Pseudomonas species using biochip technology. Sequences ABD01397-
CC   ABD17967 represent P. aeruginosa polynucleotides of the invention. Note:
CC   The sequence data for this patent did not form part of the printed
CC   specification but was obtained in electronic format from USPTO at
CC   seqdata.uspto.gov/sequence.html
XX
SQ   Sequence 1287 BP; 276 A; 437 C; 408 G; 166 T; 0 U; 0 Other;

  Query Match             3.8%;  Score 43.6;  DB 11;  Length 1287;
  Best Local Similarity   47.4%;  Pred. No. 0.1;
  Matches  130;  Conservative    0;  Mismatches  144;  Indels    0;  Gaps    0;

Qy        134 TCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCA 193
              ||||| | || |   | | | || ||| |  |      |       | | |||| |
Db        908 TCCAGCCTTCGGAGATCGCCAAGGTCTGCGTGGTGATCTTCATGGCCGGCTACCTGATCC 849

Qy        194 TGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGT 253
              | || || | |  ||| | |    || | | ||| |   | | |||| |||||
Db        848 GCCGCCAGCAGGAGGTCCGGGAAAGCTGGATGGGCTTCTTCAAGCCCTTCGTGGTGTTGC 789

Qy        254 CGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCC 313
              |   |||||   || |  || |     || |||| | | |   ||||  ||  | |
Db        788 TGCCGATGGCCGGCCTGCTGCTGCGCGAGCCGGACTTCGGCGCCACCGTGGTAATGATGG 729

Qy        314 TCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGT 373
              |     | ||  |  |  ||| |  | | ||  ||  ||  | |||  |   || |
Db        728 GCGCTGCCGCGGCCATGCTGTTCCTCGGCGGGGTGGGGCTGTTCCGCTTCGGCCTGATGG 669

Qy        374 TTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACAT 407
              | | | |  | ||||| ||  | |   | |  ||
Db        668 TGCTGCTGGCGGTCGGCGCGGTGGTCCTGCTGAT 635


Search completed: October 17, 2004, 16:46:32
Job time : 601.515 secs
```

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 17, 2004, 15:27:13 ; Search time 586.198 Seconds
(without alignments)
10035.691 Million cell updates/sec

Title: US-10-679-999-8
Perfect score: 1150
Sequence: 1 GTATACCTTGGGTTTAGAAC.....AGGCCCAACAATTACCTAGG 1150

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3403857 seqs, 2557783690 residues

Total number of hits satisfying chosen parameters: 6807714

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
18: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
19: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
20: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1150	100.0	1150	16	US-10-679-999-8	Sequence 8, Appli
2	1134	98.6	1150	16	US-10-679-999-11	Sequence 11, Appl
3	1117.8	97.2	1135	16	US-10-679-999-14	Sequence 14, Appl
4	1105	96.1	1135	16	US-10-679-999-17	Sequence 17, Appl
5	680.6	59.2	780	17	US-10-666-480-62	Sequence 62, Appl
6	676.2	58.8	1142	15	US-10-157-408-9	Sequence 9, Appli
7	676.2	58.8	1142	15	US-10-097-044A-9	Sequence 9, Appli
8	676.2	58.8	1142	18	US-10-769-247-9	Sequence 9, Appli
9	674.4	58.6	777	17	US-10-666-480-122	Sequence 122, App
10	622.4	54.1	7033	17	US-10-630-406-4	Sequence 4, Appli
11	502.8	43.7	2366	9	US-09-229-200A-12	Sequence 12, Appl
12	440.8	38.3	454	9	US-09-366-133-5	Sequence 5, Appli
13	440.8	38.3	454	14	US-10-214-037-5	Sequence 5, Appli
14	440.8	38.3	454	16	US-10-679-999-5	Sequence 5, Appli
15	378.4	32.9	491	9	US-09-366-133-2	Sequence 2, Appli
16	378.4	32.9	491	14	US-10-214-037-2	Sequence 2, Appli
17	378.4	32.9	491	16	US-10-679-999-2	Sequence 2, Appli
c 18	71	6.2	23770	14	US-10-035-637-8	Sequence 8, Appli
c 19	44.6	3.9	1188	17	US-10-437-963-65538	Sequence 65538, A
20	43.6	3.8	1200	9	US-09-815-242-4132	Sequence 4132, Ap
21	43.6	3.8	1200	16	US-10-282-122A-7411	Sequence 7411, Ap
c 22	43.2	3.8	2034	17	US-10-441-949-56	Sequence 56, Appl
23	43	3.7	468	15	US-10-157-408-12	Sequence 12, Appl
24	43	3.7	468	15	US-10-097-044A-12	Sequence 12, Appl
25	43	3.7	468	18	US-10-769-247-12	Sequence 12, Appl
26	43	3.7	8874	17	US-10-630-406-7	Sequence 7, Appli
c 27	42.4	3.7	1116	15	US-10-156-761-6640	Sequence 6640, Ap
c 28	42.4	3.7	9025608	15	US-10-156-761-1	Sequence 1, Appli
c 29	42.2	3.7	2034	17	US-10-441-949-57	Sequence 57, Appl
c 30	41.8	3.6	1182	16	US-10-354-437-15	Sequence 15, Appl
c 31	41.8	3.6	3489	11	US-09-894-273-1	Sequence 1, Appli
c 32	41.8	3.6	3489	15	US-10-294-804-1	Sequence 1, Appli
33	41.8	3.6	34460	13	US-10-087-192-115	Sequence 115, App
c 34	41.8	3.6	135638	15	US-10-314-657-1	Sequence 1, Appli
c 35	41.6	3.6	1986	17	US-10-441-949-47	Sequence 47, Appl
c 36	41.6	3.6	1986	17	US-10-441-949-51	Sequence 51, Appl
c 37	41.6	3.6	2034	17	US-10-441-949-49	Sequence 49, Appl
c 38	41.6	3.6	2034	17	US-10-441-949-50	Sequence 50, Appl
39	41.6	3.6	2171	9	US-09-925-300-721	Sequence 721, App
40	41.6	3.6	2172	16	US-10-264-049-843	Sequence 843, App
41	41.6	3.6	2300	9	US-09-823-245A-506	Sequence 506, App
42	41.6	3.6	2300	9	US-09-822-830A-33	Sequence 33, Appl
c 43	41.2	3.6	1236	14	US-10-077-584-3	Sequence 3, Appli
c 44	40.4	3.5	486	15	US-10-465-217-13	Sequence 13, Appl
45	40.4	3.5	754	9	US-09-229-200A-13	Sequence 13, Appl

ALIGNMENTS

```
RESULT 1
US-10-679-999-8
; Sequence 8, Application US/10679999
; Publication No. US20040067520A1
;  GENERAL INFORMATION:
;       APPLICANT: Mann, Michael B.
;                  Hecht, Randy I.
;       TITLE OF INVENTION: OB FUSION PROTEIN COMPOSITIONS AND
;                           METHODS
;       NUMBER OF SEQUENCES: 18
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Amgen Inc.
;            STREET: 1840 DeHavilland Drive
;            CITY: Thousand Oaks
;            STATE: CA
;            COUNTRY: USA
;            ZIP: 91320-1789
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/679,999
;            FILING DATE: 06-Oct-2003
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/09/568,528
;            FILING DATE: 09-May-2000
;            APPLICATION NUMBER: 09/267,517
;            FILING DATE: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Knight, Matthew W.
;            REGISTRATION NUMBER: 36,846
;            REFERENCE/DOCKET NUMBER: A-416
;  INFORMATION FOR SEQ ID NO: 8:
```

```
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 1150 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: double
;            TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-679-999-8

  Query Match           100.0%;  Score 1150;  DB 16;  Length 1150;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1150;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GTATACCTTGGGTTTAGAACACTGTTTTGAGTGTGTACGGGTGGCACGGGTCGTGGACTT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GTATACCTTGGGTTTAGAACACTGTTTTGAGTGTGTACGGGTGGCACGGGTCGTGGACTT 60

Qy         61 GAGGACCCCCCTGGCAGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GAGGACCCCCCTGGCAGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAG 120

Qy        121 AGGGCCTGGGGACTCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AGGGCCTGGGGACTCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAG 180

Qy        181 TTCAAGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TTCAAGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTC 240

Qy        241 CTCGTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTCGTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACC 300

Qy        301 GACTTACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GACTTACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTC 360

Qy        361 TTTTGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TTTTGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGT 420

Qy        421 AGGGCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AGGGCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATA 480

Qy        481 GGGTCGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGGTCGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGG 540

Qy        541 TGCGGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TGCGGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTG 600

Qy        601 TTCTCGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TTCTCGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTG 660

Qy        661 TTGGTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCATTTCATGGCTAGGTCTTTCAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TTGGTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCATTTCATGGCTAGGTCTTTCAA 720

Qy        721 GTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATGCGCATAGTTGCTGTAGTCAGTG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATGCGCATAGTTGCTGTAGTCAGTG 780

Qy        781 TGGGTCAGCCACTCGAGATTTGTCTTTCAATGTCCGGACCTGAAGTAGGGCCCAGACGTG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TGGGTCAGCCACTCGAGATTTGTCTTTCAATGTCCGGACCTGAAGTAGGGCCCAGACGTG 840

Qy        841 GGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCGACATATGGTCGTCTAGAATTGG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCGACATATGGTCGTCTAGAATTGG 900

Qy        901 AGGTACGGCAGGGCATTGCAATAGGTCTAGAGATTGCTGGAGCTCTTGGAAGCGCTGGAC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 AGGTACGGCAGGGCATTGCAATAGGTCTAGAGATTGCTGGAGCTCTTGGAAGCGCTGGAC 960

Qy        961 GACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGGTACCCGAAGTCCAGAACTCTGA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGGTACCCGAAGTCCAGAACTCTGA 1020

Qy       1021 GACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCAATGTCGTGGCTTCAACAACGAGAC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCAATGTCGTGGCTTCAACAACGAGAC 1080

Qy       1081 AGGGCAGACGTCCCAAGGGAAGTCCTGTACGAAACCGTCGACCTGGACAGAGGCCCAACA 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 AGGGCAGACGTCCCAAGGGAAGTCCTGTACGAAACCGTCGACCTGGACAGAGGCCCAACA 1140

Qy       1141 ATTACCTAGG 1150
              ||||||||||
Db       1141 ATTACCTAGG 1150


RESULT 2
US-10-679-999-11
; Sequence 11, Application US/10679999
; Publication No. US20040067520A1
;   GENERAL INFORMATION:
;        APPLICANT: Mann, Michael B.
;                   Hecht, Randy I.
;        TITLE OF INVENTION: OB FUSION PROTEIN COMPOSITIONS AND
;                            METHODS
;        NUMBER OF SEQUENCES: 18
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Amgen Inc.
;             STREET: 1840 DeHavilland Drive
;             CITY: Thousand Oaks
;             STATE: CA
;             COUNTRY: USA
;             ZIP: 91320-1789
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/679,999
;             FILING DATE: 06-Oct-2003
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/568,528
;             FILING DATE: 09-May-2000
;             APPLICATION NUMBER: 09/267,517
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Knight, Matthew W.
;             REGISTRATION NUMBER: 36,846
;             REFERENCE/DOCKET NUMBER: A-416
;   INFORMATION FOR SEQ ID NO: 11:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1150 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-679-999-11

  Query Match           98.6%;  Score 1134;  DB 16;  Length 1150;
  Best Local Similarity  99.1%;  Pred. No. 0;
  Matches 1140;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          1 GTATACCTTGGGTTTAGAACACTGTTTTGAGTGTGTACGGGTGGCACGGGTCGTGGACTT 60
              |||||||||||  ||||||  ||||||||||||||||||  |||||  ||  |||||  || |||
Db          1 GTATACCTTGGTTTTAGACGACTGTTTTGAGTGTGTACAGGTGGAACAGGTCGAGGCCTT 60
```

```
Qy         61 GAGGACCCCCCTGGCAGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAG 120
              |||||||||| || ||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GAGGACCCCCCAGGAAGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAG 120

Qy        121 AGGGCCTGGGGACTCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AGGGCCTGGGGACTCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAG 180

Qy        181 TTCAAGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TTCAAGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTC 240

Qy        241 CTCGTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTCGTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACC 300

Qy        301 GACTTACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GACTTACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTC 360

Qy        361 TTTTGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TTTTGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGT 420

Qy        421 AGGGCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AGGGCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATA 480

Qy        481 GGGTCGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGGTCGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGG 540

Qy        541 TGCGGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TGCGGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTG 600

Qy        601 TTCTCGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TTCTCGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTG 660

Qy        661 TTGGTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCATTTCATGGCTAGGTCTTTCAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TTGGTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCATTTCATGGCTAGGTCTTTCAA 720

Qy        721 GTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATGCGCATAGTTGCTGTAGTCAGTG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATGCGCATAGTTGCTGTAGTCAGTG 780

Qy        781 TGGGTCAGCCACTCGAGATTTGTCTTTCAATGTCCGGACCTGAAGTAGGGCCCAGACGTG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TGGGTCAGCCACTCGAGATTTGTCTTTCAATGTCCGGACCTGAAGTAGGGCCCAGACGTG 840

Qy        841 GGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCGACATATGGTCGTCTAGAATTGG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCGACATATGGTCGTCTAGAATTGG 900

Qy        901 AGGTACGGCAGGGCATTGCAATAGGTCTAGAGATTGCTGGAGCTCTTGGAAGCGCTGGAC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 AGGTACGGCAGGGCATTGCAATAGGTCTAGAGATTGCTGGAGCTCTTGGAAGCGCTGGAC 960

Qy        961 GACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGGTACCCGAAGTCCAGAACTCTGA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGGTACCCGAAGTCCAGAACTCTGA 1020

Qy       1021 GACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCAATGTCGTGGCTTCAACAACGAGAC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCAATGTCGTGGCTTCAACAACGAGAC 1080

Qy       1081 AGGGCAGACGTCCCAAGGGAAGTCCTGTACGAAACCGTCGACCTGGACAGAGGCCCAACA 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 AGGGCAGACGTCCCAAGGGAAGTCCTGTACGAAACCGTCGACCTGGACAGAGGCCCAACA 1140

Qy       1141 ATTACCTAGG 1150
              ||||||||||
Db       1141 ATTACCTAGG 1150
```

RESULT 3
US-10-679-999-14
; Sequence 14, Application US/10679999
; Publication No. US20040067520A1
; GENERAL INFORMATION:
; APPLICANT: Mann, Michael B.
; Hecht, Randy I.
; TITLE OF INVENTION: OB FUSION PROTEIN COMPOSITIONS AND
; METHODS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: CA
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/679,999
; FILING DATE: 06-Oct-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/568,528
; FILING DATE: 09-May-2000
; APPLICATION NUMBER: 09/267,517
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Knight, Matthew W.
; REGISTRATION NUMBER: 36,846
; REFERENCE/DOCKET NUMBER: A-416
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1135 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-10-679-999-14

Query Match 97.2%; Score 1117.8; DB 16; Length 1135;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 1122; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

```
Qy         22 CTGTTTTGAGTGTGTACGGGTGGCACGGGTCGTGGACTTGAGGACCCCCCTGGCAGTCAG 81
              |||||||||||||||| ||||| || ||||| || |||||||||||||| || ||||||
Db          7 CTGTTTTGAGTGTGTACAGGTGGAACAGGTCGAGGCCTTGAGGACCCCCCAGGAAGTCAG 66

Qy         82 AAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGT 141
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 AAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGT 126

Qy        142 ACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTG 201
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 ACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTG 186

Qy        202 CCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATG 261
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 CCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATG 246

Qy        262 GCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATGTTC 321
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 GCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATGTTC 306
```

```
Qy        322 ACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTT 381
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 ACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTT 366

Qy        382 CCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTC 441
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 CCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTC 426

Qy        442 TTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTC 501
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 TTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTC 486

Qy        502 ACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGG 561
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 ACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGG 546

Qy        562 CTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCC 621
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 CTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCC 606

Qy        622 TTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCG 681
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 TTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCG 666

Qy        682 GAGAGGGACAGAGGCCCATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAAT 741
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 GAGAGGGACAGAGGCCCATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAAT 726

Qy        742 TAATTTTGCTAGCAATGCGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTT 801
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        727 TAATTTTGCTAGCAATGCGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTT 786

Qy        802 GTCTTTCAATGTCCGGACCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTT 861
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 GTCTTTCAATGTCCGGACCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTT 846

Qy        862 TACCTGGTCTGGGACCGACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAA 921
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 TACCTGGTCTGGGACCGACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAA 906

Qy        922 TAGGTCTAGAGATTGCTGGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGG 981
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        907 TAGGTCTAGAGATTGCTGGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGG 966

Qy        982 TTTAGGACGGTGGACGGTACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAG 1041
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        967 TTTAGGACGGTGGACGGTACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAG 1026

Qy       1042 GACCTTCGTAGGCCAATGTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAA 1101
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1027 GACCTTCGTAGGCCAATGTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAA 1086

Qy       1102 GTCCTGTACGAAACCGTCGACCTGGACAGAGGCCCAACAATTACCTAGG 1150
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db       1087 GTCCTGTACGAAACCGTCGACCTGGACAGAGGCCCAACAATTACCTAGG 1135
```

```
RESULT 4
US-10-679-999-17
; Sequence 17, Application US/10679999
; Publication No. US20040067520A1
;   GENERAL INFORMATION:
;        APPLICANT: Mann, Michael B.
;                   Hecht, Randy I.
;        TITLE OF INVENTION: OB FUSION PROTEIN COMPOSITIONS AND
;                            METHODS
;        NUMBER OF SEQUENCES: 18
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Amgen Inc.
;             STREET: 1840 DeHavilland Drive
;             CITY: Thousand Oaks
;             STATE: CA
;             COUNTRY: USA
;             ZIP: 91320-1789
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/679,999
;             FILING DATE: 06-Oct-2003
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/568,528
;             FILING DATE: 09-May-2000
;             APPLICATION NUMBER: 09/267,517
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Knight, Matthew W.
;             REGISTRATION NUMBER: 36,846
;             REFERENCE/DOCKET NUMBER: A-416
;   INFORMATION FOR SEQ ID NO: 17:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1135 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-10-679-999-17

  Query Match             96.1%;  Score 1105;  DB 16;  Length 1135;
  Best Local Similarity   98.7%;  Pred. No. 0;
  Matches 1114;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy         22 CTGTTTTGAGTGTGTACGGGTGGCACGGGTCGTGGACTTGAGGACCCCCCTGGCAGTCAG 81
              ||||||||||||||||||||||||||||||||| || ||||||   || || |||||||||
Db          7 CTGTTTTGAGTGTGTACGGGTGGCACGGGTCGAGGCCTTGAGCTTCCACCAGGCAGTCAG 66

Qy         82 AAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGT 141
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 AAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGT 126

Qy        142 ACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTG 201
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 ACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTG 186

Qy        202 CCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATG 261
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 CCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATG 246

Qy        262 GCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATGTTC 321
              ||||||||||||||||||||||||||||||||||||||||||||||||| | |||
Db        247 GCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTTCGAATGCGT 306

Qy        322 ACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTT 381
              ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 ACGCGCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTT 366

Qy        382 CCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTC 441
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 CCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTC 426

Qy        442 TTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTC 501
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 TTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTC 486

Qy        502 ACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGG 561
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 ACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGG 546

Qy        562 CTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCC 621
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 CTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCC 606
```

```
Qy        622 TTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCG 681
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 TTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCG 666

Qy        682 GAGAGGGACAGAGGCCCATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAAT 741
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 GAGAGGGACAGAGGCCCATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAAT 726

Qy        742 TAATTTTGCTAGCAATGCGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTT 801
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        727 TAATTTTGCTAGCAATGCGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTT 786

Qy        802 GTCTTTCAATGTCCGGACCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTT 861
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 GTCTTTCAATGTCCGGACCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTT 846

Qy        862 TACCTGGTCTGGGACCGACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAA 921
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 TACCTGGTCTGGGACCGACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAA 906

Qy        922 TAGGTCTAGAGATTGCTGGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGG 981
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        907 TAGGTCTAGAGATTGCTGGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGG 966

Qy        982 TTTAGGACGGTGGACGGTACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAG 1041
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        967 TTTAGGACGGTGGACGGTACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAG 1026

Qy       1042 GACCTTCGTAGGCCAATGTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAA 1101
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1027 GACCTTCGTAGGCCAATGTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAA 1086

Qy       1102 GTCCTGTACGAAACCGTCGACCTGGACAGAGGCCCAACAATTACCTAGG 1150
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db       1087 GTCCTGTACGAAACCGTCGACCTGGACAGAGGCCCAACAATTACCTAGG 1135
```

RESULT 5
US-10-666-480-62
; Sequence 62, Application US/10666480
; Publication No. US20040121959A1
; GENERAL INFORMATION:
; APPLICANT: Boone, Thomas C
; APPLICANT: Wild, Kenneth D
; APPLICANT: Sitney, Karen C
; APPLICANT: Min, Hosung
; APPLICANT: Kimmel, Bruce
; TITLE OF INVENTION: Peptides and Related Molecules That Modulate Nerve Growth Factor
; FILE REFERENCE: A-827US
; CURRENT APPLICATION NUMBER: US/10/666,480
; CURRENT FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: 60/412,524
; PRIOR FILING DATE: 2002-09-19
; NUMBER OF SEQ ID NOS: 286
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 62
; LENGTH: 780
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Expression vector component
US-10-666-480-62

Query Match 59.2%; Score 680.6; DB 17; Length 780;
Best Local Similarity 98.7%; Pred. No. 3e-205;
Matches 686; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

```
Qy         18 AACACTGTTTTGAGTGTGTACGGGTGGCACGGGTCGTGGACTTGAGGACCCCCCTGGCAG 77
              | | |||||||||||||||||| ||||| ||||||||||||||||||||||||||||||||
Db         86 ACCCCTGTTTTGAGTGTGTACAGGTGGAACGGGTCGTGGACTTGAGGACCCCCCTGGCAG 145

Qy         78 TCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCA 137
              ||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        146 TCAAAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCA 205

Qy        138 GTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCA 197
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        206 GTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCA 265

Qy        198 CCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTG 257
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        266 CCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTG 325

Qy        258 CATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCAT 317
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        326 CATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCAT 385

Qy        318 GTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCG 377
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        386 GTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCG 445

Qy        378 GTTTCCCGTCGGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTG 437
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        446 GTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTG 505

Qy        438 GTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCA 497
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        506 GTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCA 565

Qy        498 CCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCT 557
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        566 CCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCT 625

Qy        558 GAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGT 617
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        626 GAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGT 685

Qy        618 CCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTT 677
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        686 CCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTT 745

Qy        678 CTCGGAGAGGGACAGAGGCCCATTTCATGGCTAGG 712
              |||||||||||||||||||||||||  |  |||||
Db        746 CTCGGAGAGGGACAGAGGCCCATTTATTACCTAGG 780
```

RESULT 6
US-10-157-408-9
; Sequence 9, Application US/10157408
; Publication No. US20030104535A1
; GENERAL INFORMATION:
; APPLICANT: Capon, Daniel J.
; Gregory, Timothy J.
; TITLE OF INVENTION: Adheson Variants
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/157,408
; FILING DATE: 28-May-2002
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/457,918
; FILING DATE: 1-JUN-1995
; APPLICATION NUMBER: 08/236311

```
;             FILING DATE: 02-MAY-1994
;             APPLICATION NUMBER: 07/936190
;             FILING DATE: 26-AUG-1992
;             APPLICATION NUMBER: 07/842777
;             FILING DATE: 18-FEB-1992
;             APPLICATION NUMBER: 07/250785
;             FILING DATE: 28-SEP-1988
;             APPLICATION NUMBER: 07/104329
;             FILING DATE: 02-OCT-1987
;       ATTORNEY/AGENT INFORMATION:
;             NAME: Kubinec, Jeffrey S.
;             REGISTRATION NUMBER: 36,575
;             REFERENCE/DOCKET NUMBER: P0444P1C3
;       TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 415/225-8228
;             TELEFAX: 415/952-9881
;             TELEX: 910/371-7168
;   INFORMATION FOR SEQ ID NO: 9:
;       SEQUENCE CHARACTERISTICS:
;             LENGTH: 1142 bases
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-157-408-9

  Query Match             58.8%;  Score 676.2;  DB 15;  Length 1142;
  Best Local Similarity   98.6%;  Pred. No. 8.8e-204;
  Matches  695;  Conservative    0;  Mismatches    3;  Indels    7;  Gaps    1;

Qy          5 ACCTTGGGTTTAGAACACTGTTTTGAGTGTGTACGGGTGGCACGGGTCGTGGACTTGAGG 64
              | || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        423 AACTCGGGTTTAGAACACTGTTTTGAGTGTGTACGGGTGGCACGGGTCGTGGACTTGAGG 482

Qy         65 ACCCCCCTGGCAGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGG 124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        483 ACCCCCCTGGCAGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGG 542

Qy        125 CCTGGGGACTCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCA 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        543 CCTGGGGACTCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCA 602

Qy        185 AGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCG 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        603 AGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCG 662

Qy        245 TCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACT 304
              |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        663 TCATGTTGTCGTGCATGGCCCACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACT 722

Qy        305 TACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTT 364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        723 TACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTT 782

Qy        365 GGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGG 424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        783 GGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGG 842

Qy        425 CCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGT 484
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        843 CCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGT 902

Qy        485 CGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCG 544
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        903 CGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCG 962

Qy        545 GAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCT 604
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        963 GAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCT 1022

Qy        605 CGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGC-------ACTACGTACTCCGAGAC 657
              ||||||||||||||||||||||||||||||||||||       ||||||||||||||||||
Db       1023 CGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTACGTACTCCGAGAC 1082

Qy        658 GTGTTGGTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCATTT 702
              |||||||||||||||||||||||||||||||||||||||||||||
Db       1083 GTGTTGGTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCATTT 1127


RESULT 7
US-10-097-044A-9
; Sequence 9, Application US/10097044A
; Publication No. US20030143220A1
;   GENERAL INFORMATION:
;       APPLICANT: Capon, Daniel J.
;                  Gregory, Timothy J.
;       TITLE OF INVENTION: Adheson Variants
;       NUMBER OF SEQUENCES: 25
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Genentech, Inc.
;            STREET: 460 Point San Bruno Blvd
;            CITY: South San Francisco
;            STATE: California
;            COUNTRY: USA
;            ZIP: 94080
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: patin (Genentech)
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/097,044A
;            FILING DATE: 28-May-2002
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/08/457,918
;            FILING DATE: 1-JUN-1995
;            APPLICATION NUMBER: 08/236311
;            FILING DATE: 02-MAY-1994
;            APPLICATION NUMBER: 07/936190
;            FILING DATE: 26-AUG-1992
;            APPLICATION NUMBER: 07/842777
;            FILING DATE: 18-FEB-1992
;            APPLICATION NUMBER: 07/250785
;            FILING DATE: 28-SEP-1988
;            APPLICATION NUMBER: 07/104329
;            FILING DATE: 02-OCT-1987
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Kubinec, Jeffrey S.
;            REGISTRATION NUMBER: 36,575
;            REFERENCE/DOCKET NUMBER: P0444P1C3
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 415/225-8228
;            TELEFAX: 415/952-9881
;            TELEX: 910/371-7168
;   INFORMATION FOR SEQ ID NO: 9:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 1142 bases
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-097-044A-9

  Query Match             58.8%;  Score 676.2;  DB 15;  Length 1142;
  Best Local Similarity   98.6%;  Pred. No. 8.8e-204;
  Matches  695;  Conservative    0;  Mismatches    3;  Indels    7;  Gaps    1;

Qy          5 ACCTTGGGTTTAGAACACTGTTTTGAGTGTGTACGGGTGGCACGGGTCGTGGACTTGAGG 64
              | || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        423 AACTCGGGTTTAGAACACTGTTTTGAGTGTGTACGGGTGGCACGGGTCGTGGACTTGAGG 482

Qy         65 ACCCCCCTGGCAGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGG 124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        483 ACCCCCCTGGCAGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGG 542
```

```
Qy        125 CCTGGGGACTCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCA 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        543 CCTGGGGACTCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCA 602

Qy        185 AGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCG 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        603 AGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCG 662

Qy        245 TCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACT 304
              |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        663 TCATGTTGTCGTGCATGGCCCACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACT 722

Qy        305 TACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTT 364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        723 TACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTT 782

Qy        365 GGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGG 424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        783 GGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGG 842

Qy        425 CCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGT 484
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        843 CCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGT 902

Qy        485 CGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCG 544
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        903 CGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCG 962

Qy        545 GAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCT 604
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        963 GAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCT 1022

Qy        605 CGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGC-------ACTACGTACTCCGAGAC 657
              |||||||||||||||||||||||||||||||||||       |||||||||||||||||
Db       1023 CGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTACGTACTCCGAGAC 1082

Qy        658 GTGTTGGTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCATTT 702
              |||||||||||||||||||||||||||||||||||||||||||||
Db       1083 GTGTTGGTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCATTT 1127
```

```
RESULT 8
US-10-769-247-9
; Sequence 9, Application US/10769247
; Publication No. US20040197809A1
;   GENERAL INFORMATION:
;        APPLICANT: Capon, Daniel J.
;                   Gregory, Timothy J.
;        TITLE OF INVENTION: Adheson Variants
;        NUMBER OF SEQUENCES: 25
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Genentech, Inc.
;             STREET: 460 Point San Bruno Blvd
;             CITY: South San Francisco
;             STATE: California
;             COUNTRY: USA
;             ZIP: 94080
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: patin (Genentech)
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/769,247
;             FILING DATE: 30-Jan-2004
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/457,918
;             FILING DATE: 1-JUN-1995
;             APPLICATION NUMBER: 08/236311
;             FILING DATE: 02-MAY-1994
;             APPLICATION NUMBER: 07/936190
;             FILING DATE: 26-AUG-1992
;             APPLICATION NUMBER: 07/842777
;             FILING DATE: 18-FEB-1992
;             APPLICATION NUMBER: 07/250785
;             FILING DATE: 28-SEP-1988
;             APPLICATION NUMBER: 07/104329
;             FILING DATE: 02-OCT-1987
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Kubinec, Jeffrey S.
;             REGISTRATION NUMBER: 36,575
;             REFERENCE/DOCKET NUMBER: P0444P1C3
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 415/225-8228
;             TELEFAX: 415/952-9881
;             TELEX: 910/371-7168
;   INFORMATION FOR SEQ ID NO: 9:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1142 bases
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-769-247-9

  Query Match             58.8%;  Score 676.2;  DB 18;  Length 1142;
  Best Local Similarity   98.6%;  Pred. No. 8.8e-204;
  Matches  695;  Conservative    0;  Mismatches    3;  Indels    7;  Gaps    1;

Qy          5 ACCTTGGGTTTAGAACACTGTTTTGAGTGTGTACGGGTGGCACGGGTCGTGGACTTGAGG 64
              | || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        423 AACTCGGGTTTAGAACACTGTTTTGAGTGTGTACGGGTGGCACGGGTCGTGGACTTGAGG 482

Qy         65 ACCCCCCTGGCAGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGG 124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        483 ACCCCCCTGGCAGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGG 542

Qy        125 CCTGGGGACTCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCA 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        543 CCTGGGGACTCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCA 602

Qy        185 AGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCG 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        603 AGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCG 662

Qy        245 TCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACT 304
              |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        663 TCATGTTGTCGTGCATGGCCCACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACT 722

Qy        305 TACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTT 364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        723 TACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTT 782

Qy        365 GGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGG 424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        783 GGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGG 842

Qy        425 CCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGT 484
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        843 CCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGT 902

Qy        485 CGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCG 544
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        903 CGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCG 962

Qy        545 GAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCT 604
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        963 GAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCT 1022

Qy        605 CGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGC-------ACTACGTACTCCGAGAC 657
              |||||||||||||||||||||||||||||||||||       |||||||||||||||||
Db       1023 CGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTACGTACTCCGAGAC 1082

Qy        658 GTGTTGGTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCATTT 702
              |||||||||||||||||||||||||||||||||||||||||||||
```

```
Db       1083 GTGTTGGTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCATTT 1127


RESULT 9
US-10-666-480-122
; Sequence 122, Application US/10666480
; Publication No. US20040121959A1
; GENERAL INFORMATION:
;  APPLICANT: Boone, Thomas C
;  APPLICANT:  Wild, Kenneth D
;  APPLICANT:  Sitney, Karen C
;  APPLICANT:  Min, Hosung
;  APPLICANT:  Kimmel, Bruce
;  TITLE OF INVENTION: Peptides and Related Molecules That Modulate Nerve Growth Factor
;  FILE REFERENCE: A-827US
;  CURRENT APPLICATION NUMBER: US/10/666,480
;  CURRENT FILING DATE:  2003-09-18
;  PRIOR APPLICATION NUMBER: 60/412,524
;  PRIOR FILING DATE: 2002-09-19
;  NUMBER OF SEQ ID NOS: 286
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 122
;   LENGTH: 777
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Expression vector
US-10-666-480-122

  Query Match             58.6%;  Score 674.4;  DB 17;  Length 777;
  Best Local Similarity   97.7%;  Pred. No. 2.8e-203;
  Matches  684;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          4 TACCTTGGGTTTAGAACACTGTTTTGAGTGTGTACGGGTGGCACGGGTCGTGGACTTGAG 63
              | |||      ||  |   ||||||||||||||||| ||||| || |||||| || ||||||
Db         24 TTCCTCCTTATTGTATACCTGTTTTGAGTGTGTACAGGTGGAACAGGTCGAGGCCTTGAG 83

Qy         64 GACCCCCCTGGCAGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGG 123
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         84 GACCCCCCTGGCAGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGG 143

Qy        124 GCCTGGGGACTCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTC 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        144 GCCTGGGGACTCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTC 203

Qy        184 AAGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTC 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        204 AAGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTC 263

Qy        244 GTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGAC 303
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        264 GTCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGAC 323

Qy        304 TTACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTT 363
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        324 TTACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTT 383

Qy        364 TGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGG 423
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        384 TGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGG 443

Qy        424 GCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGG 483
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        444 GCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGG 503

Qy        484 TCGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGC 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        504 TCGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGC 563

Qy        544 GGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTC 603
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        564 GGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTC 623

Qy        604 TCGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTG 663
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        624 TCGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTG 683

Qy        664 GTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCATTTC 703
              |||||||||||||||||||||||||||||||||||||||
Db        684 GTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCATTTC 723


RESULT 10
US-10-630-406-4
; Sequence 4, Application US/10630406
; Publication No. US20040105855A1
; GENERAL INFORMATION:
;  APPLICANT: Jure-Kunkel, Maria
;  APPLICANT:  Ganguly, Subinay
;  APPLICANT:  Abraham, Ralph
;  APPLICANT:  Hollenbaugh, Diane L.
;  APPLICANT:  Rillema, Jill
;  APPLICANT:  Thorne, Barbara
;  APPLICANT:  Shuford, Walter W.
;  APPLICANT:  Mittler, Robert S.
;  TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST HUMAN 4-1BB
;  FILE REFERENCE: D0288 NP
;  CURRENT APPLICATION NUMBER: US/10/630,406
;  CURRENT FILING DATE:  2003-07-30
;  PRIOR APPLICATION NUMBER: US 60/399,646
;  PRIOR FILING DATE: 2002-07-30
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
;   LENGTH: 7033
;   TYPE: DNA
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Synthetic
US-10-630-406-4

  Query Match             54.1%;  Score 622.4;  DB 17;  Length 7033;
  Best Local Similarity   94.7%;  Pred. No. 2.1e-186;
  Matches  644;  Conservative    0;  Mismatches   36;  Indels    0;  Gaps    0;

Qy         30 AGTGTGTACGGGTGGCACGGGTCGTGGACTTGAGGACCCCCCTGGCAGTCAGAAGGAGAA 89
              ||   | |||||||| |||||||||||||| |||||||||||| |||||||||||| ||
Db       1400 AGGTGGAACGGGTGGAACGGGTCGTGGACTCAAGGACCCCCCTGGTAGTCAGAAGGACAA 1459

Qy         90 GGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGCACCA 149
              |||||||||||||||||||| |||||||||||||||||||||||||||| ||||||||
Db       1460 GGGGGGTTTTGGGTTCCTGTGAGAGTACTAGAGGGCCTGGGGACTCCAGTGCACGCACCA 1519

Qy        150 CCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGCACCT 209
              |||||||||||||| |||||||| |||||| |||||||||||||||||| ||||||||
Db       1520 CCACCTGCACTCGGTCCTTCTGGGGCTCCAGGTCAAGTTGACCATGCACCTACCGCACCT 1579

Qy        210 CCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATGGCACACCA 269
              |||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db       1580 CCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCAAGTTGTCGTGCATGGCACACCA 1639

Qy        270 GTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATGTTCACGTTCCA 329
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db       1640 GTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTGCCGTTCCTCATGTTCACGTTCCA 1699

Qy        330 GAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTTCCCGTCGG 389
              |||||||||||| ||||||  || ||||||||||||||||||||||||||||||||||||
Db       1700 GAGGTTGTTTCCGGAGGGCAGGAGGTAGCTCTTTTGGTAGAGGTTTCGGTTTCCCGTCGG 1759

Qy        390 GGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTCTTGGTCCA 449
              ||||| |||||||||||||||||||||||||||||| ||| ||| |||||||||||||||
Db       1760 GGCTCTCGGTGTCCACATGTGGGACGGGGGTAGGGTCCTCCTCTACTGGTTCTTGGTCCA 1819

Qy        450 GTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCACCCTCTC 509
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db       1820 GTCGGACTGGACGGACCAGTTTCCGAAGATGGGGTCGCTGTAGCGGCACCTCACCCTCTC 1879
```

```
Qy        510 GTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGGCTGCCGAG 569
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1880 GTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGGCTGCCGAG 1939

Qy        570 GAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCCTTGCAGAA 629
              |||||||||||||||||| ||| ||||||||||||||||||||||| ||||||| |||||
Db       1940 GAAGAAGGAGATGTCGTCCGATTGGCACCTGTTCTCGTCCACCGTCCTCCCCTTACAGAA 1999

Qy        630 GAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCGGAGAGGGA 689
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2000 GAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGTGTCTTCTCGGAGAGGGA 2059

Qy        690 CAGAGGCCCATTTCATGGCT 709
              ||||| |||||||  | | |
Db       2060 CAGAGACCCATTTACTAGAT 2079


RESULT 11
US-09-229-200A-12
; Sequence 12, Application US/09229200A
; Patent No. US20020099179A1
;   GENERAL INFORMATION:
;        APPLICANT: Jolliffe et al.
;        TITLE OF INVENTION: CD4 Specific Recombinant Antibody
;        NUMBER OF SEQUENCES: 28
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Johnson & Johnson
;             STREET: One Johnson & Johnson Plaza
;             CITY: New Brunswick
;             STATE: NJ
;             COUNTRY: USA
;             ZIP: 08933-7003
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
;             COMPUTER: IBM
;             OPERATING SYSTEM: PC-DOS
;             SOFTWARE: <Unknown>
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/229,200A
;             FILING DATE: 13-Jan-1999
;             CLASSIFICATION: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: John W. Wallen, III
;             REGISTRATION NUMBER: 35,403
;             REFERENCE/DOCKET NUMBER: ORT-948
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (858) 784-3239
;             TELEFAX: (908) 524-2808
;   INFORMATION FOR SEQ ID NO: 12:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 2366
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: linear
;        ANTI-SENSE: no
;        SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-229-200A-12

  Query Match             43.7%;  Score 502.8;  DB 9;  Length 2366;
  Best Local Similarity   81.1%;  Pred. No. 1.3e-148;
  Matches  641;  Conservative    0;  Mismatches   52;  Indels   97;  Gaps    1;

Qy         10 GGGTTTAGAACACTGTTTTGAGTGTGTACGGGTGGCACGGGTCGTGGACTTGAGGACCCC 69
              ||| |  |  |||   |  |   ||| | |    | | | ||||||||||  ||||||||
Db       1230 GGGGTCGGCCCACGACTGCGTAGGTGGAGGTAGAGAAGGAGTCGTGGACTCAAGGACCCC 1289

Qy         70 CCTGGCAGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGG 129
              ||||| |||||||||||| ||||||||||||||||||||||| ||||||||||||||||||
Db       1290 CCTGGTAGTCAGAAGGACAAGGGGGGTTTTGGGTTCCTGTGAGAGTACTAGAGGGCCTGG 1349

Qy        130 GGACTCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTG 189
              |||||||||||| |||||||||||||||||||||||| |||||||| |||||| ||||||||
```

```
Db       1350 GGACTCCAGTGCACGCACCACCACCTGCACTCGGTCCTTCTGGGGCTCCAGGTCAAGTTG 1409

Qy        190 ACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATG 249
              |||||||||||  |||||||||||||||||||||||||||||||||||  ||||||| |
Db       1410 ACCATGCACCTACCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCGTCTCGTCAAG 1469

Qy        250 TTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCG 309
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db       1470 TTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTGCCG 1529

Qy        310 TTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAG 369
              |||||||||||||||||||||||||||||| ||||||  || ||||||||||||||||||
Db       1530 TTCCTCATGTTCACGTTCCAGAGGTTGTTTCCGGAGGGCAGGAGGTAGCTCTTTTGGTAG 1589

Qy        370 AGGTTTCGGTT---------------------------------------------------- 380
              |||||||||||
Db       1590 AGGTTTCGGTTTCCACCCTGGGTGCCCCACGCTCCCGGTGTGCCTGTCTCCGGTCGAGCC 1649

Qy        381 ----------------------------------------------------TCCCGTCGGGGC 392
                                                                   ||||||||||||
Db       1650 GGGTGGGAGACGGGACCCTCACTGGCGACACGGTTGGAGACAGGGATGTCCCGTCGGGGC 1709

Qy        393 TCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTCTTGGTCCAGTC 452
              ||| |||||||||||||||||||||||| ||| ||| ||||||||||||||||||||||
Db       1710 TCTCGGTGTCCACATGTGGGACGGGGGTAGGGTCCTCCTCTACTGGTTCTTGGTCCAGTC 1769

Qy        453 GGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCACCCTCTCGTT 512
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db       1770 GGACTGGACGGACCAGTTTCCGAAGATGGGGTCGCTGTAGCGGCACCTCACCCTCTCGTT 1829

Qy        513 ACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGGCTGCCGAGGAA 572
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1830 ACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGGCTGCCGAGGAA 1889

Qy        573 GAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCCTTGCAGAAGAG 632
              |||||||||||||| ||| |||||||||||||||||||||| ||||| | ||||||||
Db       1890 GAAGGAGATGTCGTCCGATTGGCACCTGTTCTCGTCCACCGTCCTCCCCCTACAGAAGAG 1949

Qy        633 TACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTTCTCGGAGAGGGACAG 692
              |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db       1950 TACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGTGTCTTCTCGGAGAGGGACAG 2009

Qy        693 AGGCCCATTT 702
              || |||||||
Db       2010 AGACCCATTT 2019


RESULT 12
US-09-366-133-5
; Sequence 5, Application US/09366133
; Patent No. US20020009798A1
;  GENERAL INFORMATION:
;    APPLICANT:  Pelleymounter, Mary Ann
;    APPLICANT:  Hecht, Randy I
;    APPLICANT:  Mann, Michael B
;    TITLE OF INVENTION:  OB PROTEIN COMPOSITIONS AND METHODS
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Amgen Inc.
;      STREET:  1840 Dehavilland Drive
;      CITY:  Thousand Oaks
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  91230-1789
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/366,133
;      FILING DATE:
;      CLASSIFICATION:
```

```
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/920,608
;       FILING DATE:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Pessin, Karol M.
;       REFERENCE/DOCKET NUMBER:  A-345
;   INFORMATION FOR SEQ ID NO:  5:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  454 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  double
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA
US-09-366-133-5

  Query Match           38.3%;  Score 440.8;  DB 9;  Length 454;
  Best Local Similarity   98.5%;  Pred. No. 3.4e-129;
  Matches  445;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy        699 ATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATG 758
              ||  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 ATACCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATG 62

Qy        759 CGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTTGTCTTTCAATGTCCGGA 818
              ||||||||||||||||||||||||||||||||||||||||||||   ||||||||||||
Db         63 CGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTTGTCGCACAATGTCCGGA 122

Qy        819 CCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCG 878
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 CCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCG 182

Qy        879 ACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAATAGGTCTAGAGATTGCT 938
              |||||||||||||||||||||||||||||||||||||| | ||||||||||||||||||
Db        183 ACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAAGAAGTCTAGAGATTGCT 242

Qy        939 GGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGG 998
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        243 GGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGG 302

Qy        999 TACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCAAT 1058
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        303 TACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCAAT 362

Qy       1059 GTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAAGTCCTGTACGAAACCGT 1118
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        363 GTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAAGTCCTGTACGAAACCGT 422

Qy       1119 CGACCTGGACAGAGGCCCAACAATTACCTAGG 1150
              |||||||||||||||||||||||||||||||
Db        423 CGACCTGGACAGAGGCCCAACAATTACCTAGG 454


RESULT 13
US-10-214-037-5
; Sequence 5, Application US/10214037
; Publication No. US20030054997A1
;   GENERAL INFORMATION:
;       APPLICANT: Pelleymounter, Mary Ann
;                  Hecht, Randy I
;                  Mann, Michael B
;       TITLE OF INVENTION: OB PROTEIN COMPOSITIONS AND METHODS
;       NUMBER OF SEQUENCES: 6
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Amgen Inc.
;            STREET: 1840 Dehavilland Drive
;            CITY: Thousand Oaks
;            STATE: California
;            COUNTRY: U.S.A.
;            ZIP: 91230-1789
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/214,037
;            FILING DATE: 05-Aug-2002
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/08/920,608
;            FILING DATE: 07-JUN-1995
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Pessin, Karol M.
;            REFERENCE/DOCKET NUMBER: A-345
;   INFORMATION FOR SEQ ID NO: 5:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 454 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: double
;            TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-214-037-5

  Query Match           38.3%;  Score 440.8;  DB 14;  Length 454;
  Best Local Similarity   98.5%;  Pred. No. 3.4e-129;
  Matches  445;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy        699 ATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATG 758
              ||  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 ATACCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATG 62

Qy        759 CGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTTGTCTTTCAATGTCCGGA 818
              ||||||||||||||||||||||||||||||||||||||||||||   ||||||||||||
Db         63 CGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTTGTCGCACAATGTCCGGA 122

Qy        819 CCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCG 878
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 CCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCG 182

Qy        879 ACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAATAGGTCTAGAGATTGCT 938
              |||||||||||||||||||||||||||||||||||||| | ||||||||||||||||||
Db        183 ACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAAGAAGTCTAGAGATTGCT 242

Qy        939 GGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGG 998
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        243 GGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGG 302

Qy        999 TACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCAAT 1058
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        303 TACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCAAT 362

Qy       1059 GTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAAGTCCTGTACGAAACCGT 1118
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        363 GTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAAGTCCTGTACGAAACCGT 422

Qy       1119 CGACCTGGACAGAGGCCCAACAATTACCTAGG 1150
              |||||||||||||||||||||||||||||||
Db        423 CGACCTGGACAGAGGCCCAACAATTACCTAGG 454


RESULT 14
US-10-679-999-5
; Sequence 5, Application US/10679999
; Publication No. US20040067520A1
;   GENERAL INFORMATION:
;       APPLICANT: Mann, Michael B.
;                  Hecht, Randy I.
;       TITLE OF INVENTION: OB FUSION PROTEIN COMPOSITIONS AND
;                           METHODS
;       NUMBER OF SEQUENCES: 18
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Amgen Inc.
;            STREET: 1840 DeHavilland Drive
;            CITY: Thousand Oaks
;            STATE: CA
```

```
;              COUNTRY: USA
;              ZIP: 91320-1789
;         COMPUTER READABLE FORM:
;              MEDIUM TYPE: Floppy disk
;              COMPUTER: IBM PC compatible
;              OPERATING SYSTEM: PC-DOS/MS-DOS
;              SOFTWARE: PatentIn Release #1.0, Version #1.30
;         CURRENT APPLICATION DATA:
;              APPLICATION NUMBER: US/10/679,999
;              FILING DATE: 06-Oct-2003
;              CLASSIFICATION: <Unknown>
;         PRIOR APPLICATION DATA:
;              APPLICATION NUMBER: US/09/568,528
;              FILING DATE: 09-May-2000
;              APPLICATION NUMBER: 09/267,517
;              FILING DATE: <Unknown>
;         ATTORNEY/AGENT INFORMATION:
;              NAME: Knight, Matthew W.
;              REGISTRATION NUMBER: 36,846
;              REFERENCE/DOCKET NUMBER: A-416
;    INFORMATION FOR SEQ ID NO: 5:
;         SEQUENCE CHARACTERISTICS:
;              LENGTH: 454 base pairs
;              TYPE: nucleic acid
;              STRANDEDNESS: double
;              TOPOLOGY: linear
;         MOLECULE TYPE: cDNA
;         SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-679-999-5

  Query Match             38.3%;  Score 440.8;  DB 16;  Length 454;
  Best Local Similarity   98.5%;  Pred. No. 3.4e-129;
  Matches  445;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy        699 ATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATG 758
              ||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 ATACCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATG 62

Qy        759 CGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTTGTCTTTCAATGTCCGGA 818
              ||||||||||||||||||||||||||||||||||||||||||||    ||||||||||
Db         63 CGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTTGTCGCACAATGTCCGGA 122

Qy        819 CCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCG 878
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 CCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCG 182

Qy        879 ACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAATAGGTCTAGAGATTGCT 938
              |||||||||||||||||||||||||||||||||||||||| | ||||||||||||||||
Db        183 ACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAAGAAGTCTAGAGATTGCT 242

Qy        939 GGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGG 998
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        243 GGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGG 302

Qy        999 TACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCAAT 1058
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        303 TACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCAAT 362

Qy       1059 GTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAAGTCCTGTACGAAACCGT 1118
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        363 GTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAAGTCCTGTACGAAACCGT 422

Qy       1119 CGACCTGGACAGAGGCCCAACAATTACCTAGG 1150
              |||||||||||||||||||||||||||||||
Db        423 CGACCTGGACAGAGGCCCAACAATTACCTAGG 454


RESULT 15
US-09-366-133-2
; Sequence 2, Application US/09366133
; Patent No. US20020009798A1
;  GENERAL INFORMATION:
;    APPLICANT:  Pelleymounter, Mary Ann
;    APPLICANT:  Hecht, Randy I
;    APPLICANT:  Mann, Michael B
;    TITLE OF INVENTION:  OB PROTEIN COMPOSITIONS AND METHODS
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Amgen Inc.
;      STREET:  1840 Dehavilland Drive
;      CITY:  Thousand Oaks
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  91230-1789
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/366,133
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/920,608
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Pessin, Karol M.
;      REFERENCE/DOCKET NUMBER:  A-345
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  491 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-366-133-2

  Query Match             32.9%;  Score 378.4;  DB 9;  Length 491;
  Best Local Similarity   89.8%;  Pred. No. 2.3e-109;
  Matches  406;  Conservative    0;  Mismatches   46;  Indels    0;  Gaps    0;

Qy        699 ATTTCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATG 758
              ||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         40 ATACCATGGCTAGGTCTTTCAAGTCCTGCTGTGGTTTTGGAATTAATTTTGCTAGCAATG 99

Qy        759 CGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCACTCGAGATTTGTCTTTCAATGTCCGGA 818
              ||||||||||||||||||||||||||||||||    | ||||||||    ||||| || ||
Db        100 CGCATAGTTGCTGTAGTCAGTGTGGGTCAGCCAGAGGCGATTTGTCGCACAATGGCCAGA 159

Qy        819 CCTGAAGTAGGGCCCAGACGTGGGCTAGGACTGGAACAGGTTTTACCTGGTCTGGGACCG 878
              |||||||||||||||||||||||||||||| | ||||||||||||||||||||||||||
Db        160 CCTGAAGTAGGGCCCAGACGTGGGCTAGGATTCGAACAGGTTTTACCTGGTCTGGGACCG 219

Qy        879 ACATATGGTCGTCTAGAATTGGAGGTACGGCAGGGCATTGCAATAGGTCTAGAGATTGCT 938
              |||||||||||||| | |||||||||  ||||||  | ||||||  |||||||||||||
Db        220 ACATATGGTCGTCCACAATTGGAGGGACGGCAGGGTCTTGCAAGAAGTCTAGCGATTGCT 279

Qy        939 GGAGCTCTTGGAAGCGCTGGACGACGTGCACGACCGTAAGAGGTTTAGGACGGTGGACGG 998
              |||||||||||||||||||||||||| ||||||||||||||||||||||  ||||||
Db        280 GGAGCTCTTGGAAGCGCTGGACGACGTGGACGACCGTAAGAGGTTTAGGACGAGGGACGG 339

Qy        999 TACCCGAAGTCCAGAACTCTGAGACCTGAGAGACCCGCCCCAGGACCTTCGTAGGCCAAT 1058
                | | ||||||||| |||  | ||| || |||| ||||||||||||||||||||   ||
Db        340 CGTCTGGAGTCCAGAAGTCTTTGGCCTTAGGGACCTGCCCCAGGACCTTCGTAGGGACAT 399

Qy       1059 GTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAAGTCCTGTACGAAACCGT 1118
              |||||||||||||||||||||||||||||||||||||||||||||||||||||  |||  |||
Db        400 GTCGTGGCTTCAACAACGAGACAGGGCAGACGTCCCAAGGGAAGTCCTGTAGGAAGTCGT 459

Qy       1119 CGACCTGGACAGAGGCCCAACAATTACCTAGG 1150
              |||||| | |||||||  ||||||||||||||
Db        460 CGACCTGCAAAGAGGCCTTACAATTACCTAGG 491


Search completed: October 17, 2004, 18:18:26
```

Job time : 595.198 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 17, 2004, 15:27:13 ; Search time 104.054 Seconds
(without alignments)
7855.635 Million cell updates/sec

Title: US-10-679-999-8
Perfect score: 1150
Sequence: 1 GTATACCTTGGGTTTAGAAC.....AGGCCCAACAATTACCTAGG 1150

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	676.2	58.8	1142	1	US-08-236-311-9	Sequence 9, Appli
	2	676.2	58.8	1142	3	US-08-457-918-9	Sequence 9, Appli
	3	676.2	58.8	1142	4	US-10-157-408-9	Sequence 9, Appli
	4	60	5.2	2287	1	US-08-480-036-1	Sequence 1, Appli
	5	60	5.2	2287	1	US-08-461-968A-1	Sequence 1, Appli
	6	60	5.2	2287	2	US-08-462-571-1	Sequence 1, Appli
	7	60	5.2	2287	4	US-08-472-888A-1	Sequence 1, Appli
	8	43.6	3.8	1161	4	US-09-252-991A-7703	Sequence 7703, Ap
c	9	43.6	3.8	1287	4	US-09-252-991A-7860	Sequence 7860, Ap
	10	43.6	3.8	1359	4	US-09-252-991A-7624	Sequence 7624, Ap
	11	43	3.7	468	1	US-08-236-311-12	Sequence 12, Appl
	12	43	3.7	468	3	US-08-457-918-12	Sequence 12, Appl
	13	43	3.7	468	4	US-10-157-408-12	Sequence 12, Appl
c	14	41.8	3.6	3489	2	US-08-728-323A-1	Sequence 1, Appli
c	15	41.8	3.6	3489	3	US-09-298-568-1	Sequence 1, Appli
c	16	41.8	3.6	3489	4	US-09-410-399-1	Sequence 1, Appli
c	17	41.8	3.6	3489	4	US-09-894-273-1	Sequence 1, Appli
	18	41.8	3.6	32207	2	US-08-770-379-20	Sequence 20, Appl
	19	41.8	3.6	32207	3	US-08-757-669A-20	Sequence 20, Appl
	20	41.8	3.6	32207	3	US-09-230-371A-20	Sequence 20, Appl
	21	40.2	3.5	1423	4	US-09-799-451-728	Sequence 728, App
c	22	40	3.5	533	6	5482709-5	Patent No. 5482709
c	23	40	3.5	543	6	5273901-6	Patent No. 5273901
c	24	39.6	3.4	1425	4	US-09-489-039A-1509	Sequence 1509, Ap
	25	39.6	3.4	2016	4	US-09-489-039A-1492	Sequence 1492, Ap
c	26	39.4	3.4	5331	4	US-09-453-956-1	Sequence 1, Appli
c	27	39.2	3.4	1482	4	US-09-977-897-1	Sequence 1, Appli
c	28	38.6	3.4	1440	4	US-09-672-749-13	Sequence 13, Appl
c	29	37.4	3.3	688	3	US-08-998-416-915	Sequence 915, App
	30	37.4	3.3	7559	2	US-08-250-848-2	Sequence 2, Appli
c	31	37.4	3.3	4403765	3	US-09-103-840A-2	Sequence 2, Appli
c	32	37.4	3.3	4411529	3	US-09-103-840A-1	Sequence 1, Appli
	33	36.6	3.2	23673	3	US-09-773-816-1	Sequence 1, Appli
	34	36.4	3.2	1125	4	US-09-252-991A-16469	Sequence 16469, A
	35	36.4	3.2	1173	4	US-09-252-991A-16248	Sequence 16248, A
c	36	36.4	3.2	1296	4	US-09-252-991A-16018	Sequence 16018, A
	37	36.4	3.2	2582	2	US-08-816-105A-2	Sequence 2, Appli
	38	36.2	3.1	505	4	US-09-621-976-15639	Sequence 15639, A
c	39	36.2	3.1	615	4	US-09-252-991A-242	Sequence 242, App
	40	36.2	3.1	1041	4	US-09-252-991A-296	Sequence 296, App
	41	36.2	3.1	1140	4	US-09-252-991A-269	Sequence 269, App
	42	36.2	3.1	1233	4	US-09-252-991A-3735	Sequence 3735, Ap
c	43	36.2	3.1	1491	4	US-09-252-991A-3636	Sequence 3636, Ap
	44	36.2	3.1	4884	4	US-09-252-991A-3824	Sequence 3824, Ap
c	45	36	3.1	909	4	US-09-252-991A-7481	Sequence 7481, Ap

ALIGNMENTS

RESULT 1
US-08-236-311-9
; Sequence 9, Application US/08236311
; Patent No. 5565335
; GENERAL INFORMATION:
; APPLICANT: Capon, Daniel J.
; APPLICANT: Gregory, Timothy J.
; TITLE OF INVENTION: Adheson Variants
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/236,311
; FILING DATE: 02-MAY-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/936190
; FILING DATE: 26-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/842777
; FILING DATE: 18-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/250785
; FILING DATE: 28-SEP-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/104329
; FILING DATE: 02-OCT-1987
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: 444P1C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1896
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1142 bases
; TYPE: nucleic acid
; STRANDEDNESS: single

```
;      TOPOLOGY:  linear
US-08-236-311-9

  Query Match             58.8%;  Score 676.2;  DB 1;  Length 1142;
  Best Local Similarity   98.6%;  Pred. No. 1.2e-177;
  Matches  695;  Conservative    0;  Mismatches    3;  Indels    7;  Gaps    1;

Qy          5 ACCTTGGGTTTAGAACACTGTTTTGAGTGTGTACGGGTGGCACGGGTCGTGGACTTGAGG 64
              | || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        423 AACTCGGGTTTAGAACACTGTTTTGAGTGTGTACGGGTGGCACGGGTCGTGGACTTGAGG 482

Qy         65 ACCCCCCTGGCAGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGG 124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        483 ACCCCCCTGGCAGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGG 542

Qy        125 CCTGGGGACTCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCA 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        543 CCTGGGGACTCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCA 602

Qy        185 AGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCG 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        603 AGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCG 662

Qy        245 TCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACT 304
              |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        663 TCATGTTGTCGTGCATGGCCCACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACT 722

Qy        305 TACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTT 364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        723 TACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTT 782

Qy        365 GGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGG 424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        783 GGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGG 842

Qy        425 CCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGT 484
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        843 CCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGT 902

Qy        485 CGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCG 544
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        903 CGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCG 962

Qy        545 GAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCT 604
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        963 GAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCT 1022

Qy        605 CGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGC-------ACTACGTACTCCGAGAC 657
              |||||||||||||||||||||||||||||||||||       |||||||||||||||||
Db       1023 CGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTACGTACTCCGAGAC 1082

Qy        658 GTGTTGGTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCATTT 702
              |||||||||||||||||||||||||||||||||||||||||||||
Db       1083 GTGTTGGTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCATTT 1127


RESULT 2
US-08-457-918-9
; Sequence 9, Application US/08457918
; Patent No. 6117655
;  GENERAL INFORMATION:
;    APPLICANT:  Capon, Daniel J.
;    APPLICANT:  Gregory, Timothy J.
;    TITLE OF INVENTION:  Adheson Variants
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  5.25 inch, 360 Kb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  patin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/457,918
;      FILING DATE:  1-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/236311
;      FILING DATE:  02-MAY-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/936190
;      FILING DATE:  26-AUG-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/842777
;      FILING DATE:  18-FEB-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/250785
;      FILING DATE:  28-SEP-1988
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/104329
;      FILING DATE:  02-OCT-1987
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kubinec, Jeffrey S.
;      REGISTRATION NUMBER:  36,575
;      REFERENCE/DOCKET NUMBER:  P0444P1C3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/225-8228
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1142 bases
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-457-918-9

  Query Match             58.8%;  Score 676.2;  DB 3;  Length 1142;
  Best Local Similarity   98.6%;  Pred. No. 1.2e-177;
  Matches  695;  Conservative    0;  Mismatches    3;  Indels    7;  Gaps    1;

Qy          5 ACCTTGGGTTTAGAACACTGTTTTGAGTGTGTACGGGTGGCACGGGTCGTGGACTTGAGG 64
              | || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        423 AACTCGGGTTTAGAACACTGTTTTGAGTGTGTACGGGTGGCACGGGTCGTGGACTTGAGG 482

Qy         65 ACCCCCCTGGCAGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGG 124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        483 ACCCCCCTGGCAGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGG 542

Qy        125 CCTGGGGACTCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCA 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        543 CCTGGGGACTCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCA 602

Qy        185 AGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCG 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        603 AGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCG 662

Qy        245 TCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACT 304
              |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        663 TCATGTTGTCGTGCATGGCCCACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACT 722

Qy        305 TACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTT 364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        723 TACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTT 782

Qy        365 GGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGG 424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        783 GGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGG 842

Qy        425 CCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGT 484
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        843 CCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGT 902

Qy        485 CGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCG 544
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        903 CGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCG 962

Qy        545 GAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCT 604
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        963 GAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCT 1022

Qy        605 CGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGC-------ACTACGTACTCCGAGAC 657
              |||||||||||||||||||||||||||||||||||       |||||||||||||||||
Db       1023 CGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTACGTACTCCGAGAC 1082

Qy        658 GTGTTGGTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCATTT 702
              |||||||||||||||||||||||||||||||||||||||||||||
Db       1083 GTGTTGGTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCATTT 1127


RESULT 3
US-10-157-408-9
; Sequence 9, Application US/10157408
; Patent No. 6710169
;  GENERAL INFORMATION:
;       APPLICANT: Capon, Daniel J.
;                  Gregory, Timothy J.
;       TITLE OF INVENTION: Adheson Variants
;       NUMBER OF SEQUENCES: 25
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Genentech, Inc.
;            STREET: 460 Point San Bruno Blvd
;            CITY: South San Francisco
;            STATE: California
;            COUNTRY: USA
;            ZIP: 94080
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: patin (Genentech)
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/157,408
;            FILING DATE: 28-May-2002
;            CLASSIFICATION: 435
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/08/457,918
;            FILING DATE: 1-JUN-1995
;            APPLICATION NUMBER: 08/236311
;            FILING DATE: 02-MAY-1994
;            APPLICATION NUMBER: 07/936190
;            FILING DATE: 26-AUG-1992
;            APPLICATION NUMBER: 07/842777
;            FILING DATE: 18-FEB-1992
;            APPLICATION NUMBER: 07/250785
;            FILING DATE: 28-SEP-1988
;            APPLICATION NUMBER: 07/104329
;            FILING DATE: 02-OCT-1987
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Kubinec, Jeffrey S.
;            REGISTRATION NUMBER: 36,575
;            REFERENCE/DOCKET NUMBER: P0444P1C3
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 415/225-8228
;            TELEFAX: 415/952-9881
;            TELEX: 910/371-7168
;   INFORMATION FOR SEQ ID NO: 9:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 1142 bases
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-157-408-9

  Query Match           58.8%;  Score 676.2;  DB 4;  Length 1142;
  Best Local Similarity  98.6%;  Pred. No. 1.2e-177;
  Matches  695;  Conservative    0;  Mismatches    3;  Indels    7;  Gaps    1;

Qy          5 ACCTTGGGTTTAGAACACTGTTTTGAGTGTGTACGGGTGGCACGGGTCGTGGACTTGAGG 64
              | || ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        423 AACTCGGGTTTAGAACACTGTTTTGAGTGTGTACGGGTGGCACGGGTCGTGGACTTGAGG 482

Qy         65 ACCCCCCTGGCAGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGG 124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        483 ACCCCCCTGGCAGTCAGAAGGAGAAGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGG 542

Qy        125 CCTGGGGACTCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCA 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        543 CCTGGGGACTCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCA 602

Qy        185 AGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCG 244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        603 AGTTGACCATGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCG 662

Qy        245 TCATGTTGTCGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACT 304
              ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        663 TCATGTTGTCGTGCATGGCCCACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACT 722

Qy        305 TACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTT 364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        723 TACCGTTCCTCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTT 782

Qy        365 GGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGG 424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        783 GGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGG 842

Qy        425 CCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGT 484
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        843 CCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGT 902

Qy        485 CGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCG 544
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        903 CGCTGTAGCGGCACCTCACCCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCG 962

Qy        545 GAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCT 604
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        963 GAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCT 1022

Qy        605 CGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGC-------ACTACGTACTCCGAGAC 657
              |||||||||||||||||||||||||||||||||||       |||||||||||||||||
Db       1023 CGTCCACCGTCGTCCCCTTGCAGAAGAGTACGAGGCACTACGTACTACGTACTCCGAGAC 1082

Qy        658 GTGTTGGTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCATTT 702
              |||||||||||||||||||||||||||||||||||||||||||||
Db       1083 GTGTTGGTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCATTT 1127


RESULT 4
US-08-480-036-1
; Sequence 1, Application US/08480036
; Patent No. 5723583
;  GENERAL INFORMATION:
;    APPLICANT:  Seed, Brian et al.
;    TITLE OF INVENTION:  INHIBITION OF CELL ADHESION
;    TITLE OF INVENTION:  PROTEIN-CARBOHYDRATE
;    TITLE OF INVENTION:  INTERACTIONS
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson
;      STREET:  225 Franklin Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  U.S.A.
;      ZIP:  02110-2804
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
```

```
;       COMPUTER:  IBM PS/2 Model 50Z or 55SX
;       OPERATING SYSTEM:  IBM P.C. DOS (Version 5.00)
;       SOFTWARE:  WordPerfect (Version 5.1)
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/480,036
;       FILING DATE:
;       CLASSIFICATION:  424
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US/07/618,314C
;       FILING DATE:  No. 5723583ember 23, 1990
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Clark, Paul T.
;       REGISTRATION NUMBER:  30,162
;       REFERENCE/DOCKET NUMBER:  00786/067001
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (617) 542-5070
;       TELEFAX:  (617) 542-8906
;       TELEX:  200154
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  2287
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
US-08-480-036-1

  Query Match             5.2%;  Score 60;  DB 1;  Length 2287;
  Best Local Similarity   100.0%;  Pred. No. 8.5e-07;
  Matches   60;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         89 AGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGCACC 148
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 AGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGCACC 1620


RESULT 5
US-08-461-968A-1
; Sequence 1, Application US/08461968A
; Patent No. 5801044
;  GENERAL INFORMATION:
;    APPLICANT:  Seed et al., Brian
;    TITLE OF INVENTION:  INHIBITION OF CELL ADHESION
;    TITLE OF INVENTION:  PROTEIN-CARBOHYDRATE INTERACTIONS
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson P.C.
;      STREET:  225 Franklin Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  0210-2804
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/461,968A
;      FILING DATE:  05-JUN-1995
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/618,314
;      FILING DATE:  23-NOV-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Lech, Karen F.
;      REGISTRATION NUMBER:  35,238
;      REFERENCE/DOCKET NUMBER:  00786/067003
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617/542-5070
;      TELEFAX:  617/542-8906
;      TELEX:  200154
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;       LENGTH:  2287
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
US-08-461-968A-1

  Query Match             5.2%;  Score 60;  DB 1;  Length 2287;
  Best Local Similarity   100.0%;  Pred. No. 8.5e-07;
  Matches   60;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         89 AGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGCACC 148
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 AGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGCACC 1620


RESULT 6
US-08-462-571-1
; Sequence 1, Application US/08462571
; Patent No. 5858983
;  GENERAL INFORMATION:
;    APPLICANT:  Seed, Brian et al.
;    TITLE OF INVENTION:  INHIBITION OF CELL ADHESION
;    TITLE OF INVENTION:  PROTEIN-CARBOHYDRATE INTERACTIONS
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson P.C.
;      STREET:  225 Franklin Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  U.S.A.
;      ZIP:  02110-2804
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      COMPUTER:  IBM PS/2 Model 50Z or 55SX
;      OPERATING SYSTEM:  IBM P.C. DOS (Version 3.30)
;      SOFTWARE:  WordPerfect (Version 5.0)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/462,571
;      FILING DATE:  05 June 1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/618,314
;      FILING DATE:  23 No. 5858983ember 1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Lech, Karen F.
;      REGISTRATION NUMBER:  35,238
;      REFERENCE/DOCKET NUMBER:  00786/067002
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 542-5070
;      TELEFAX:  (617) 542-8906
;      TELEX:  200154
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;       LENGTH:  2287
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
US-08-462-571-1

  Query Match             5.2%;  Score 60;  DB 2;  Length 2287;
  Best Local Similarity   100.0%;  Pred. No. 8.5e-07;
  Matches   60;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         89 AGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGCACC 148
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 AGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGCACC 1620


RESULT 7
US-08-472-888A-1
; Sequence 1, Application US/08472888A
; Patent No. 6613746
;  GENERAL INFORMATION:
```

```
;    APPLICANT:  Seed, Brian
;    APPLICANT:  Walz, Gerd
;    TITLE OF INVENTION:  AGP-ANTIBODY FUSION PROTEINS
;    TITLE OF INVENTION:  AND RELATED MOLECULES AND METHODS
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Clark & Elbing LLP
;      STREET:  176 Federal Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02110
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/472,888A
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/618,314
;      FILING DATE:  23-NOV-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Elbing, Karen L
;      REGISTRATION NUMBER:  35,238
;      REFERENCE/DOCKET NUMBER:  00786/258001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-428-0200
;      TELEFAX:  617-428-7045
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2287 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Genomic DNA
;    FEATURE:
;      NAME/KEY:  Coding Sequence
;      LOCATION:  1...300, 361...453, 679...903, 961...972,
;      LOCATION:  1360...1404, 1524...1853, 1950...2270
;      OTHER INFORMATION:
US-08-472-888A-1

  Query Match             5.2%;  Score 60;  DB 4;  Length 2287;
  Best Local Similarity   100.0%;  Pred. No. 8.5e-07;
  Matches   60;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          89 AGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGCACC 148
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1561 AGGGGGGTTTTGGGTTCCTGTGGGAGTACTAGAGGGCCTGGGGACTCCAGTGTACGCACC 1620


RESULT 8
US-09-252-991A-7703
; Sequence 7703, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 7703
;   LENGTH: 1161
;   TYPE: DNA
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-7703

  Query Match             3.8%;  Score 43.6;  DB 4;  Length 1161;
  Best Local Similarity   47.4%;  Pred. No. 0.023;
  Matches  130;  Conservative    0;  Mismatches  144;  Indels    0;  Gaps    0;

Qy         134 TCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCA 193
               |||||  | || |   |  |  |  ||  ||| |  |     |       | |  ||| |
Db         332 TCCAGCCTTCGGAGATCGCCAAGGTCTGCGTGGTGATCTTCATGGCCGGCTACCTGATCC 391

Qy         194 TGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGT 253
                 || || | |  |||  | |    || |  | |||  |   | | ||||  |||||
Db         392 GCCGCCAGCAGGAGGTCCGGGAAAGCTGGATGGGCTTCTTCAAGCCCTTCGTGGTGTTGC 451

Qy         254 CGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCC 313
                 |  |||||   || |  || |      || |||| | | |   ||||   ||  | |
Db         452 TGCCGATGGCCGGCCTGCTGCTGCGCGAGCCGGACTTCGGCGCCACCGTGGTAATGATGG 511

Qy         314 TCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGT 373
               |    | ||  |  |  |||  |  | | ||   ||  ||  | |||  |   || |
Db         512 GCGCTGCCGCGGCCATGCTGTTCCTCGGCGGGGTGGGGCTGTTCCGCTTCGGCCTGATGG 571

Qy         374 TTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACAT 407
               | | | |  |||||  ||  | |   | | ||
Db         572 TGCTGCTGGCGGTCGGCGCGGTGGTCCTGCTGAT 605


RESULT 9
US-09-252-991A-7860/c
; Sequence 7860, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 7860
;   LENGTH: 1287
;   TYPE: DNA
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-7860

  Query Match             3.8%;  Score 43.6;  DB 4;  Length 1287;
  Best Local Similarity   47.4%;  Pred. No. 0.024;
  Matches  130;  Conservative    0;  Mismatches  144;  Indels    0;  Gaps    0;

Qy         134 TCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCA 193
               |||||  | || |   |  |  |  ||  ||| |  |     |       | |  ||| |
Db         908 TCCAGCCTTCGGAGATCGCCAAGGTCTGCGTGGTGATCTTCATGGCCGGCTACCTGATCC 849

Qy         194 TGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGT 253
                 || || | |  |||  | |    || |  | |||  |   | | ||||  |||||
Db         848 GCCGCCAGCAGGAGGTCCGGGAAAGCTGGATGGGCTTCTTCAAGCCCTTCGTGGTGTTGC 789

Qy         254 CGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCC 313
                 |  |||||   || |  || |      || |||| | | |   ||||   ||  | |
Db         788 TGCCGATGGCCGGCCTGCTGCTGCGCGAGCCGGACTTCGGCGCCACCGTGGTAATGATGG 729

Qy         314 TCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGT 373
               |    | ||  |  |  |||  |  | | ||   ||  ||  | |||  |   || |
Db         728 GCGCTGCCGCGGCCATGCTGTTCCTCGGCGGGGTGGGGCTGTTCCGCTTCGGCCTGATGG 669

Qy         374 TTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACAT 407
               | | | |  |||||  ||  | |   | | ||
```

```
Db        668 TGCTGCTGGCGGTCGGCGCGGTGGTCCTGCTGAT 635


RESULT 10
US-09-252-991A-7624
; Sequence 7624, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 7624
;   LENGTH: 1359
;   TYPE: DNA
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-7624

  Query Match             3.8%;  Score 43.6;  DB 4;  Length 1359;
  Best Local Similarity   47.4%;  Pred. No. 0.024;
  Matches  130;  Conservative    0;  Mismatches  144;  Indels    0;  Gaps    0;

Qy        134 TCCAGTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCA 193
              |||||  | || |   |  |  |  ||  ||| |  |     |     | |  ||| |
Db        576 TCCAGCCTTCGGAGATCGCCAAGGTCTGCGTGGTGATCTTCATGGCCGGCTACCTGATCC 635

Qy        194 TGCACCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGT 253
              | || || | |  ||| | |    || |  | |||  |   | | ||||  |||||
Db        636 GCCGCCAGCAGGAGGTCCGGGAAAGCTGGATGGGCTTCTTCAAGCCCTTCGTGGTGTTGC 695

Qy        254 CGTGCATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCC 313
              |   |||||   || |  || |     || |||| | | |   ||||   ||  | |
Db        696 TGCCGATGGCCGGCCTGCTGCTGCGCGAGCCGGACTTCGGCGCCACCGTGGTAATGATGG 755

Qy        314 TCATGTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGT 373
              |   | ||  |  |  |||  |  | | ||   ||  ||  | |||  |   || |
Db        756 GCGCTGCCGCGGCCATGCTGTTCCTCGGCGGGGTGGGGCTGTTCCGCTTCGGCCTGATGG 815

Qy        374 TTCGGTTTCCCGTCGGGGCTCTTGGTGTCCACAT 407
              | | | |  | ||||| ||  | |   | |  ||
Db        816 TGCTGCTGGCGGTCGGCGCGGTGGTCCTGCTGAT 849


RESULT 11
US-08-236-311-12
; Sequence 12, Application US/08236311
; Patent No. 5565335
;  GENERAL INFORMATION:
;    APPLICANT:  Capon, Daniel J.
;    APPLICANT:  Gregory, Timothy J.
;    TITLE OF INVENTION:  Adheson Variants
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  5.25 inch, 360 Kb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  patin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/236,311
;      FILING DATE:  02-MAY-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/936190
;      FILING DATE:  26-AUG-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/842777
;      FILING DATE:  18-FEB-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/250785
;      FILING DATE:  28-SEP-1988
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/104329
;      FILING DATE:  02-OCT-1987
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hasak, Janet E.
;      REGISTRATION NUMBER:  28,616
;      REFERENCE/DOCKET NUMBER:  444P1C2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/225-1896
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  468 bases
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-236-311-12

  Query Match             3.7%;  Score 43;  DB 1;  Length 468;
  Best Local Similarity   49.5%;  Pred. No. 0.023;
  Matches  143;  Conservative    0;  Mismatches  140;  Indels    6;  Gaps    1;

Qy        394 CTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTCTTGGTCCAGTCG 453
              | ||||   || | || | | || |||||    ||  || |||              | |
Db        127 CGTGGTAGACAGAAGTAGAAGGGCGGTAGACTACTCGTCAACTTTAGACCTTGACGGAGA 186

Qy        454 GACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCAC------CCTC 507
              |    |||||| | ||  ||||||||||||| ||   |   ||  ||||      |||
Db        187 CAACACACGGACGACTTATTGAAGATAGGGTCTCTCCGGTTTCATGTCACCTTCCACCTA 246

Qy        508 TCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGGCTGCCG 567
              | |       ||  |||  |||  | |  |||         |       |   ||| ||
Db        247 TTGCGGGAGGTTAGCCCATTGAGGGTCCTCTCACAGTGTCTCGTCCTGTCGTTCCTGTCG 306

Qy        568 AGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCCTTGCAG 627
              |||  |  ||||  |||||  || ||  ||  |||       |   || |   || |||
Db        307 TGGATGTCGGAGTCGTCGTGGGACTGCGACTCGTTTCGTCTGATGCTCTTTGTGTTTCAG 366

Qy        628 AAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCT 676
              | | | |||   || |  ||| |||  |||  |   | |  |||  |||
Db        367 ATGCGGACGCTTCAGTGGGTAGTCCCGGACTCGAGCGGGCAGTGTTTCT 415


RESULT 12
US-08-457-918-12
; Sequence 12, Application US/08457918
; Patent No. 6117655
;  GENERAL INFORMATION:
;    APPLICANT:  Capon, Daniel J.
;    APPLICANT:  Gregory, Timothy J.
;    TITLE OF INVENTION:  Adheson Variants
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  5.25 inch, 360 Kb floppy disk
```

```
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  patin (Genentech)
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/457,918
;       FILING DATE:  1-JUN-1995
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/236311
;       FILING DATE:  02-MAY-1994
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  07/936190
;       FILING DATE:  26-AUG-1992
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  07/842777
;       FILING DATE:  18-FEB-1992
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  07/250785
;       FILING DATE:  28-SEP-1988
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  07/104329
;       FILING DATE:  02-OCT-1987
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Kubinec, Jeffrey S.
;       REGISTRATION NUMBER:  36,575
;       REFERENCE/DOCKET NUMBER:  P0444P1C3
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  415/225-8228
;       TELEFAX:  415/952-9881
;       TELEX:  910/371-7168
;   INFORMATION FOR SEQ ID NO:  12:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  468 bases
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
US-08-457-918-12

  Query Match             3.7%;  Score 43;  DB 3;  Length 468;
  Best Local Similarity   49.5%;  Pred. No. 0.023;
  Matches  143;  Conservative    0;  Mismatches  140;  Indels    6;  Gaps    1;

Qy        394 CTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTCTTGGTCCAGTCG 453
              | ||||   || | || | | || |||||    ||  || |||           | |
Db        127 CGTGGTAGACAGAAGTAGAAGGGCGGTAGACTACTCGTCAACTTTAGACCTTGACGGAGA 186

Qy        454 GACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCAC------CCTC 507
              |    |||||| | ||   |||||||||||| ||   |   ||  ||||      |||
Db        187 CAACACACGGACGACTTATTGAAGATAGGGTCTCTCCGGTTTCATGTCACCTTCCACCTA 246

Qy        508 TCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGGCTGCCG 567
              | |       ||  |||  |||  | |  |||       |       |      |  ||| ||
Db        247 TTGCGGGAGGTTAGCCCATTGAGGGTCCTCTCACAGTGTCTCGTCCTGTCGTTCCTGTCG 306

Qy        568 AGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCCTTGCAG 627
              |||  |  ||||  |||||  || ||  ||  |||       |  || |    || |||
Db        307 TGGATGTCGGAGTCGTCGTGGGACTGCGACTCGTTTCGTCTGATGCTCTTTGTGTTTCAG 366

Qy        628 AAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCT 676
              | | | |||   || |  ||| |||  |||  |   | |  |||  |||
Db        367 ATGCGGACGCTTCAGTGGGTAGTCCCGGACTCGAGCGGGCAGTGTTTCT 415


RESULT 13
US-10-157-408-12
; Sequence 12, Application US/10157408
; Patent No. 6710169
;   GENERAL INFORMATION:
;       APPLICANT: Capon, Daniel J.
;                  Gregory, Timothy J.
;       TITLE OF INVENTION: Adheson Variants
;       NUMBER OF SEQUENCES: 25
;       CORRESPONDENCE ADDRESS:
;           ADDRESSEE: Genentech, Inc.
;           STREET: 460 Point San Bruno Blvd
;           CITY: South San Francisco
;           STATE: California
;           COUNTRY: USA
;           ZIP: 94080
;       COMPUTER READABLE FORM:
;           MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
;           COMPUTER: IBM PC compatible
;           OPERATING SYSTEM: PC-DOS/MS-DOS
;           SOFTWARE: patin (Genentech)
;       CURRENT APPLICATION DATA:
;           APPLICATION NUMBER: US/10/157,408
;           FILING DATE: 28-May-2002
;           CLASSIFICATION: 435
;       PRIOR APPLICATION DATA:
;           APPLICATION NUMBER: US/08/457,918
;           FILING DATE: 1-JUN-1995
;           APPLICATION NUMBER: 08/236311
;           FILING DATE: 02-MAY-1994
;           APPLICATION NUMBER: 07/936190
;           FILING DATE: 26-AUG-1992
;           APPLICATION NUMBER: 07/842777
;           FILING DATE: 18-FEB-1992
;           APPLICATION NUMBER: 07/250785
;           FILING DATE: 28-SEP-1988
;           APPLICATION NUMBER: 07/104329
;           FILING DATE: 02-OCT-1987
;       ATTORNEY/AGENT INFORMATION:
;           NAME: Kubinec, Jeffrey S.
;           REGISTRATION NUMBER: 36,575
;           REFERENCE/DOCKET NUMBER: P0444P1C3
;       TELECOMMUNICATION INFORMATION:
;           TELEPHONE: 415/225-8228
;           TELEFAX: 415/952-9881
;           TELEX: 910/371-7168
;   INFORMATION FOR SEQ ID NO: 12:
;       SEQUENCE CHARACTERISTICS:
;           LENGTH: 468 bases
;           TYPE: nucleic acid
;           STRANDEDNESS: single
;           TOPOLOGY: linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-10-157-408-12

  Query Match             3.7%;  Score 43;  DB 4;  Length 468;
  Best Local Similarity   49.5%;  Pred. No. 0.023;
  Matches  143;  Conservative    0;  Mismatches  140;  Indels    6;  Gaps    1;

Qy        394 CTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTCTTGGTCCAGTCG 453
              | ||||   || | || | | || |||||    ||  || |||           | |
Db        127 CGTGGTAGACAGAAGTAGAAGGGCGGTAGACTACTCGTCAACTTTAGACCTTGACGGAGA 186

Qy        454 GACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCAC------CCTC 507
              |    |||||| | ||   |||||||||||| ||   |   ||  ||||      |||
Db        187 CAACACACGGACGACTTATTGAAGATAGGGTCTCTCCGGTTTCATGTCACCTTCCACCTA 246

Qy        508 TCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGGCTGCCG 567
              | |       ||  |||  |||  | |  |||       |       |      |  ||| ||
Db        247 TTGCGGGAGGTTAGCCCATTGAGGGTCCTCTCACAGTGTCTCGTCCTGTCGTTCCTGTCG 306

Qy        568 AGGAAGAAGGAGATGTCGTTCGAGTGGCACCTGTTCTCGTCCACCGTCGTCCCCTTGCAG 627
              |||  |  ||||  |||||  || ||  ||  |||       |  || |    || |||
Db        307 TGGATGTCGGAGTCGTCGTGGGACTGCGACTCGTTTCGTCTGATGCTCTTTGTGTTTCAG 366

Qy        628 AAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCT 676
              | | | |||   || |  ||| |||  |||  |   | |  |||  |||
Db        367 ATGCGGACGCTTCAGTGGGTAGTCCCGGACTCGAGCGGGCAGTGTTTCT 415


RESULT 14
US-08-728-323A-1/c
; Sequence 1, Application US/08728323A
```

```
; Patent No. 5948676
;  GENERAL INFORMATION:
;    APPLICANT:  Chang, Yuan
;    APPLICANT:  Bohenzky, Roy A.
;    APPLICANT:  Russo, James J.
;    APPLICANT:  Edelman, Isidore S.
;    APPLICANT:  Moore, Patrick S.
;    TITLE OF INVENTION:  Immediate Early Protein From Kaposi's
;    TITLE OF INVENTION:  Sarcoma-Associated Herpesvirus, DNA
;    TITLE OF INVENTION:  Encoding Same And Uses Thereof
;    NUMBER OF SEQUENCES:  21
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Cooper & Dunham LLP
;      STREET:  1185 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/728,323A
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  White, John P.
;      REGISTRATION NUMBER:  28,678
;      REFERENCE/DOCKET NUMBER:  0575/52268/JPW/MSC/SKS
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-278-0400
;      TELEFAX:  212-391-0525
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3489 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..3489
US-08-728-323A-1

  Query Match             3.6%;  Score 41.8;  DB 2;  Length 3489;
  Best Local Similarity   43.4%;  Pred. No. 0.11;
  Matches  193;  Conservative    0;  Mismatches  252;  Indels    0;  Gaps    0;

Qy        144 GCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCC 203
              ||  |  | | | |    | ||||  |    || | | |||  ||    ||| | | |
Db       1894 GCTGCTGCTCATCCTGCTGCTGCTCATCCTGCTGCTGCTCATCCTGCTGCTGCTCATCCT 1835

Qy        204 GCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATGGC 263
              ||  || | | |  | | | |    ||      || ||| || || ||  |||  | |
Db       1834 GCTGCTGCTCATCCTGCTGCTGCTCATCCTGCTGCTGCTCATCCTGCTGCTGTGGCTCCC 1775

Qy        264 ACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATGTTCAC 323
                | |  || ||    |  || |    |  |||       | ||| | ||   | || |
Db       1774 GCTGCTGTGGCTCCCGCTGCTGTGGCTCCCGCTGCTGTGGCTCCCGCTGCTGTGGCTCCC 1715

Qy        324 GTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTTCC 383
              | | | | ||  |  | | | |  | |||         |  | |  || | | ||
Db       1714 GCTGCTGTGGCTCCCGCTGCTGTGGCTCCCGCTGCTGGGGCTCCCGCTGCTGTGGCTCCC 1655

Qy        384 CGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTCTT 443
                |   |  ||   | |  |      |   ||  ||| ||    ||| || | |
Db       1654 GCTGCTGTGGCTCCTGCTGCTGTGGCTCCTGCTGCTGTGGCTCCTGCTGCTGTGGCTCCT 1595

Qy        444 GGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCAC 503
              | | | ||  | |  | |    | | | |  | |  ||  |||  || |  |||
Db       1594 GCTGCTGTGGCTCCTGCTGCTGTGGCTCCTGCTGCTGTGGCTCCTGCTGCTGTGGCTCCT 1535

Qy        504 CCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGGCT 563
              ||  ||  | | |    | | | |  || | | |||       ||| |  ||   |||
Db       1534 GCTGCTGTGGCTCCTGCTGTTGTGGCTCCTGCTGTTGTGGCTCCTGCAGGGGCTCCTGCT 1475

Qy        564 GCCGAGGAAGAAGGAGATGTCGTTC 588
              || | ||      |  | ||| | ||
Db       1474 GCTGTGGCTCCTGCTGTTGTGGCTC 1450


RESULT 15
US-09-298-568-1/c
; Sequence 1, Application US/09298568
; Patent No. 6322792
; GENERAL INFORMATION:
;  APPLICANT: Kieff, Elliott D.
;  APPLICANT: Ballestas, Mary E.
;  APPLICANT: Kaye, Kenneth M.
;  TITLE OF INVENTION: RHADINO VIRUS LANA ACTS IN TRANS ON A UNIT OF RHADINO
;  TITLE OF INVENTION: VIRUS DNA TO MEDIATE EFFICIENT EPISOME PERSISTENCE
;  FILE REFERENCE: 16412-10001R
;  CURRENT APPLICATION NUMBER: US/09/298,568
;  CURRENT FILING DATE: 1999-04-21
;  EARLIER APPLICATION NUMBER: US 60/109,422
;  EARLIER FILING DATE: 1998-11-19
;  NUMBER OF SEQ ID NOS: 3
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 3489
;   TYPE: DNA
;   ORGANISM: Kaposi's sarcoma-associated herpesvirus
US-09-298-568-1

  Query Match             3.6%;  Score 41.8;  DB 3;  Length 3489;
  Best Local Similarity   43.4%;  Pred. No. 0.11;
  Matches  193;  Conservative    0;  Mismatches  252;  Indels    0;  Gaps    0;

Qy        144 GCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCC 203
              ||  |  | | | |    | ||||  |    || | | |||  ||    ||| | | |
Db       1894 GCTGCTGCTCATCCTGCTGCTGCTCATCCTGCTGCTGCTCATCCTGCTGCTGCTCATCCT 1835

Qy        204 GCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATGGC 263
              ||  || | | |  | | | |    ||      || ||| || || ||  |||  | |
Db       1834 GCTGCTGCTCATCCTGCTGCTGCTCATCCTGCTGCTGCTCATCCTGCTGCTGTGGCTCCC 1775

Qy        264 ACACCAGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATGTTCAC 323
                | |  || ||    |  || |    |  |||       | ||| | ||   | || |
Db       1774 GCTGCTGTGGCTCCCGCTGCTGTGGCTCCCGCTGCTGTGGCTCCCGCTGCTGTGGCTCCC 1715

Qy        324 GTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTTCC 383
              | | | | ||  |  | | | |  | |||         |  | |  || | | ||
Db       1714 GCTGCTGTGGCTCCCGCTGCTGTGGCTCCCGCTGCTGGGGCTCCCGCTGCTGTGGCTCCC 1655

Qy        384 CGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTGGTTCTT 443
                |   |  ||   | |  |      |   ||  ||| ||    ||| || | |
Db       1654 GCTGCTGTGGCTCCTGCTGCTGTGGCTCCTGCTGCTGTGGCTCCTGCTGCTGTGGCTCCT 1595

Qy        444 GGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCACCTCAC 503
              | | | ||  | |  | |    | | | |  | |  ||  |||  || |  |||
Db       1594 GCTGCTGTGGCTCCTGCTGCTGTGGCTCCTGCTGCTGTGGCTCCTGCTGCTGTGGCTCCT 1535

Qy        504 CCTCTCGTTACCCGTCGGCCTCTTGTTGATGTTCTGGTGCGGAGGGCACGACCTGAGGCT 563
              ||  ||  | | |    | | | |  || | | |||       ||| |  ||   |||
Db       1534 GCTGCTGTGGCTCCTGCTGTTGTGGCTCCTGCTGTTGTGGCTCCTGCAGGGGCTCCTGCT 1475

Qy        564 GCCGAGGAAGAAGGAGATGTCGTTC 588
              || | ||      |  | ||| | ||
Db       1474 GCTGTGGCTCCTGCTGTTGTGGCTC 1450


Search completed: October 17, 2004, 17:00:26
Job time : 111.054 secs
```